



wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 06:41 pm BST

PDB ID : 5JA8
Title : Crystal structure of the HigB2 toxin in complex with Nb2
Authors : Hadzi, S.; Loris, R.
Deposited on : 2016-04-12
Resolution : 2.49 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

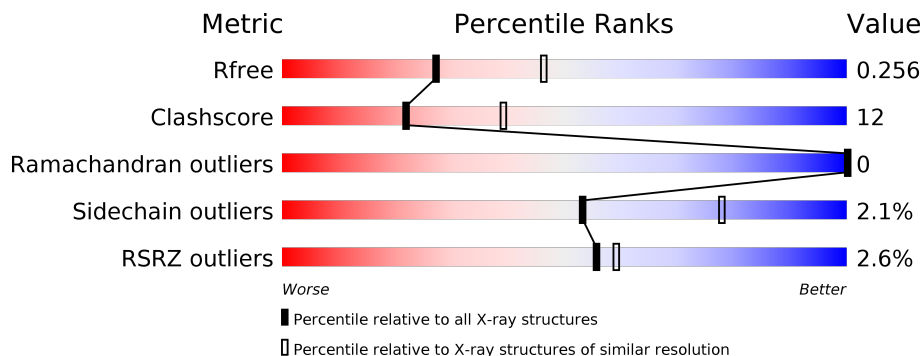
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	111	 2% 73% 20% • 5%
1	C	111	 2% 77% 20% • •
1	E	111	 4% 75% 20% • •
1	G	111	 5% 70% 23% • 5%
2	B	127	 % 69% 24% • 5%
2	D	127	 % 77% 23%

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Mol	Chain	Length	Quality of chain
2	F	127	
2	H	127	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	PO4	D	202	-	X	-	-
3	PO4	E	202	-	-	X	-
7	PDO	D	204	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7542 atoms, of which 59 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 Toxin HigB-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	105	Total 847	C 541	N 145	O 156	S 5	0	0	0
1	C	108	Total 870	C 554	N 148	O 163	S 5	0	0	0
1	E	107	Total 861	C 549	N 146	O 161	S 5	0	0	0
1	G	105	Total 863	C 550	N 149	O 159	S 5	0	0	0

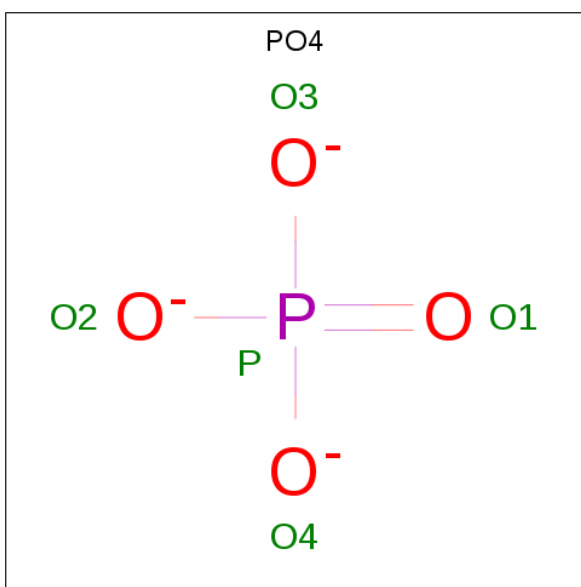
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	expression tag	UNP Q9KMA6
C	0	HIS	-	expression tag	UNP Q9KMA6
E	0	HIS	-	expression tag	UNP Q9KMA6
G	0	HIS	-	expression tag	UNP Q9KMA6

- Molecule 2 is a protein called Nanobody 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	121	Total 920	C 574	N 157	O 184	S 5	0	0	0
2	D	127	Total 980	C 610	N 175	O 190	S 5	0	0	0
2	F	127	Total 980	C 610	N 175	O 190	S 5	0	0	0
2	H	122	Total 934	C 582	N 160	O 187	S 5	0	1	0

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O P 5 4 1	0	0
3	A	1	Total O P 5 4 1	0	0
3	B	1	Total O P 5 4 1	0	0
3	C	1	Total O P 5 4 1	0	0
3	C	1	Total O P 5 4 1	0	0
3	D	1	Total O P 5 4 1	0	0
3	D	1	Total O P 5 4 1	0	0
3	E	1	Total O P 5 4 1	0	0
3	E	1	Total O P 5 4 1	0	0
3	G	1	Total O P 5 4 1	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



