



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 03:16 am GMT

PDB ID : 3TZQ
Title : Crystal structure of a short-chain type dehydrogenase/reductase from Mycobacterium marinum
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2011-09-27
Resolution : 2.50 Å(reported)

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

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

A user guide is available at

<http://wwpdb.org/validation/2016/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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

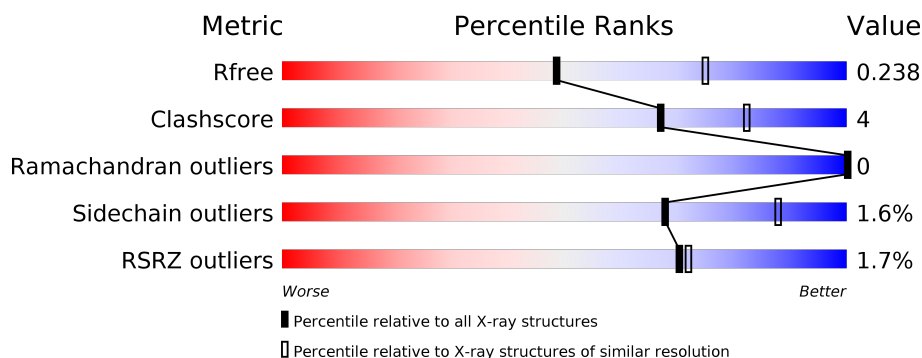
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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.



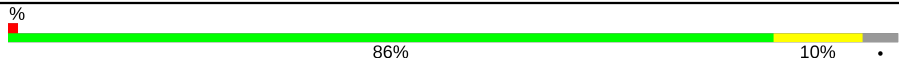

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

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. 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	271	<div> <div>2%</div> <div> <div></div> <div>90%</div> <div>6%</div> <div>.</div> </div> </div>
1	B	271	<div> <div>3%</div> <div> <div></div> <div>82%</div> <div>13%</div> <div>5%</div> </div> </div>
1	C	271	<div> <div>%</div> <div> <div></div> <div>87%</div> <div>10%</div> <div>.</div> </div> </div>
1	D	271	<div> <div>2%</div> <div> <div></div> <div>86%</div> <div>8%</div> <div>.</div> </div> </div>
1	E	271	<div> <div>2%</div> <div> <div></div> <div>86%</div> <div>10%</div> <div>.</div> </div> </div>
1	F	271	<div> <div>2%</div> <div> <div></div> <div>86%</div> <div>10%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	271	
1	H	271	

