wwPDB X-ray Structure Validation Summary Report (i)

Aug 6, 2023 – 03:02 AM EDT

PDB ID	:	1K1E
Title	:	Structure Of the cobalt-bound form of the deoxy-D-mannose-octulosonate 8-phosphate phosphatase (YrbI) From Haemophilus Influenzae (HI1679)
Authors	:	Lim, K.; Herzberg, O.; Structure 2 Function Project (S2F)
Deposited on	:	2001-09-25
Resolution	:	1.67 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

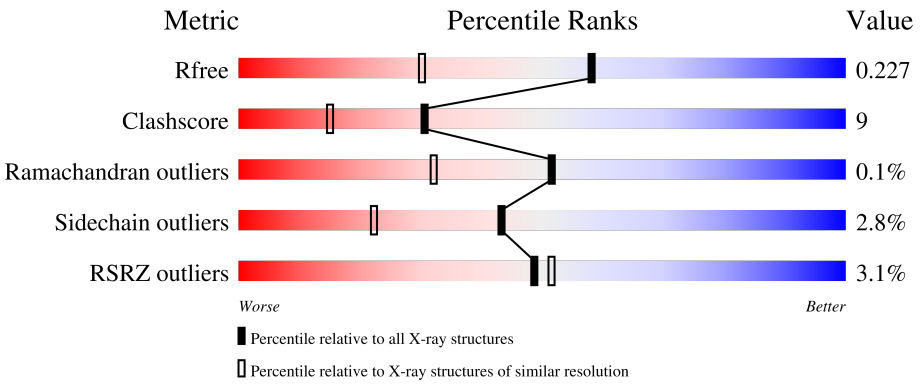
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.67 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	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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 of 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 <=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	180	% 79% 17% • •
1	B	180	6% 82% 14% • •
1	C	180	3% 80% 16% • •
1	D	180	3% 82% 11% • 6%
1	E	180	4% 80% 18% • •

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Mol	Chain	Length	Quality of chain
1	F	180	3% 83% 15%
1	G	180	2% 81% 13% 6%
1	H	180	3% 76% 16% 5%
1	I	180	2% 85% 13%
1	J	180	% 78% 18%
1	K	180	3% 89% 7%
1	L	180	3% 76% 18% 6%

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
4	SO4	B	2402	-	-	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 17393 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 deoxy-D-mannose-octulosonate 8-phosphate phosphatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	177	1336	844	227	257	8	7	0	0
1	B	177	1336	844	227	257	8	12	0	0
1	C	174	1317	833	224	253	7	5	0	0
1	D	170	1283	812	217	247	7	6	0	0
1	E	177	1336	844	227	257	8	10	0	0
1	F	177	1336	844	227	257	8	7	0	0
1	G	170	1286	815	218	246	7	6	0	0
1	H	171	1295	820	220	248	7	6	0	0
1	I	177	1336	844	227	257	8	12	0	0
1	J	177	1336	844	227	257	8	0	0	0
1	K	173	1310	828	223	252	7	15	0	0
1	L	170	1286	815	218	246	7	9	0	0

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Co		
2	A	1	1	1	0	0
2	B	1	1	1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total Co 1 1	0	0
2	D	1	Total Co 1 1	0	0
2	E	1	Total Co 1 1	0	0
2	F	1	Total Co 1 1	0	0
2	G	1	Total Co 1 1	0	0
2	H	1	Total Co 1 1	0	0
2	I	1	Total Co 1 1	0	0
2	J	1	Total Co 1 1	0	0
2	K	1	Total Co 1 1	0	0
2	L	1	Total Co 1 1	0	0

- Molecule 3 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Hg 1 1	0	0
3	B	1	Total Hg 1 1	0	0
3	C	1	Total Hg 1 1	0	0
3	D	1	Total Hg 1 1	0	0
3	E	1	Total Hg 1 1	0	0
3	F	1	Total Hg 1 1	0	0
3	G	1	Total Hg 1 1	0	0
3	H	1	Total Hg 1 1	0	0
3	I	1	Total Hg 1 1	0	0

