



wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 07:28 pm BST

PDB ID : 5LTW
Title : Complex of human 14-3-3 sigma CLU1 mutant with phosphorylated heat shock protein B6
Authors : Sluchanko, N.N.; Beelen, S.; Kulikova, A.A.; Weeks, S.D.; Antson, A.A.; Gusev, N.B.; Strelkov, S.V.
Deposited on : 2016-09-07
Resolution : 4.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

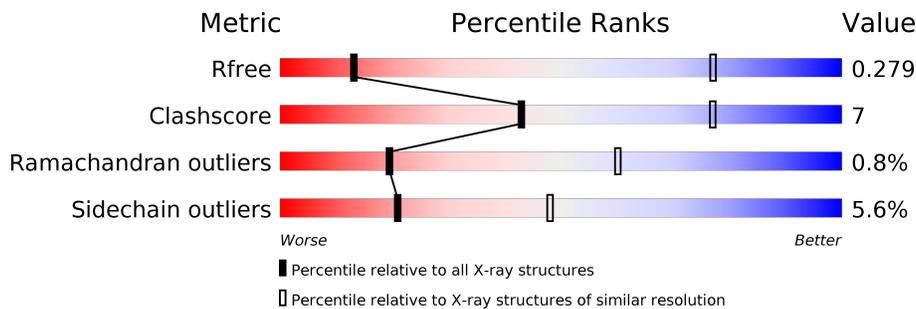
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1055 (5.20-3.80)
Clashscore	141614	1123 (5.20-3.80)
Ramachandran outliers	138981	1069 (5.20-3.80)
Sidechain outliers	138945	1050 (5.20-3.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	234	
1	B	234	
1	E	234	
1	F	234	
1	I	234	
1	J	234	
2	C	149	

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Mol	Chain	Length	Quality of chain
2	D	149	 <p>50% 15% 34%</p>
2	G	149	 <p>46% 30% 21%</p>
2	H	149	 <p>50% 14% 34%</p>
2	K	149	 <p>55% 18% 23%</p>
2	L	149	 <p>54% 13% 33%</p>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15884 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 14-3-3 protein sigma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	227	1791	1119	305	357	10	0	0	0
1	B	226	1777	1109	301	358	9	0	0	0
1	E	227	1790	1118	303	359	10	0	0	0
1	F	229	1809	1129	307	363	10	0	0	0
1	I	232	1828	1139	310	369	10	0	0	0
1	J	229	1809	1129	307	363	10	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P31947
A	-1	PRO	-	expression tag	UNP P31947
A	0	HIS	-	expression tag	UNP P31947
A	159	ALA	LYS	engineered mutation	UNP P31947
A	160	ALA	LYS	engineered mutation	UNP P31947
A	161	ALA	GLU	engineered mutation	UNP P31947
B	-2	GLY	-	expression tag	UNP P31947
B	-1	PRO	-	expression tag	UNP P31947
B	0	HIS	-	expression tag	UNP P31947
B	159	ALA	LYS	engineered mutation	UNP P31947
B	160	ALA	LYS	engineered mutation	UNP P31947
B	161	ALA	GLU	engineered mutation	UNP P31947
E	-2	GLY	-	expression tag	UNP P31947
E	-1	PRO	-	expression tag	UNP P31947
E	0	HIS	-	expression tag	UNP P31947
E	159	ALA	LYS	engineered mutation	UNP P31947
E	160	ALA	LYS	engineered mutation	UNP P31947

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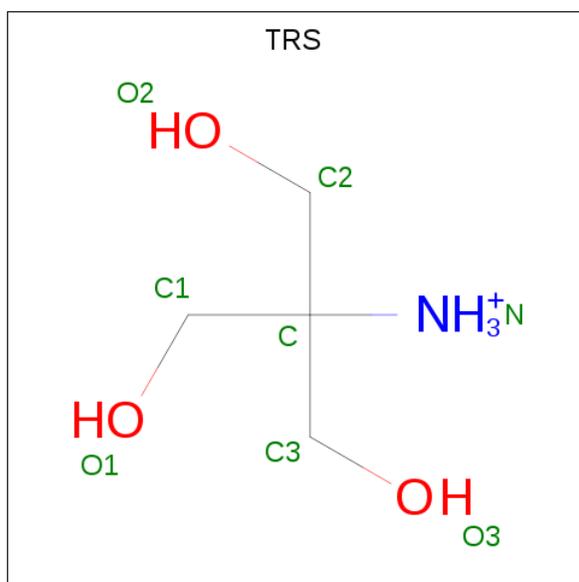
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Chain	Residue	Modelled	Actual	Comment	Reference
E	161	ALA	GLU	engineered mutation	UNP P31947
F	-2	GLY	-	expression tag	UNP P31947
F	-1	PRO	-	expression tag	UNP P31947
F	0	HIS	-	expression tag	UNP P31947
F	159	ALA	LYS	engineered mutation	UNP P31947
F	160	ALA	LYS	engineered mutation	UNP P31947
F	161	ALA	GLU	engineered mutation	UNP P31947
I	-2	GLY	-	expression tag	UNP P31947
I	-1	PRO	-	expression tag	UNP P31947
I	0	HIS	-	expression tag	UNP P31947
I	159	ALA	LYS	engineered mutation	UNP P31947
I	160	ALA	LYS	engineered mutation	UNP P31947
I	161	ALA	GLU	engineered mutation	UNP P31947
J	-2	GLY	-	expression tag	UNP P31947
J	-1	PRO	-	expression tag	UNP P31947
J	0	HIS	-	expression tag	UNP P31947
J	159	ALA	LYS	engineered mutation	UNP P31947
J	160	ALA	LYS	engineered mutation	UNP P31947
J	161	ALA	GLU	engineered mutation	UNP P31947