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
2	GOL	A	270	-	-	-	X
2	GOL	B	268	-	-	-	X
2	GOL	C	271	-	-	-	X
2	GOL	E	270	-	-	-	X
2	GOL	F	269	-	-	-	X
2	GOL	G	269	-	-	-	X
2	GOL	G	270	-	-	-	X
2	GOL	H	269	-	-	-	X
3	EDO	A	269	-	-	-	X
3	EDO	C	268	-	-	-	X
4	PEG	E	268	-	-	-	X
4	PEG	E	269	-	-	-	X
4	PEG	F	268	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15934 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 Short-chain type dehydrogenase/reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	258	Total	C	N	O	S	0	0	0
			1871	1173	334	354	10			
1	A	259	Total	C	N	O	S	0	1	0
			1894	1186	341	357	10			
1	D	259	Total	C	N	O	S	0	0	0
			1877	1179	334	354	10			
1	C	261	Total	C	N	O	S	0	0	0
			1884	1182	336	356	10			
1	F	261	Total	C	N	O	S	0	0	0
			1901	1192	339	360	10			
1	E	260	Total	C	N	O	S	0	1	0
			1913	1198	345	360	10			
1	H	261	Total	C	N	O	S	0	0	0
			1907	1196	340	361	10			
1	G	260	Total	C	N	O	S	0	0	0
			1890	1186	335	359	10			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	EXPRESSION TAG	UNP B2HKN3
B	-2	PRO	-	EXPRESSION TAG	UNP B2HKN3
B	-1	GLY	-	EXPRESSION TAG	UNP B2HKN3
B	0	SER	-	EXPRESSION TAG	UNP B2HKN3
A	-3	GLY	-	EXPRESSION TAG	UNP B2HKN3
A	-2	PRO	-	EXPRESSION TAG	UNP B2HKN3
A	-1	GLY	-	EXPRESSION TAG	UNP B2HKN3
A	0	SER	-	EXPRESSION TAG	UNP B2HKN3
D	-3	GLY	-	EXPRESSION TAG	UNP B2HKN3
D	-2	PRO	-	EXPRESSION TAG	UNP B2HKN3
D	-1	GLY	-	EXPRESSION TAG	UNP B2HKN3
D	0	SER	-	EXPRESSION TAG	UNP B2HKN3
C	-3	GLY	-	EXPRESSION TAG	UNP B2HKN3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	PRO	-	EXPRESSION TAG	UNP B2HKN3
C	-1	GLY	-	EXPRESSION TAG	UNP B2HKN3
C	0	SER	-	EXPRESSION TAG	UNP B2HKN3
F	-3	GLY	-	EXPRESSION TAG	UNP B2HKN3
F	-2	PRO	-	EXPRESSION TAG	UNP B2HKN3
F	-1	GLY	-	EXPRESSION TAG	UNP B2HKN3
F	0	SER	-	EXPRESSION TAG	UNP B2HKN3
E	-3	GLY	-	EXPRESSION TAG	UNP B2HKN3
E	-2	PRO	-	EXPRESSION TAG	UNP B2HKN3
E	-1	GLY	-	EXPRESSION TAG	UNP B2HKN3
E	0	SER	-	EXPRESSION TAG	UNP B2HKN3
H	-3	GLY	-	EXPRESSION TAG	UNP B2HKN3
H	-2	PRO	-	EXPRESSION TAG	UNP B2HKN3
H	-1	GLY	-	EXPRESSION TAG	UNP B2HKN3
H	0	SER	-	EXPRESSION TAG	UNP B2HKN3
G	-3	GLY	-	EXPRESSION TAG	UNP B2HKN3
G	-2	PRO	-	EXPRESSION TAG	UNP B2HKN3
G	-1	GLY	-	EXPRESSION TAG	UNP B2HKN3
G	0	SER	-	EXPRESSION TAG	UNP B2HKN3

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



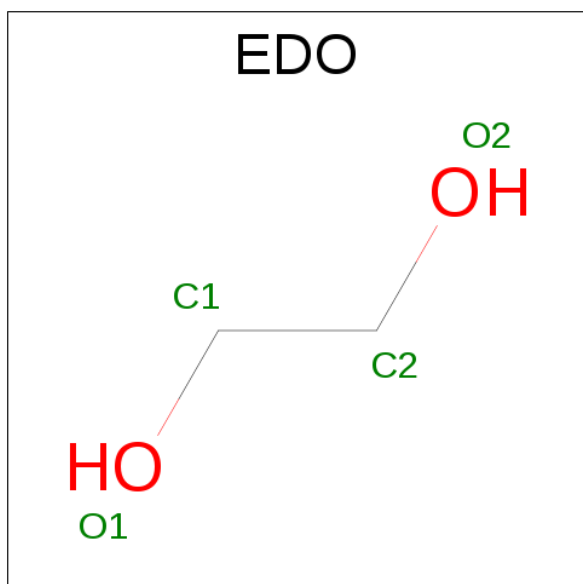
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			6	3	3		
2	F	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	H	1	Total	C	O	0	0
			6	3	3		
2	G	1	Total	C	O	0	0
			6	3	3		
2	G	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



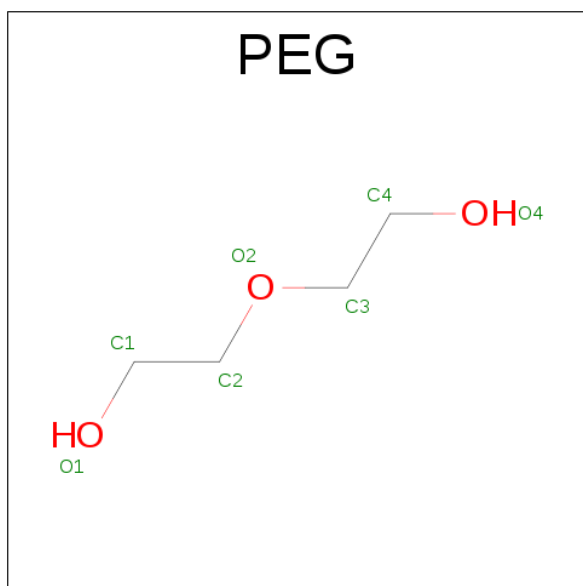
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	H	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	G	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			7	4	3		
4	F	1	Total	C	O	0	0
			7	4	3		
4	E	1	Total	C	O	0	0
			7	4	3		
4	E	1	Total	C	O	0	0
			7	4	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	81	Total	O	0	0
			81	81		
5	A	91	Total	O	0	1
			92	92		
5	D	77	Total	O	0	0
			77	77		
5	C	81	Total	O	0	0
			81	81		