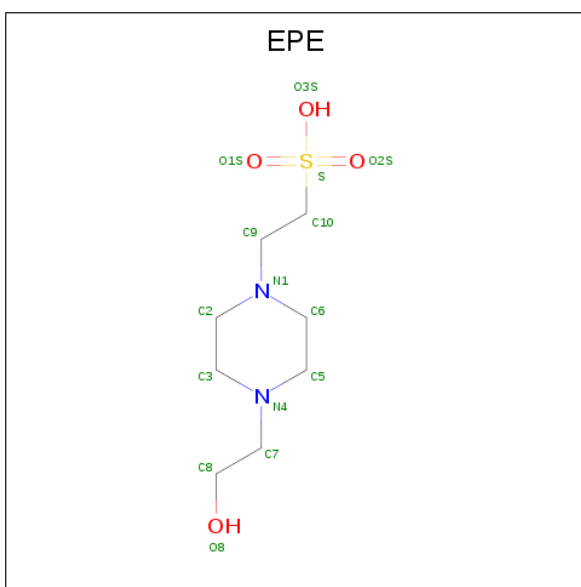
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
4	A	1	7	2	3	2	0	0

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



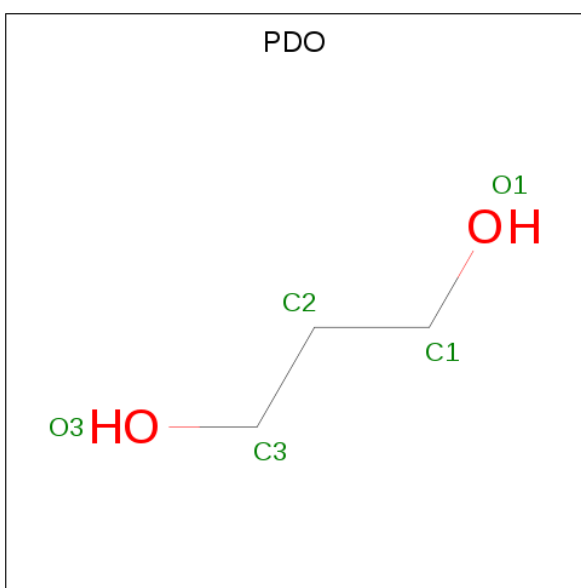
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
5	B	1	10	2	6	2	0	0

- Molecule 6 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf		
			Total	C	H	N	O			S	
6	D	1	Total	32	8	17	2	4	1	0	0
6	F	1	Total	32	8	17	2	4	1	0	0

- Molecule 7 is 1,3-PROPANDIOL (three-letter code: PDO) (formula: $C_3H_8O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	H	O			
7	D	1	Total	13	3	8	2	0	0
7	G	1	Total	13	3	8	2	0	0

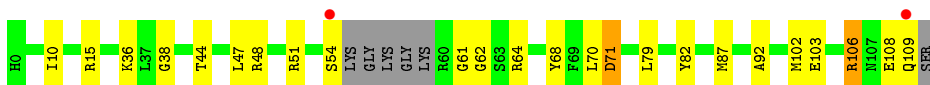
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	17	Total O 17 17	0	0
8	B	23	Total O 23 23	0	0
8	C	16	Total O 16 16	0	0
8	D	14	Total O 14 14	0	0
8	E	15	Total O 15 15	0	0
8	F	20	Total O 20 20	0	0
8	G	10	Total O 10 10	0	0
8	H	15	Total O 15 15	0	0

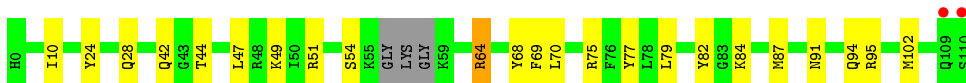
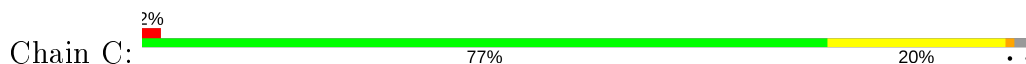
3 Residue-property plots [i](#)