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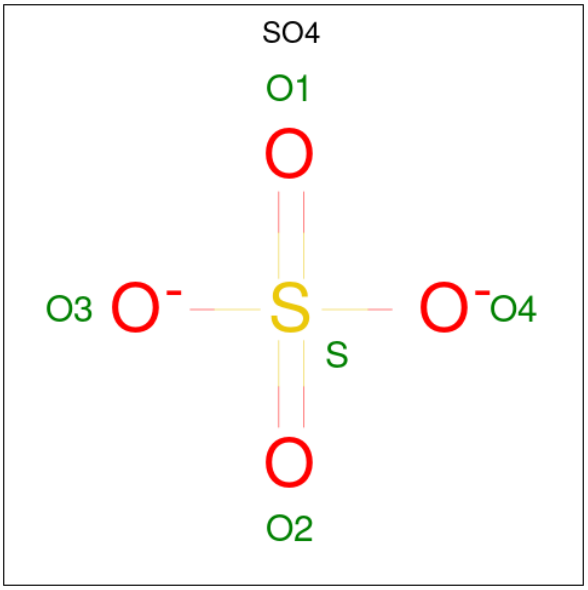
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	J	1	Total Hg 1 1	0	0
3	K	1	Total Hg 1 1	0	0
3	L	1	Total Hg 1 1	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

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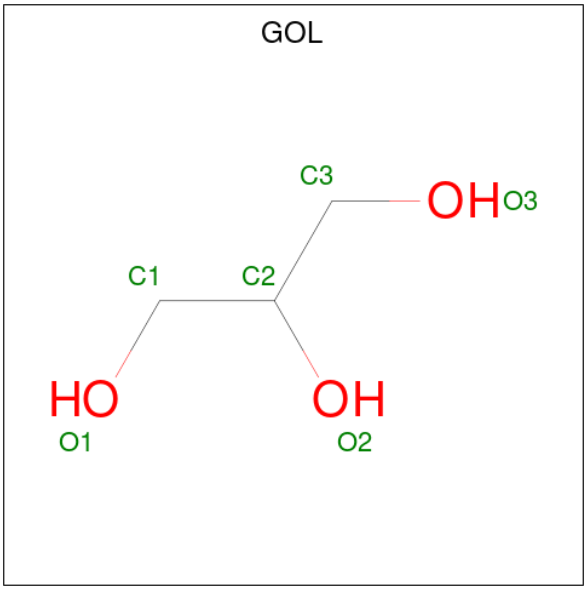
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
4	F	1	5	4	1	0	0
			Total	O	S		
4	F	1	5	4	1	0	0
			Total	O	S		
4	G	1	5	4	1	0	0
			Total	O	S		
4	H	1	5	4	1	0	0
			Total	O	S		
4	I	1	5	4	1	0	0
			Total	O	S		
4	I	1	5	4	1	0	0
			Total	O	S		
4	J	1	5	4	1	0	0
			Total	O	S		
4	J	1	5	4	1	0	0
			Total	O	S		
4	K	1	5	4	1	0	0
			Total	O	S		
4	L	1	5	4	1	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	A	1	6	3	3	0	0

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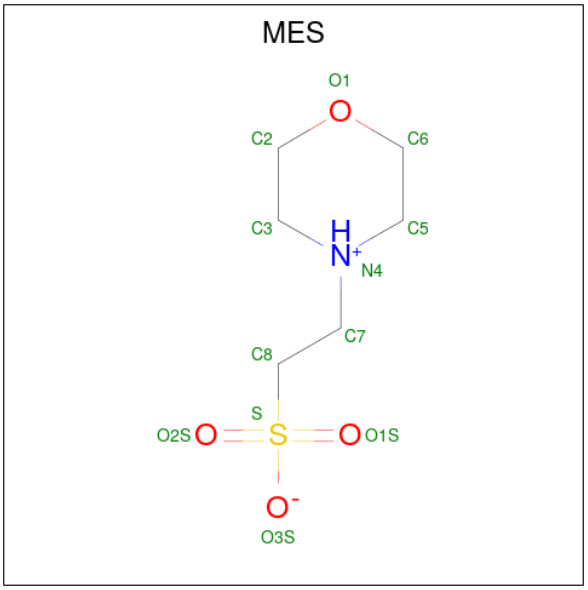
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	C	1	6	3	3	0	0
			Total	C	O		
5	G	1	6	3	3	0	0
			Total	C	O		
5	I	1	6	3	3	0	0
			Total	C	O		
5	K	1	6	3	3	0	0
			Total	C	O		
5	K	1	6	3	3	0	0

- Molecule 6 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
6	C	1	12	6	1	4	1	0	0
			Total	C	N	O	S		
6	H	1	12	6	1	4	1	0	0
			Total	C	N	O	S		
6	J	1	12	6	1	4	1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	137	137	137	0	0