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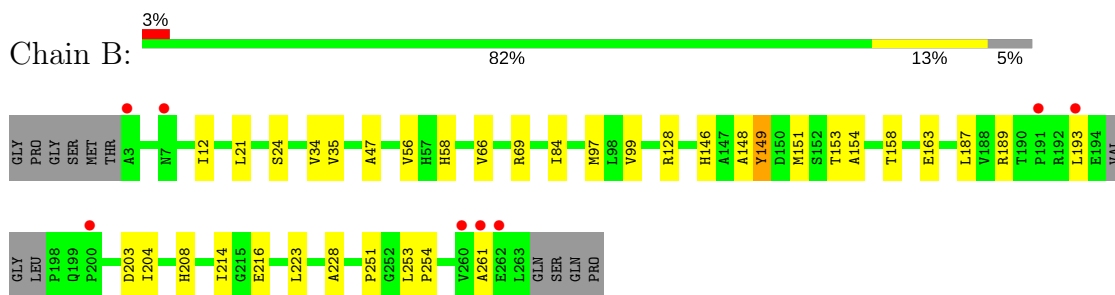
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	F	95	Total 95	O 95	0	0
5	E	77	Total 77	O 77	0	0
5	H	107	Total 107	O 107	0	0
5	G	87	Total 87	O 87	0	0

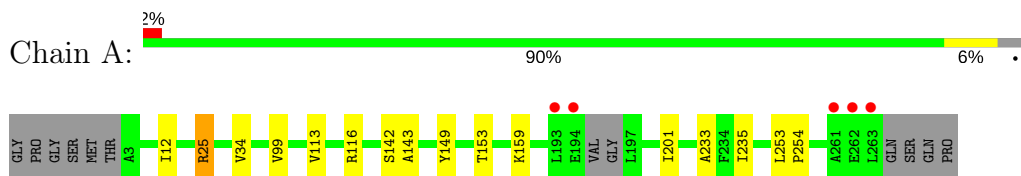
3 Residue-property plots [i](#)

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.

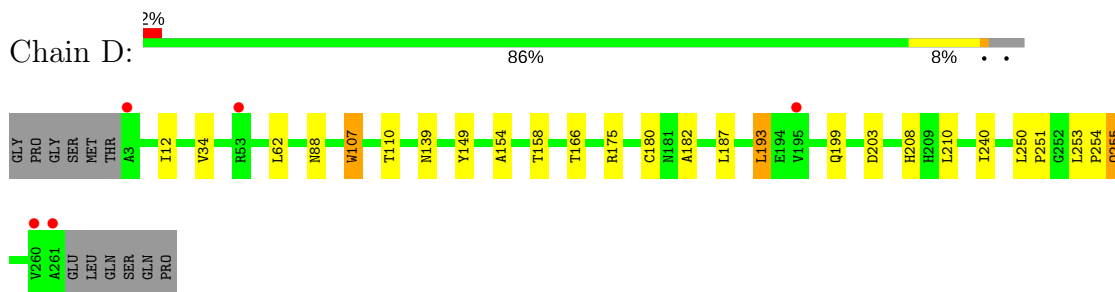
- Molecule 1: Short-chain type dehydrogenase/reductase