- Molecule 2 is a protein called Heat shock protein beta-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
2	C	113	Total	C	N	O	P	S	0	0	0
			890	565	163	160	1	1			
2	D	98	Total	C	N	O	P	S	0	0	0
			769	488	141	138	1	1			
2	G	118	Total	C	N	O	P	S	0	0	0
			920	584	168	166	1	1			
2	H	98	Total	C	N	O	P	S	0	0	0
			769	488	141	138	1	1			
2	K	114	Total	C	N	O	P	S	0	0	0
			897	569	164	162	1	1			
2	L	100	Total	C	N	O	P	S	0	0	0
			784	497	143	142	1	1			

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	8	4	1	3	0	0
3	B	1	8	4	1	3	0	0
3	E	1	8	4	1	3	0	0
3	F	1	8	4	1	3	0	0
3	I	1	8	4	1	3	0	0
3	J	1	8	4	1	3	0	0

- Molecule 4 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ni		
4	H	1	1	1	0	0
4	L	1	1	1	0	0
4	D	1	1	1	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 14-3-3 protein sigma

Chain A: 



- Molecule 1: 14-3-3 protein sigma

Chain B: 



- Molecule 1: 14-3-3 protein sigma

Chain E: 



- Molecule 1: 14-3-3 protein sigma

Chain F: 



- Molecule 1: 14-3-3 protein sigma

Chain I: 

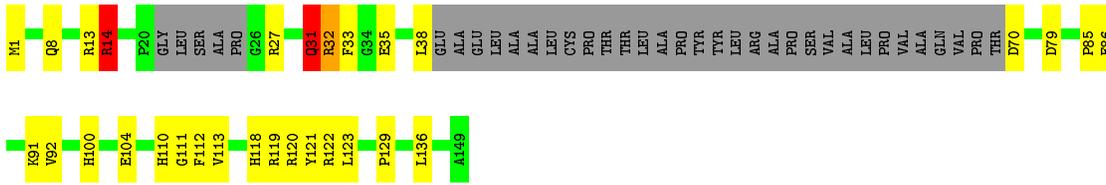


- Molecule 1: 14-3-3 protein sigma

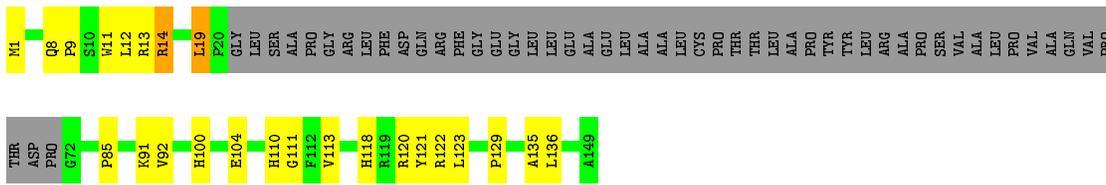
Chain J: 