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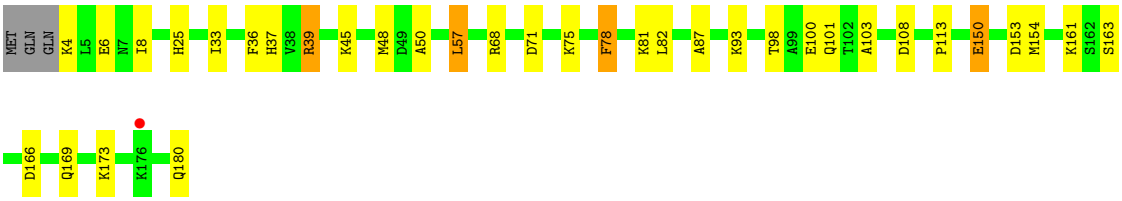
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	B	133	133	133	0	0
			Total	O		
7	C	133	133	133	0	0
			Total	O		
7	D	133	133	133	0	0
			Total	O		
7	E	125	125	125	0	0
			Total	O		
7	F	113	113	113	0	0
			Total	O		
7	G	124	124	124	0	0
			Total	O		
7	H	102	102	102	0	0
			Total	O		
7	I	108	108	108	0	0
			Total	O		
7	J	93	93	93	0	0
			Total	O		
7	K	115	115	115	0	0
			Total	O		
7	L	98	98	98	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

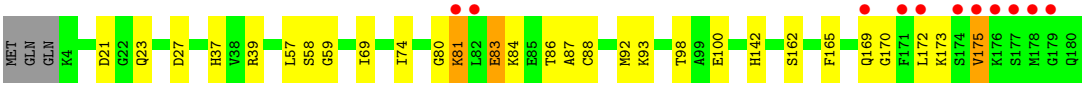
• Molecule 1: deoxy-D-mannose-octulosonate 8-phosphate phosphatase

Chain A:



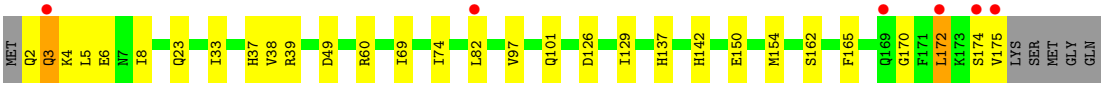
• Molecule 1: deoxy-D-mannose-octulosonate 8-phosphate phosphatase

Chain B:



• Molecule 1: deoxy-D-mannose-octulosonate 8-phosphate phosphatase

Chain C:

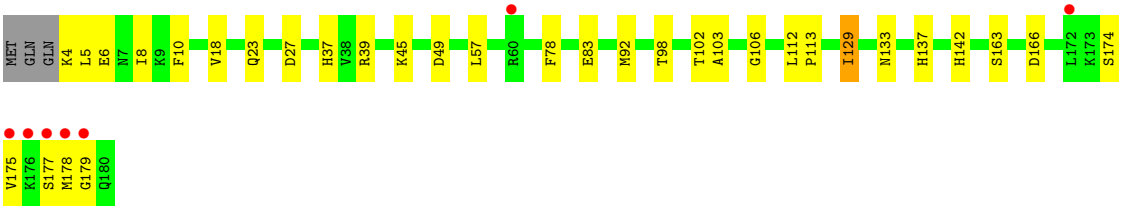


• Molecule 1: deoxy-D-mannose-octulosonate 8-phosphate phosphatase

Chain D:

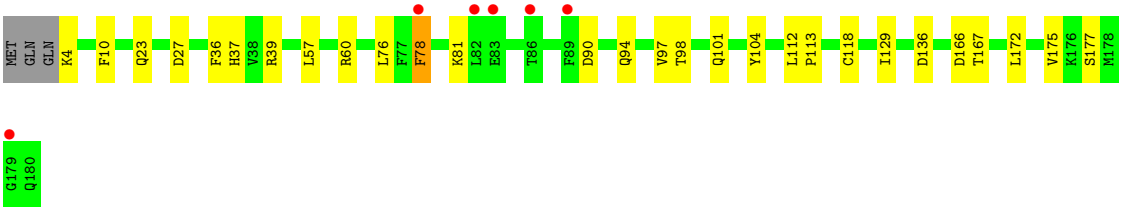
• Molecule 1: deoxy-D-mannose-octulosonate 8-phosphate phosphatase