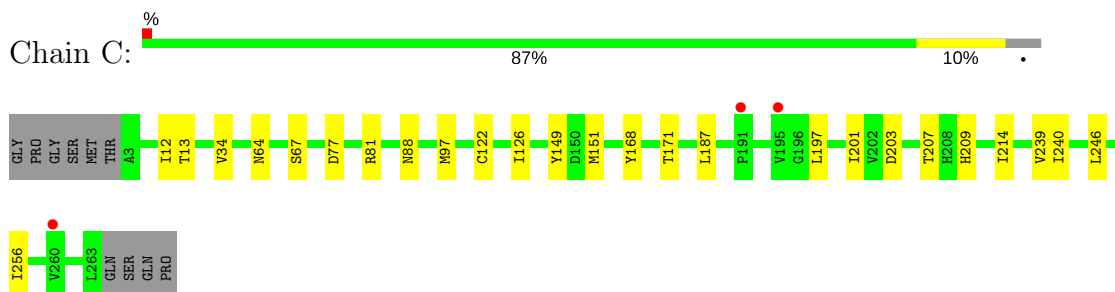
- Molecule 1: Short-chain type dehydrogenase/reductase



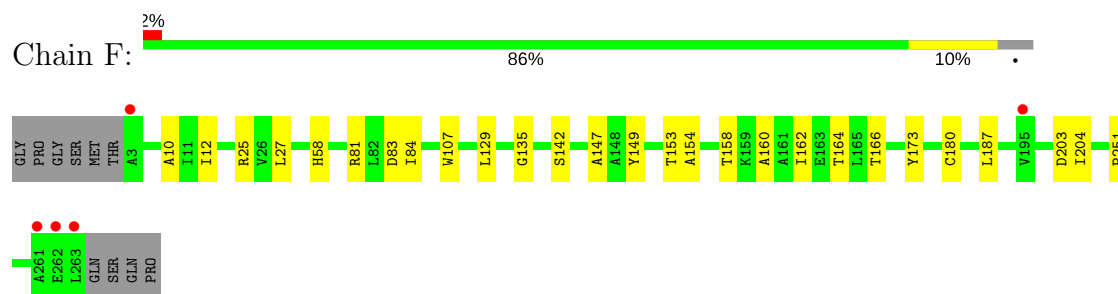
- Molecule 1: Short-chain type dehydrogenase/reductase



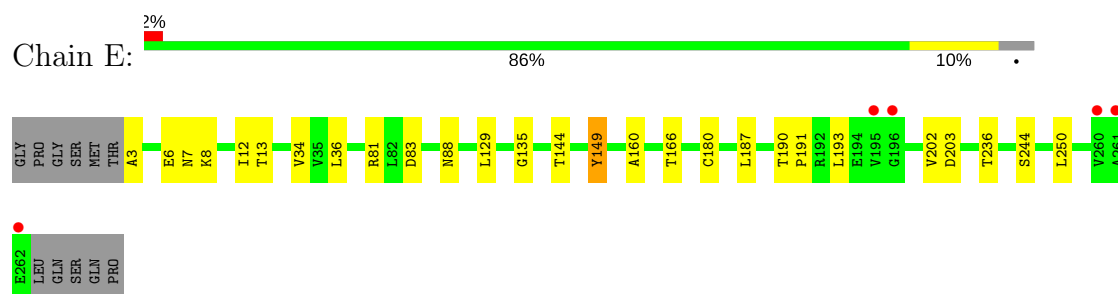
- Molecule 1: Short-chain type dehydrogenase/reductase



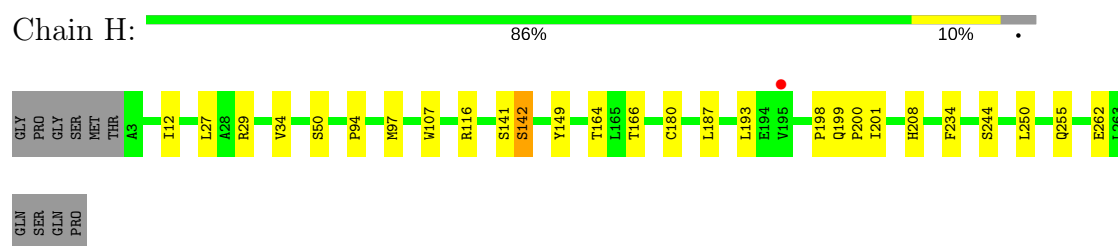
- Molecule 1: Short-chain type dehydrogenase/reductase