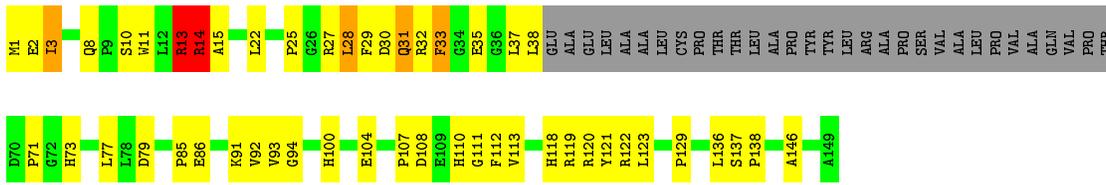
• Molecule 2: Heat shock protein beta-6



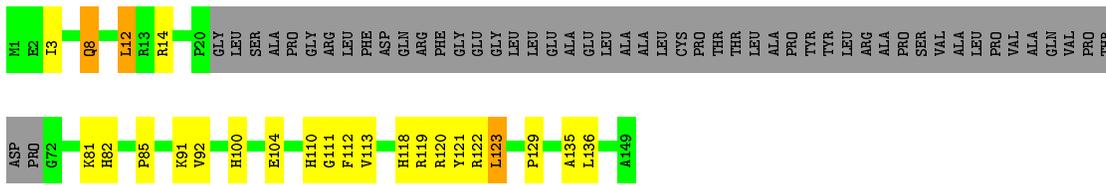
• Molecule 2: Heat shock protein beta-6



• Molecule 2: Heat shock protein beta-6



• Molecule 2: Heat shock protein beta-6



• Molecule 2: Heat shock protein beta-6





- Molecule 2: Heat shock protein beta-6



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	125.06Å 341.29Å 144.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.17 – 4.50 47.62 – 4.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (45.17-4.50) 99.7 (47.62-4.50)	Depositor EDS
R_{merge}	0.31	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 4.45Å)	Xtrriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.236 , 0.256 0.264 , 0.279	Depositor DCC
R_{free} test set	935 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	227.4	Xtrriage
Anisotropy	0.377	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 68.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.21$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	15884	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.54% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NI, TRS, SEP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.41	0/1817	0.63	0/2445
1	B	0.42	0/1802	0.66	1/2426 (0.0%)
1	E	0.41	0/1815	0.64	0/2442
1	F	0.42	0/1835	0.66	0/2469
1	I	0.43	0/1855	0.67	0/2497
1	J	0.42	0/1835	0.65	0/2469
2	C	0.42	0/905	0.71	1/1229 (0.1%)
2	D	0.39	0/782	0.70	0/1066
2	G	0.48	0/937	0.74	0/1275
2	H	0.40	0/782	0.65	0/1066
2	K	0.45	0/912	0.72	0/1239
2	L	0.40	0/798	0.69	0/1089
All	All	0.42	0/16075	0.67	2/21712 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	70	ASN	C-N-CA	5.82	136.24	121.70
2	C	31	GLN	C-N-CA	5.67	135.87	121.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1791	0	1769	24	0
1	B	1777	0	1746	23	0
1	E	1790	0	1768	24	0
1	F	1809	0	1781	23	0
1	I	1828	0	1796	34	0
1	J	1809	0	1781	11	0
2	C	890	0	867	23	0
2	D	769	0	753	23	0
2	G	920	0	899	43	0
2	H	769	0	753	37	0
2	K	897	0	874	16	0
2	L	784	0	764	13	0
3	A	8	0	12	1	0
3	B	8	0	12	1	0
3	E	8	0	12	1	0
3	F	8	0	12	1	0
3	I	8	0	12	1	0
3	J	8	0	12	1	0
4	D	1	0	0	0	0
4	H	1	0	0	0	0
4	L	1	0	0	0	0
All	All	15884	0	15623	214	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 214 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:202:MET:SD	2:G:107:PRO:HD2	1.86	1.14
1:E:165:THR:HB	1:E:208:LEU:HD11	1.31	1.09
1:A:165:THR:HB	1:A:208:LEU:HD11	1.31	1.08
1:J:228:THR:HG21	2:K:85:PRO:HG2	1.38	1.05
1:F:165:THR:HB	1:F:208:LEU:HD11	1.34	1.05

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	223/234 (95%)	215 (96%)	8 (4%)	0	100	100
1	B	222/234 (95%)	213 (96%)	9 (4%)	0	100	100
1	E	223/234 (95%)	214 (96%)	9 (4%)	0	100	100
1	F	225/234 (96%)	216 (96%)	8 (4%)	1 (0%)	34	72
1	I	230/234 (98%)	218 (95%)	11 (5%)	1 (0%)	34	72
1	J	225/234 (96%)	216 (96%)	8 (4%)	1 (0%)	34	72
2	C	106/149 (71%)	96 (91%)	7 (7%)	3 (3%)	5	33
2	D	93/149 (62%)	86 (92%)	6 (6%)	1 (1%)	14	52
2	G	113/149 (76%)	97 (86%)	10 (9%)	6 (5%)	2	22
2	H	93/149 (62%)	85 (91%)	8 (9%)	0	100	100
2	K	107/149 (72%)	93 (87%)	11 (10%)	3 (3%)	5	33
2	L	95/149 (64%)	87 (92%)	8 (8%)	0	100	100
All	All	1955/2298 (85%)	1836 (94%)	103 (5%)	16 (1%)	19	60