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

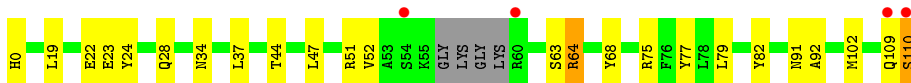
- Molecule 1: Toxin HigB-2



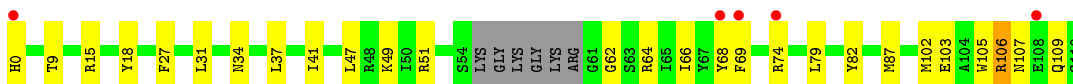
- Molecule 1: Toxin HigB-2



- Molecule 1: Toxin HigB-2



- Molecule 1: Toxin HigB-2

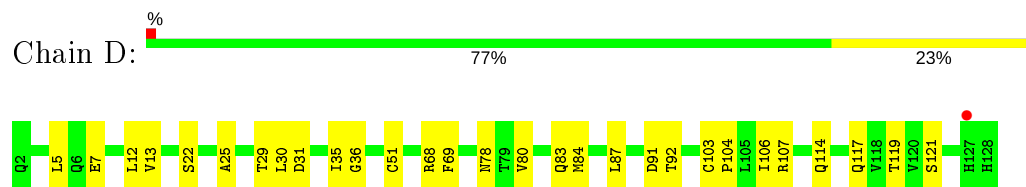


- Molecule 2: Nanobody 2

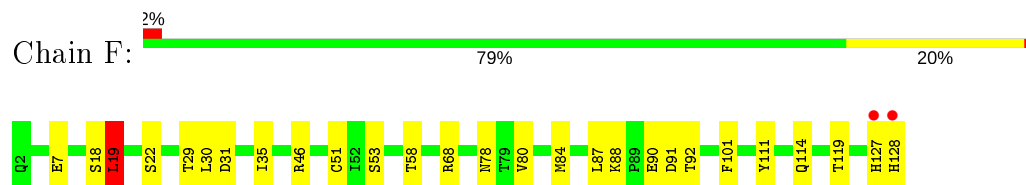


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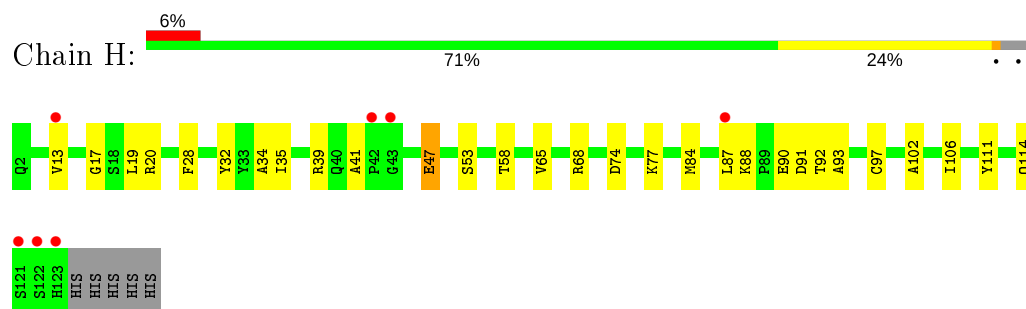
- Molecule 2: Nanobody 2



- Molecule 2: Nanobody 2



- Molecule 2: Nanobody 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.00Å 109.28Å 117.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.48 – 2.49 46.48 – 2.49	Depositor EDS
% Data completeness (in resolution range)	99.4 (46.48-2.49) 99.4 (46.48-2.49)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.04 (at 2.48Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.201 , 0.248 0.216 , 0.256	Depositor DCC
R_{free} test set	1742 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	43.9	Xtrriage
Anisotropy	0.146	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 33.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7542	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 35.75 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.5561e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: PDO, PO4, EPE, EDO, ACT

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	0.56	1/862 (0.1%)	0.56	0/1157
1	C	0.75	2/884 (0.2%)	0.66	3/1185 (0.3%)
1	E	0.57	0/875	0.55	0/1173
1	G	0.47	0/878	0.51	0/1175
2	B	0.75	1/939 (0.1%)	0.69	3/1273 (0.2%)
2	D	0.39	0/1005	0.53	0/1363
2	F	0.50	2/1005 (0.2%)	0.60	1/1363 (0.1%)
2	H	0.61	2/953 (0.2%)	0.95	9/1292 (0.7%)
All	All	0.59	8/7401 (0.1%)	0.65	16/9981 (0.2%)

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	69	PHE	C-N	-14.28	1.01	1.34
2	B	98	VAL	C-N	-13.97	1.01	1.34
2	H	20	ARG	C-N	-12.43	1.05	1.34
2	H	19	LEU	C-N	-9.75	1.11	1.34
2	F	19	LEU	C-N	-9.26	1.12	1.34