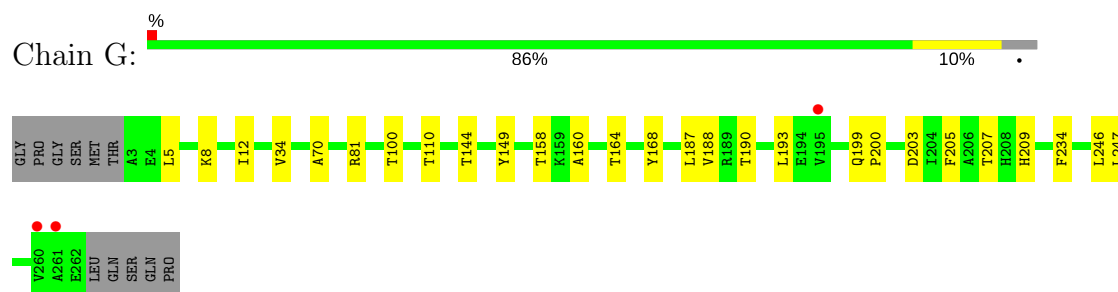
- Molecule 1: Short-chain type dehydrogenase/reductase



- Molecule 1: Short-chain type dehydrogenase/reductase



- Molecule 1: Short-chain type dehydrogenase/reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	69.67Å 122.07Å 125.29Å 90.00° 101.03° 90.00°	Depositor
Resolution (Å)	19.92 – 2.50 19.92 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.9 (19.92-2.50) 98.1 (19.92-2.50)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.180 , 0.244 0.179 , 0.238	Depositor DCC
R_{free} test set	3526 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	19.2	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 35.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15934	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.53% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, PEG, EDO

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	0.60	0/1927	0.72	0/2629
1	B	0.56	0/1901	0.70	0/2595
1	C	0.59	0/1915	0.73	1/2617 (0.0%)
1	D	0.58	1/1908 (0.1%)	0.68	0/2607
1	E	0.60	0/1947	0.70	0/2656
1	F	0.59	1/1932 (0.1%)	0.71	0/2638
1	G	0.60	0/1921	0.71	1/2624 (0.0%)
1	H	0.62	1/1938 (0.1%)	0.74	1/2646 (0.0%)
All	All	0.59	3/15389 (0.0%)	0.71	3/21012 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	107	TRP	CD2-CE2	6.07	1.48	1.41
1	F	107	TRP	CD2-CE2	5.10	1.47	1.41
1	D	107	TRP	CD2-CE2	5.02	1.47	1.41

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	116	ARG	NE-CZ-NH2	-5.93	117.33	120.30
1	C	81	ARG	NE-CZ-NH1	5.86	123.23	120.30
1	G	81	ARG	NE-CZ-NH1	5.75	123.17	120.30

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	1894	0	1893	14	0
1	B	1871	0	1864	29	0
1	C	1884	0	1874	18	0
1	D	1877	0	1879	22	0
1	E	1913	0	1928	19	0
1	F	1901	0	1902	19	0
1	G	1890	0	1889	22	0
1	H	1907	0	1915	17	0
2	A	6	0	8	1	0
2	B	6	0	8	1	0
2	C	6	0	8	0	0
2	E	6	0	8	1	0
2	F	6	0	8	0	0
2	G	12	0	16	1	0
2	H	6	0	8	1	0
3	A	8	0	12	0	0
3	C	8	0	12	1	0
3	G	4	0	6	0	0
3	H	4	0	6	0	0
4	C	7	0	10	0	0
4	E	14	0	20	4	0
4	F	7	0	10	2	0
5	A	92	0	0	3	0
5	B	81	0	0	4	0
5	C	81	0	0	0	0
5	D	77	0	0	0	0
5	E	77	0	0	2	0
5	F	95	0	0	3	0
5	G	87	0	0	1	0
5	H	107	0	0	2	0
All	All	15934	0	15284	137	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 4.