Chain E:



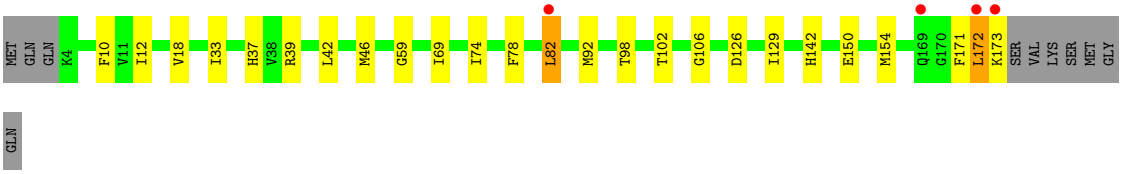
• Molecule 1: deoxy-D-mannose-octulosonate 8-phosphate phosphatase

Chain F:



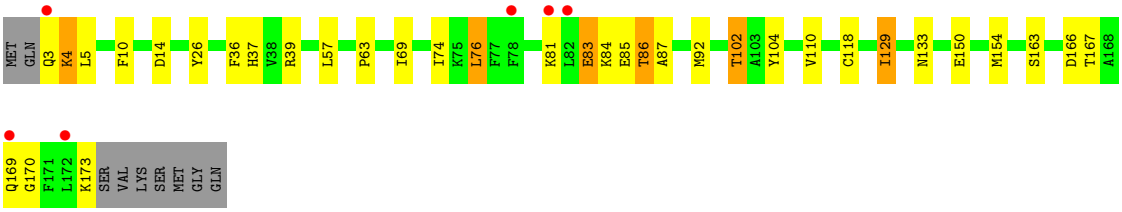
• Molecule 1: deoxy-D-mannose-octulosonate 8-phosphate phosphatase

Chain G:



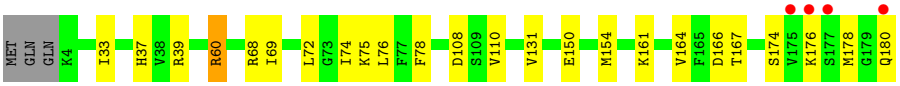
• Molecule 1: deoxy-D-mannose-octulosonate 8-phosphate phosphatase

Chain H:



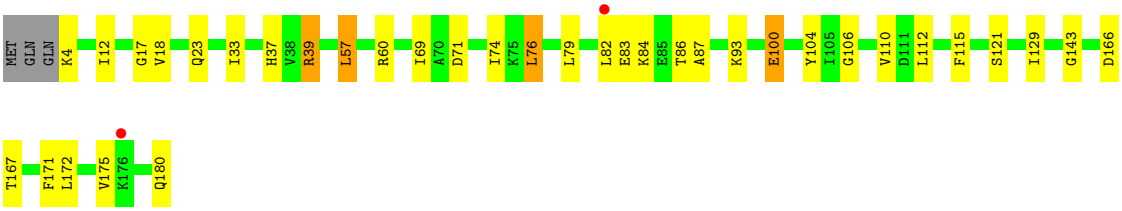
• Molecule 1: deoxy-D-mannose-octulosonate 8-phosphate phosphatase

Chain I:



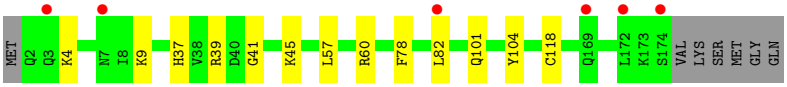
• Molecule 1: deoxy-D-mannose-octulosonate 8-phosphate phosphatase

Chain J:



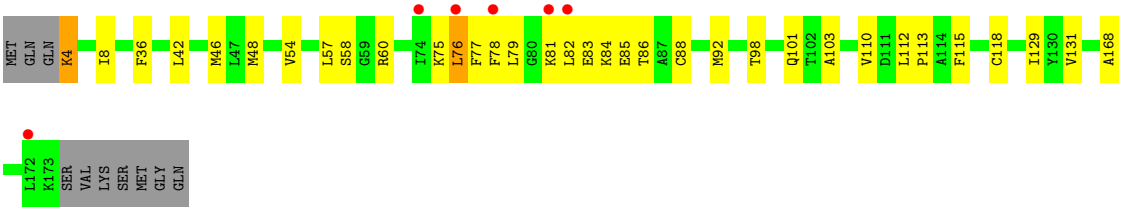
- Molecule 1: deoxy-D-mannose-octulosonate 8-phosphate phosphatase