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	20	ARG	O-C-N	-14.92	98.83	122.70
2	H	19	LEU	O-C-N	-10.71	105.57	122.70
2	H	20	ARG	CA-C-N	10.49	140.28	117.20
2	B	97	CYS	O-C-N	-10.31	106.20	122.70
2	H	97	CYS	O-C-N	-10.22	106.35	122.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	847	0	808	18	0
1	C	870	0	829	17	0
1	E	861	0	826	20	0
1	G	863	0	838	29	0
2	B	920	0	870	27	0
2	D	980	0	913	22	0
2	F	980	0	912	19	0
2	H	934	0	878	23	0
3	A	10	0	0	1	0
3	B	5	0	0	0	0
3	C	10	0	0	1	0
3	D	10	0	0	0	0
3	E	10	0	0	3	0
3	G	5	0	0	1	0
4	A	4	3	3	0	0
5	B	4	6	6	3	0
6	D	15	17	17	2	0
6	F	15	17	17	2	0
7	D	5	8	8	8	0
7	G	5	8	8	0	0
8	A	17	0	0	0	0
8	B	23	0	0	1	0
8	C	16	0	0	1	0
8	D	14	0	0	0	0
8	E	15	0	0	0	0
8	F	20	0	0	1	0
8	G	10	0	0	1	0
8	H	15	0	0	0	0
All	All	7483	59	6933	169	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 12.

The worst 5 of 169 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:C:95:ARG:NH2	3:C:202:PO4:O1	1.87	1.07
2:B:68:ARG:NH2	2:B:91:ASP:OD2	1.86	1.07
2:F:19:LEU:HD12	2:F:87:LEU:HD11	1.32	1.04
2:F:46:ARG:NH1	8:F:301:HOH:O	1.98	0.96
1:E:92:ALA:N	3:E:202:PO4:O2	1.98	0.95

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	101/111 (91%)	100 (99%)	1 (1%)	0	100	100
1	C	104/111 (94%)	103 (99%)	1 (1%)	0	100	100
1	E	103/111 (93%)	102 (99%)	1 (1%)	0	100	100
1	G	101/111 (91%)	100 (99%)	1 (1%)	0	100	100
2	B	119/127 (94%)	118 (99%)	1 (1%)	0	100	100
2	D	125/127 (98%)	123 (98%)	2 (2%)	0	100	100
2	F	125/127 (98%)	123 (98%)	2 (2%)	0	100	100
2	H	121/127 (95%)	120 (99%)	1 (1%)	0	100	100
All	All	899/952 (94%)	889 (99%)	10 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	85/97 (88%)	82 (96%)	3 (4%)	36	62
1	C	88/97 (91%)	86 (98%)	2 (2%)	50	76
1	E	87/97 (90%)	84 (97%)	3 (3%)	37	63
1	G	89/97 (92%)	88 (99%)	1 (1%)	73	89
2	B	98/104 (94%)	94 (96%)	4 (4%)	30	55
2	D	104/104 (100%)	104 (100%)	0	100	100
2	F	104/104 (100%)	102 (98%)	2 (2%)	57	80
2	H	99/104 (95%)	98 (99%)	1 (1%)	76	90
All	All	754/804 (94%)	738 (98%)	16 (2%)	53	78

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	51	ARG
1	C	64	ARG
2	F	19	LEU
2	B	116	THR
2	F	51	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	F	60	ASN
2	F	127	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry

16 ligands 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
3	PO4	A	201	-	4,4,4	1.74	2 (50%)	6,6,6	0.62	0
3	PO4	E	202	-	4,4,4	1.82	1 (25%)	6,6,6	0.78	0
3	PO4	C	202	-	4,4,4	1.59	0	6,6,6	0.88	0
3	PO4	A	202	-	4,4,4	1.41	0	6,6,6	0.91	0
3	PO4	G	201	-	4,4,4	0.95	0	6,6,6	0.45	0
4	ACT	A	203	-	1,3,3	1.89	0	0,3,3	0.00	-
3	PO4	C	201	-	4,4,4	0.92	0	6,6,6	0.40	0
3	PO4	E	201	-	4,4,4	0.91	0	6,6,6	0.37	0
3	PO4	B	201	-	4,4,4	1.62	0	6,6,6	0.49	0
3	PO4	D	202	-	4,4,4	3.00	4 (100%)	6,6,6	1.01	0
6	EPE	F	201	-	15,15,15	2.51	1 (6%)	18,20,20	2.05	7 (38%)
5	EDO	B	202	-	3,3,3	0.48	0	2,2,2	0.16	0
6	EPE	D	201	-	15,15,15	2.40	1 (6%)	18,20,20	1.93	6 (33%)
7	PDO	G	202	-	4,4,4	0.17	0	3,3,3	0.29	0
3	PO4	D	203	-	4,4,4	0.94	0	6,6,6	0.64	0
7	PDO	D	204	-	4,4,4	0.23	0	3,3,3	0.24	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
6	EPE	F	201	-	-	0/9/19/19	0/1/1/1
7	PDO	G	202	-	-	1/2/2/2	-
5	EDO	B	202	-	-	1/1/1/1	-
6	EPE	D	201	-	-	4/9/19/19	0/1/1/1
7	PDO	D	204	-	-	2/2/2/2	-