All (137) 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:197:LEU:HD22	1:C:201:ILE:HG21	1.59	0.84
1:A:201:ILE:HD12	1:C:256:ILE:HG23	1.65	0.80
1:E:12:ILE:CD1	1:E:34:VAL:HG13	2.13	0.79
1:E:166:THR:HG23	1:E:180:CYS:SG	2.25	0.76
1:E:236:THR:HG21	4:E:269:PEG:H32	1.68	0.75
1:G:187:LEU:HD11	1:G:193:LEU:CD1	2.19	0.72
4:E:268:PEG:H22	1:G:247:LEU:O	1.90	0.71
1:A:12:ILE:CD1	1:A:34:VAL:HG13	2.22	0.69
1:B:187:LEU:HD23	1:B:214:ILE:HG21	1.77	0.66
1:G:187:LEU:HD11	1:G:193:LEU:HD11	1.77	0.66
1:D:110:THR:HG22	1:D:158:THR:HG21	1.78	0.65
1:B:66:VAL:HG21	1:H:262:GLU:HG2	1.77	0.65
1:F:166:THR:HG23	1:F:180:CYS:SG	2.37	0.65
1:G:110:THR:HG22	1:G:158:THR:HG21	1.80	0.64
1:E:12:ILE:HD13	1:E:34:VAL:CG1	2.28	0.63
1:C:97:MET:HE2	1:C:151:MET:HB2	1.79	0.63
1:B:187:LEU:HD23	1:B:214:ILE:CG2	2.28	0.63
1:F:203:ASP:CG	5:F:464:HOH:O	2.39	0.61
1:H:166:THR:HG23	1:H:180:CYS:SG	2.42	0.60
1:D:12:ILE:HD13	1:D:34:VAL:CG1	2.32	0.59
1:D:166:THR:HG23	1:D:180:CYS:SG	2.43	0.58
1:G:203:ASP:O	1:G:207:THR:HG23	2.03	0.58
1:H:187:LEU:HD11	1:H:193:LEU:HD13	1.85	0.58
1:H:187:LEU:HD11	1:H:193:LEU:CD1	2.33	0.58
1:E:81:ARG:NH1	1:E:83:ASP:OD1	2.37	0.57
1:B:187:LEU:HD13	2:B:268:GOL:H31	1.87	0.56
1:H:187:LEU:HD13	2:H:269:GOL:H11	1.88	0.55
1:B:189:ARG:NH2	1:B:216:GLU:OE2	2.39	0.55
1:D:187:LEU:HD11	1:D:193:LEU:HD11	1.87	0.55
1:H:12:ILE:CD1	1:H:34:VAL:HG13	2.36	0.54
1:C:203:ASP:O	1:C:207:THR:HG23	2.08	0.53
1:F:25:ARG:NH1	5:F:511:HOH:O	2.40	0.53
1:C:239:VAL:HB	3:C:269:EDO:H11	1.90	0.53
1:C:13:THR:O	1:C:88:ASN:HB3	2.09	0.52
1:A:116:ARG:HG3	1:D:107:TRP:CD1	2.45	0.52
1:A:12:ILE:HD13	1:A:34:VAL:HG13	1.90	0.52
1:E:34:VAL:HG12	1:E:36:LEU:HD12	1.92	0.51
1:G:187:LEU:HD11	1:G:193:LEU:HD13	1.90	0.51
1:E:236:THR:CG2	4:E:269:PEG:H32	2.40	0.51
1:C:12:ILE:CD1	1:C:34:VAL:HG13	2.41	0.51
1:E:187:LEU:HD11	1:E:193:LEU:CD1	2.41	0.51
1:E:3:ALA:HB3	1:E:6:GLU:OE1	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:144:THR:HG23	2:G:269:GOL:H2	1.93	0.51
1:G:209:HIS:CE1	1:G:246:LEU:HD13	2.46	0.51
1:A:12:ILE:HD13	1:A:34:VAL:CG1	2.42	0.50
1:B:251:PRO:HB2	1:D:208:HIS:CD2	2.46	0.50
1:E:144:THR:HG23	2:E:270:GOL:H2	1.94	0.50
1:B:12:ILE:HD12	1:B:34:VAL:CG1	2.41	0.50
1:B:149:TYR:CE1	1:B:151:MET:HG2	2.47	0.50