Chain K:



- Molecule 1: deoxy-D-mannose-octulosonate 8-phosphate phosphatase

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	109.30Å 109.10Å 179.10Å 90.00° 107.60° 90.00°	Depositor
Resolution (Å)	20.00 – 1.67 45.97 – 1.60	Depositor EDS
% Data completeness (in resolution range)	82.5 (20.00-1.67) 77.2 (45.97-1.60)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.68 (at 1.60Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.178 , 0.225 0.184 , 0.227	Depositor DCC
R_{free} test set	12274 reflections (5.99%)	wwPDB-VP
Wilson B-factor (Å^2)	16.7	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 33.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.24$	Xtriage
Estimated twinning fraction	0.155 for k,h,-1/2*h-1/2*k-l 0.155 for -k,-h,-1/2*h+1/2*k-l 0.105 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	17393	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.34% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: MES, CO, HG, GOL, SO4

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	0.90	1/1355 (0.1%)	0.97	3/1821 (0.2%)
1	B	0.94	0/1355	0.96	2/1821 (0.1%)
1	C	0.97	0/1336	0.99	1/1799 (0.1%)
1	D	0.96	1/1302 (0.1%)	1.03	2/1754 (0.1%)
1	E	0.90	0/1355	0.94	2/1821 (0.1%)
1	F	0.91	0/1355	0.90	1/1821 (0.1%)
1	G	0.99	0/1305	0.98	1/1757 (0.1%)
1	H	0.86	0/1314	0.95	1/1769 (0.1%)
1	I	0.91	0/1355	0.92	0/1821
1	J	0.92	2/1355 (0.1%)	0.94	1/1821 (0.1%)
1	K	0.89	0/1329	0.94	0/1789
1	L	0.91	1/1305 (0.1%)	1.02	2/1757 (0.1%)
All	All	0.92	5/16021 (0.0%)	0.96	16/21551 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	100	GLU	CG-CD	6.10	1.61	1.51
1	A	150	GLU	CD-OE1	-5.94	1.19	1.25
1	L	118	CYS	CB-SG	-5.69	1.72	1.81
1	D	104	TYR	CD2-CE2	5.43	1.47	1.39
1	J	100	GLU	CB-CG	5.24	1.62	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L	60	ARG	NE-CZ-NH1	11.11	125.86	120.30
1	L	60	ARG	NE-CZ-NH2	-9.32	115.64	120.30
1	B	27	ASP	CB-CG-OD1	-6.10	112.81	118.30
1	E	27	ASP	CB-CG-OD2	6.04	123.73	118.30
1	E	27	ASP	CB-CG-OD1	-5.87	113.01	118.30

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	1336	0	1340	33	0
1	B	1336	0	1340	31	0
1	C	1317	0	1318	36	0
1	D	1283	0	1280	23	0
1	E	1336	0	1340	30	0
1	F	1336	0	1340	21	0
1	G	1286	0	1288	21	0
1	H	1295	0	1297	37	0
1	I	1336	0	1340	27	0
1	J	1336	0	1340	33	0
1	K	1310	0	1309	8	0
1	L	1286	0	1288	27	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	J	1	0	0	0	0
3	K	1	0	0	0	0
3	L	1	0	0	0	0
4	A	10	0	0	0	0
4	B	10	0	0	2	0
4	C	5	0	0	0	0
4	D	5	0	0	0	0
4	E	10	0	0	0	0
4	F	10	0	0	0	0
4	G	5	0	0	0	0
4	H	5	0	0	0	0
4	I	10	0	0	0	0
4	J	10	0	0	1	0
4	K	5	0	0	0	0
4	L	5	0	0	1	0
5	A	6	0	8	1	0
5	C	6	0	8	0	0
5	G	6	0	8	0	0
5	I	6	0	8	0	0
5	K	12	0	16	0	0
6	C	12	0	12	3	0
6	H	12	0	13	0	0
6	J	12	0	12	0	0
7	A	137	0	0	5	0
7	B	133	0	0	2	0
7	C	133	0	0	5	0
7	D	133	0	0	4	0
7	E	125	0	0	8	0
7	F	113	0	0	2	0
7	G	124	0	0	3	0
7	H	102	0	0	8	0
7	I	108	0	0	2	0
7	J	93	0	0	4	0
7	K	115	0	0	0	0
7	L	98	0	0	4	0
All	All	17393	0	15905	290	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 9.