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	13	ARG
2	C	32	ARG
2	G	32	ARG
1	I	72	GLU
2	K	13	ARG

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	190/195 (97%)	187 (98%)	3 (2%)	62	79
1	B	188/195 (96%)	183 (97%)	5 (3%)	44	66
1	E	190/195 (97%)	184 (97%)	6 (3%)	39	62
1	F	192/195 (98%)	188 (98%)	4 (2%)	53	72
1	I	194/195 (100%)	185 (95%)	9 (5%)	27	53
1	J	192/195 (98%)	187 (97%)	5 (3%)	46	67
2	C	93/120 (78%)	81 (87%)	12 (13%)	4	20
2	D	81/120 (68%)	75 (93%)	6 (7%)	13	40
2	G	96/120 (80%)	82 (85%)	14 (15%)	3	17
2	H	81/120 (68%)	74 (91%)	7 (9%)	10	35
2	K	94/120 (78%)	78 (83%)	16 (17%)	2	13
2	L	83/120 (69%)	76 (92%)	7 (8%)	11	36
All	All	1674/1890 (89%)	1580 (94%)	94 (6%)	21	48

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	28	LEU
2	H	12	LEU
2	K	123	LEU
2	G	31	GLN
2	G	104	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	G	8	GLN
1	I	8	GLN
1	I	152	GLN
2	K	31	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

6 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SEP	H	16	2	8,9,10	0.81	0	8,12,14	2.26	4 (50%)
2	SEP	L	16	2	8,9,10	0.79	0	8,12,14	2.20	4 (50%)
2	SEP	K	16	2	8,9,10	1.02	1 (12%)	8,12,14	1.89	3 (37%)
2	SEP	D	16	2	8,9,10	0.67	0	8,12,14	3.38	3 (37%)
2	SEP	G	16	2	8,9,10	1.07	1 (12%)	8,12,14	1.56	2 (25%)
2	SEP	C	16	2	8,9,10	0.88	0	8,12,14	2.13	4 (50%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SEP	H	16	2	-	0/5/8/10	-
2	SEP	L	16	2	-	0/5/8/10	-
2	SEP	K	16	2	-	0/5/8/10	-
2	SEP	D	16	2	-	4/5/8/10	-
2	SEP	G	16	2	-	0/5/8/10	-
2	SEP	C	16	2	-	0/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	16	SEP	P-OG	-2.41	1.52	1.60
2	K	16	SEP	P-OG	-2.36	1.52	1.60

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	D	16	SEP	OG-CB-CA	8.48	116.40	108.14
2	C	16	SEP	OG-CB-CA	3.97	112.01	108.14
2	H	16	SEP	OG-CB-CA	3.94	111.97	108.14
2	L	16	SEP	OG-CB-CA	3.70	111.75	108.14
2	K	16	SEP	OG-CB-CA	3.15	111.21	108.14

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	16	SEP	N-CA-CB-OG
2	D	16	SEP	CB-OG-P-O1P
2	D	16	SEP	CB-OG-P-O3P
2	D	16	SEP	CB-OG-P-O2P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	TRS	F	501	-	7,7,7	0.18	0	9,9,9	0.30	0
3	TRS	E	501	-	7,7,7	0.21	0	9,9,9	0.31	0
3	TRS	J	501	-	7,7,7	0.20	0	9,9,9	0.32	0
3	TRS	I	501	-	7,7,7	0.21	0	9,9,9	0.34	0
3	TRS	B	501	-	7,7,7	0.19	0	9,9,9	0.31	0
3	TRS	A	501	-	7,7,7	0.20	0	9,9,9	0.30	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TRS	F	501	-	-	3/9/9/9	-
3	TRS	E	501	-	-	2/9/9/9	-
3	TRS	J	501	-	-	2/9/9/9	-
3	TRS	I	501	-	-	3/9/9/9	-
3	TRS	B	501	-	-	2/9/9/9	-
3	TRS	A	501	-	-	3/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	F	501	TRS	N-C-C3-O3
3	E	501	TRS	N-C-C3-O3
3	J	501	TRS	N-C-C3-O3
3	I	501	TRS	N-C-C3-O3
3	B	501	TRS	N-C-C3-O3

There are no ring outliers.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	501	TRS	1	0
3	E	501	TRS	1	0
3	J	501	TRS	1	0
3	I	501	TRS	1	0
3	B	501	TRS	1	0
3	A	501	TRS	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.