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	201	EPE	C10-S	-9.60	1.63	1.77
6	D	201	EPE	C10-S	-9.21	1.64	1.77
3	D	202	PO4	P-O2	-3.28	1.44	1.54
3	D	202	PO4	P-O3	-3.27	1.44	1.54
3	D	202	PO4	P-O4	-3.06	1.45	1.54

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	201	EPE	O1S-S-C10	4.63	112.49	106.92
6	F	201	EPE	C6-N1-C2	4.24	118.38	108.83
6	F	201	EPE	O1S-S-C10	3.39	111.00	106.92
6	F	201	EPE	C6-C5-N4	3.35	117.51	110.64
6	D	201	EPE	C9-N1-C2	-3.29	102.83	111.23

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	D	201	EPE	C9-C10-S-O2S
6	D	201	EPE	C9-C10-S-O3S
7	G	202	PDO	C1-C2-C3-O3
7	D	204	PDO	O1-C1-C2-C3
7	D	204	PDO	C1-C2-C3-O3

There are no ring outliers.

9 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	202	PO4	2	0
3	C	202	PO4	1	0
3	A	202	PO4	1	0
3	G	201	PO4	1	0
3	E	201	PO4	1	0
6	F	201	EPE	2	0
5	B	202	EDO	3	0
6	D	201	EPE	2	0
7	D	204	PDO	8	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	H	2
1	C	2
2	B	1
1	A	1
2	F	1

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	103:GLU	C	104:ALA	N	1.14
1	C	70:LEU	C	71:ASP	N	1.13
1	F	19:LEU	C	20:ARG	N	1.12
1	H	19:LEU	C	20:ARG	N	1.11
1	H	20:ARG	C	21:LEU	N	1.05

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	105/111 (94%)	-0.11	2 (1%) 66 69	25, 44, 88, 116	0
1	C	108/111 (97%)	-0.10	2 (1%) 66 69	27, 48, 87, 116	0
1	E	107/111 (96%)	0.02	4 (3%) 41 45	27, 43, 87, 123	0
1	G	105/111 (94%)	0.19	5 (4%) 30 32	36, 62, 101, 138	0
2	B	121/127 (95%)	-0.29	1 (0%) 86 87	24, 42, 61, 80	0
2	D	127/127 (100%)	-0.25	1 (0%) 86 87	25, 44, 70, 95	0
2	F	127/127 (100%)	-0.21	2 (1%) 72 74	23, 36, 59, 155	0
2	H	122/127 (96%)	0.17	7 (5%) 23 25	32, 57, 79, 127	0
All	All	922/952 (96%)	-0.08	24 (2%) 56 59	23, 46, 86, 155	0

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	127	HIS	7.6
2	H	122	SER	4.4
1	A	109	GLN	4.1
2	H	13	VAL	4.0
1	E	109	GLN	3.9

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	PO4	A	202	5/5	0.62	0.26	113,113,114,114	0
7	PDO	G	202	5/5	0.64	0.21	69,83,88,89	0
3	PO4	D	203	5/5	0.77	0.26	113,114,114,115	0
4	ACT	A	203	4/4	0.79	0.26	57,61,69,69	0
3	PO4	C	202	5/5	0.80	0.18	118,119,119,120	0
6	EPE	D	201	15/15	0.83	0.20	57,77,104,104	0
3	PO4	E	202	5/5	0.85	0.25	104,105,106,106	0
6	EPE	F	201	15/15	0.88	0.22	76,91,98,101	0
5	EDO	B	202	4/4	0.89	0.28	50,61,66,73	0
3	PO4	C	201	5/5	0.90	0.19	86,87,88,89	0
3	PO4	B	201	5/5	0.91	0.44	30,30,30,30	0
3	PO4	A	201	5/5	0.92	0.10	85,86,88,88	0
7	PDO	D	204	5/5	0.93	0.34	43,52,60,60	0
3	PO4	E	201	5/5	0.94	0.13	79,82,84,84	0
3	PO4	G	201	5/5	0.97	0.14	69,70,71,72	0
3	PO4	D	202	5/5	0.98	0.13	67,69,70,72	0

6.5 Other polymers [i](#)

There are no such residues in this entry.