The worst 5 of 290 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:B:169:GLN:HG2	1:B:173:LYS:NZ	1.65	1.09
1:L:83:GLU:OE1	1:L:86:THR:HG23	1.59	1.01
1:J:82:LEU:HD23	7:J:2652:HOH:O	1.61	1.01
1:L:76:LEU:HD12	1:L:76:LEU:N	1.79	0.98
1:I:60:ARG:NH1	1:I:60:ARG:HG2	1.82	0.93

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	175/180 (97%)	173 (99%)	2 (1%)	0	100	100
1	B	175/180 (97%)	171 (98%)	3 (2%)	1 (1%)	25	10
1	C	172/180 (96%)	167 (97%)	4 (2%)	1 (1%)	25	10
1	D	168/180 (93%)	163 (97%)	5 (3%)	0	100	100
1	E	175/180 (97%)	170 (97%)	5 (3%)	0	100	100
1	F	175/180 (97%)	169 (97%)	6 (3%)	0	100	100
1	G	168/180 (93%)	162 (96%)	5 (3%)	1 (1%)	25	10
1	H	169/180 (94%)	164 (97%)	5 (3%)	0	100	100
1	I	175/180 (97%)	171 (98%)	4 (2%)	0	100	100
1	J	175/180 (97%)	170 (97%)	5 (3%)	0	100	100
1	K	171/180 (95%)	167 (98%)	4 (2%)	0	100	100
1	L	168/180 (93%)	161 (96%)	7 (4%)	0	100	100
All	All	2066/2160 (96%)	2008 (97%)	55 (3%)	3 (0%)	51	32

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	172	LEU
1	G	172	LEU
1	B	175	VAL

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	141/144 (98%)	138 (98%)	3 (2%)	53	33
1	B	141/144 (98%)	138 (98%)	3 (2%)	53	33
1	C	139/144 (96%)	136 (98%)	3 (2%)	52	32
1	D	135/144 (94%)	131 (97%)	4 (3%)	41	20
1	E	141/144 (98%)	134 (95%)	7 (5%)	24	7
1	F	141/144 (98%)	137 (97%)	4 (3%)	43	22
1	G	135/144 (94%)	133 (98%)	2 (2%)	65	48
1	H	136/144 (94%)	130 (96%)	6 (4%)	28	9
1	I	141/144 (98%)	138 (98%)	3 (2%)	53	33
1	J	141/144 (98%)	137 (97%)	4 (3%)	43	22
1	K	138/144 (96%)	134 (97%)	4 (3%)	42	21
1	L	135/144 (94%)	131 (97%)	4 (3%)	41	20
All	All	1664/1728 (96%)	1617 (97%)	47 (3%)	43	22

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	83	GLU
1	J	57	LEU
1	H	86	THR
1	I	60	ARG
1	J	79	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	94	GLN
1	L	133	ASN
1	G	37	HIS
1	J	169	GLN
1	F	37	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 51 ligands modelled in this entry, 24 are monoatomic - leaving 27 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	$\#\|Z\| > 2$
4	SO4	H	2408	-	4,4,4	0.31	0	6,6,6	0.33	0
6	MES	H	2602	-	12,12,12	1.68	3 (25%)	14,16,16	2.53	4 (28%)
4	SO4	E	2405	-	4,4,4	0.32	0	6,6,6	0.36	0
4	SO4	E	2418	-	4,4,4	0.65	0	6,6,6	0.33	0
5	GOL	K	2506	-	5,5,5	0.68	0	5,5,5	0.65	0
4	SO4	B	2402	-	4,4,4	0.22	0	6,6,6	0.44	0
5	GOL	I	2501	-	5,5,5	0.42	0	5,5,5	0.51	0
4	SO4	D	2404	-	4,4,4	0.29	0	6,6,6	0.54	0
4	SO4	L	2412	-	4,4,4	0.21	0	6,6,6	0.40	0
4	SO4	F	2415	-	4,4,4	0.55	0	6,6,6	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	SO4	C	2403	-	4,4,4	0.36	0	6,6,6	0.93	0
5	GOL	A	2502	-	5,5,5	0.55	0	5,5,5	0.38	0
4	SO4	J	2410	-	4,4,4	0.30	0	6,6,6	0.38	0
4	SO4	I	2416	-	4,4,4	0.65	0	6,6,6	0.44	0
5	GOL	G	2504	-	5,5,5	0.84	0	5,5,5	0.58	0
4	SO4	F	2406	-	4,4,4	0.22	0	6,6,6	0.42	0
4	SO4	G	2407	-	4,4,4	0.53	0	6,6,6	0.65	0
6	MES	C	2601	-	12,12,12	0.82	0	14,16,16	2.50	5 (35%)
4	SO4	J	2417	-	4,4,4	0.43	0	6,6,6	0.41	0
6	MES	J	2603	-	12,12,12	1.73	1 (8%)	14,16,16	2.80	8 (57%)
5	GOL	K	2505	-	5,5,5	0.64	0	5,5,5	0.52	0
4	SO4	K	2411	-	4,4,4	0.58	0	6,6,6	0.42	0
4	SO4	A	2414	-	4,4,4	0.59	0	6,6,6	0.42	0
4	SO4	I	2409	-	4,4,4	0.40	0	6,6,6	0.61	0
4	SO4	B	2413	-	4,4,4	0.44	0	6,6,6	0.29	0
5	GOL	C	2503	-	5,5,5	0.59	0	5,5,5	0.41	0
4	SO4	A	2401	-	4,4,4	0.38	0	6,6,6	0.54	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
5	GOL	A	2502	-	-	0/4/4/4	-
6	MES	J	2603	-	-	1/6/14/14	0/1/1/1
5	GOL	K	2505	-	-	0/4/4/4	-
6	MES	H	2602	-	-	1/6/14/14	0/1/1/1
5	GOL	K	2506	-	-	0/4/4/4	-
6	MES	C	2601	-	-	2/6/14/14	0/1/1/1
5	GOL	G	2504	-	-	0/4/4/4	-
5	GOL	I	2501	-	-	0/4/4/4	-
5	GOL	C	2503	-	-	0/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	2603	MES	C8-S	5.07	1.84	1.77
6	H	2602	MES	C8-S	3.42	1.82	1.77
6	H	2602	MES	O2S-S	-2.41	1.37	1.45
6	H	2602	MES	C3-C2	2.30	1.59	1.50

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	H	2602	MES	O2S-S-C8	7.32	115.73	106.92
6	C	2601	MES	O2S-S-C8	6.40	114.62	106.92
6	J	2603	MES	O2S-S-C8	6.18	114.35	106.92
6	J	2603	MES	O1S-S-C8	4.38	112.19	106.92
6	C	2601	MES	C5-N4-C3	3.55	116.82	108.83

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	2601	MES	C8-C7-N4-C3
6	H	2602	MES	C8-C7-N4-C3
6	J	2603	MES	C8-C7-N4-C3
6	C	2601	MES	C8-C7-N4-C5

There are no ring outliers.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	2402	SO4	2	0
4	L	2412	SO4	1	0
5	A	2502	GOL	1	0
4	J	2410	SO4	1	0
6	C	2601	MES	3	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

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	177/180 (98%)	-0.19	1 (0%)	89	91	10, 17, 31, 35	2 (1%)
1	B	177/180 (98%)	0.03	11 (6%)	20	21	12, 17, 34, 38	4 (2%)
1	C	174/180 (96%)	-0.06	6 (3%)	45	48	10, 16, 32, 41	2 (1%)
1	D	170/180 (94%)	-0.13	6 (3%)	44	47	11, 17, 32, 41	2 (1%)
1	E	177/180 (98%)	-0.02	7 (3%)	38	41	10, 18, 31, 37	3 (1%)
1	F	177/180 (98%)	-0.07	6 (3%)	45	48	12, 19, 32, 38	2 (1%)
1	G	170/180 (94%)	-0.07	4 (2%)	59	62	11, 18, 32, 38	2 (1%)
1	H	171/180 (95%)	0.04	6 (3%)	44	47	13, 21, 34, 39	2 (1%)
1	I	177/180 (98%)	-0.28	4 (2%)	60	64	12, 19, 32, 38	4 (2%)
1	J	177/180 (98%)	-0.11	2 (1%)	80	83	13, 21, 33, 38	0
1	K	173/180 (96%)	-0.21	6 (3%)	44	47	13, 18, 33, 41	4 (2%)
1	L	170/180 (94%)	-0.03	6 (3%)	44	47	13, 21, 34, 39	3 (1%)
All	All	2090/2160 (96%)	-0.09	65 (3%)	49	51	10, 18, 33, 41	30 (1%)

The worst 5 of 65 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	82	LEU	8.9
1	H	82	LEU	8.5
1	E	175	VAL	7.7
1	C	175	VAL	7.6
1	B	172	LEU	7.3

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 monosaccharides 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
5	GOL	G	2504	6/6	0.84	0.13	19,25,26,31	0
4	SO4	E	2418	5/5	0.86	0.25	33,39,40,42	0
5	GOL	I	2501	6/6	0.88	0.12	17,22,28,30	0
5	GOL	C	2503	6/6	0.90	0.11	14,19,23,29	0
4	SO4	A	2414	5/5	0.90	0.23	32,34,43,49	0
4	SO4	J	2417	5/5	0.90	0.21	33,34,39,43	0
6	MES	J	2603	12/12	0.90	0.17	27,33,40,40	0
6	MES	H	2602	12/12	0.92	0.16	29,31,42,43	0
6	MES	C	2601	12/12	0.92	0.13	26,34,42,43	0
5	GOL	K	2506	6/6	0.93	0.10	19,27,28,32	0
5	GOL	A	2502	6/6	0.94	0.10	18,25,30,36	0
4	SO4	F	2415	5/5	0.94	0.20	22,35,39,44	0
4	SO4	I	2416	5/5	0.94	0.18	32,39,40,48	0
4	SO4	B	2413	5/5	0.94	0.24	35,39,41,46	0
5	GOL	K	2505	6/6	0.95	0.08	20,22,28,31	0
4	SO4	G	2407	5/5	0.97	0.10	16,20,28,29	0
3	HG	E	305	1/1	0.97	0.04	18,18,18,18	0
4	SO4	H	2408	5/5	0.98	0.09	22,27,33,39	0
4	SO4	I	2409	5/5	0.98	0.07	18,20,23,23	0
4	SO4	A	2401	5/5	0.98	0.09	21,22,25,32	0
4	SO4	J	2410	5/5	0.98	0.09	19,26,30,32	0
3	HG	C	303	1/1	0.98	0.04	17,17,17,17	0
4	SO4	L	2412	5/5	0.98	0.08	26,29,34,39	0
4	SO4	B	2402	5/5	0.98	0.10	26,34,36,38	0
2	CO	F	206	1/1	0.98	0.05	12,12,12,12	0
4	SO4	C	2403	5/5	0.98	0.09	12,16,18,21	0
4	SO4	D	2404	5/5	0.98	0.08	17,20,28,37	0
4	SO4	E	2405	5/5	0.98	0.07	16,16,22,23	0
3	HG	F	306	1/1	0.98	0.03	22,22,22,22	0
4	SO4	F	2406	5/5	0.98	0.08	20,21,31,34	0
3	HG	G	307	1/1	0.98	0.05	19,19,19,19	0
3	HG	H	308	1/1	0.98	0.04	25,25,25,25	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	HG	D	304	1/1	0.99	0.02	19,19,19,19	0
4	SO4	K	2411	5/5	0.99	0.07	17,20,21,23	0
2	CO	C	203	1/1	0.99	0.04	9,9,9,9	0
2	CO	D	204	1/1	0.99	0.03	10,10,10,10	0
2	CO	E	205	1/1	0.99	0.04	8,8,8,8	0
2	CO	A	201	1/1	0.99	0.04	12,12,12,12	0
3	HG	J	310	1/1	0.99	0.02	24,24,24,24	0
3	HG	L	312	1/1	0.99	0.02	25,25,25,25	0
2	CO	G	207	1/1	0.99	0.05	12,12,12,12	0
2	CO	H	208	1/1	0.99	0.04	12,12,12,12	0
3	HG	A	301	1/1	0.99	0.02	19,19,19,19	0
2	CO	B	202	1/1	0.99	0.05	12,12,12,12	0
2	CO	L	212	1/1	1.00	0.02	13,13,13,13	0
2	CO	I	209	1/1	1.00	0.01	12,12,12,12	0
3	HG	B	302	1/1	1.00	0.02	18,18,18,18	0
2	CO	J	210	1/1	1.00	0.02	12,12,12,12	0
3	HG	I	309	1/1	1.00	0.02	19,19,19,19	0
2	CO	K	211	1/1	1.00	0.04	13,13,13,13	0
3	HG	K	311	1/1	1.00	0.02	22,22,22,22	0

6.5 Other polymers (i)

There are no such residues in this entry.