1:D:154:ALA:O	1:D:158:THR:HG23	2.11	0.50
1:G:5:LEU:O	1:G:8:LYS:HB2	2.11	0.49
1:D:12:ILE:CD1	1:D:34:VAL:HG13	2.41	0.49
1:G:199:GLN:N	1:G:200:PRO:HD2	2.28	0.49
1:D:253:LEU:HB3	1:D:254:PRO:HD3	1.95	0.49
1:F:142:SER:OG	4:F:268:PEG:H12	2.13	0.49
1:G:12:ILE:HD13	1:G:34:VAL:HG13	1.95	0.49
1:B:99:VAL:HG22	1:B:153:THR:HG21	1.95	0.48
1:E:13:THR:O	1:E:88:ASN:HB3	2.14	0.48
1:H:199:GLN:HB3	1:H:200:PRO:HD3	1.95	0.48
1:A:143:ALA:HB2	5:A:425:HOH:O	2.13	0.48
1:D:240:ILE:HD11	1:C:240:ILE:HG23	1.95	0.48
1:A:25:ARG:NH1	5:A:346:HOH:O	2.46	0.48
1:D:210:LEU:HD22	1:C:171:THR:HA	1.96	0.48
1:B:154:ALA:O	1:B:158:THR:HG23	2.14	0.47
1:B:12:ILE:HD12	1:B:34:VAL:HG11	1.97	0.47
1:G:12:ILE:CD1	1:G:34:VAL:HG13	2.44	0.47
1:D:139:ASN:O	1:D:182:ALA:HA	2.14	0.47
1:F:251:PRO:HB2	1:H:208:HIS:CD2	2.50	0.47
1:F:12:ILE:HD11	1:F:27:LEU:HD22	1.97	0.46
1:F:58:HIS:NE2	5:F:362:HOH:O	2.27	0.46
1:E:129:LEU:HD22	1:E:135:GLY:HA3	1.97	0.46
1:C:187:LEU:HD23	1:C:214:ILE:HG21	1.98	0.46
1:D:12:ILE:HD13	1:D:34:VAL:HG13	1.98	0.46
1:B:208:HIS:CD2	1:D:251:PRO:HB2	2.51	0.46
1:B:21:LEU:HD13	1:B:47:ALA:HB1	1.98	0.45
1:H:12:ILE:HD13	1:H:34:VAL:CG1	2.47	0.45
1:A:233:ALA:HB1	5:A:605:HOH:O	2.16	0.44
1:D:12:ILE:HD13	1:D:34:VAL:HG11	1.99	0.44
1:D:187:LEU:HD11	1:D:193:LEU:CD1	2.47	0.44
1:H:12:ILE:HD12	1:H:12:ILE:N	2.32	0.44
1:B:128:ARG:HD3	5:B:541:HOH:O	2.16	0.44
1:B:148:ALA:HA	1:C:168:TYR:CZ	2.53	0.44
1:F:153:THR:HG1	1:G:168:TYR:HD2	1.63	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:198:PRO:HG2	1:H:201:ILE:HD12	2.00	0.44
1:B:97:MET:HE1	1:B:151:MET:HB2	2.00	0.44
1:F:164:THR:OG1	1:G:160:ALA:HB2	2.18	0.44
1:H:244:SER:HB2	1:G:234:PHE:CE1	2.52	0.43
1:C:64:ASN:HB3	1:C:67:SER:HB3	1.98	0.43
1:F:81:ARG:HD3	1:F:83:ASP:OD2	2.18	0.43
1:B:204:ILE:HD13	1:D:255:GLN:CB	2.48	0.43
1:B:149:TYR:CD2	1:D:250:LEU:HD12	2.53	0.43
1:B:204:ILE:HD13	1:D:255:GLN:HB3	2.01	0.43
1:B:35:VAL:HG22	1:B:56:VAL:CG2	2.49	0.43
1:B:261:ALA:HB3	5:B:534:HOH:O	2.19	0.43
1:E:149:TYR:HB2	5:E:279:HOH:O	2.18	0.43
1:E:250:LEU:HD13	1:G:205:PHE:CE1	2.54	0.43
1:E:187:LEU:HD11	1:E:193:LEU:HD13	2.01	0.42
1:F:129:LEU:HD22	1:F:135:GLY:HA3	2.01	0.42
1:D:240:ILE:CD1	1:C:240:ILE:HG23	2.49	0.42
1:B:223:LEU:HD22	1:A:235:ILE:HD11	2.02	0.42
1:F:204:ILE:HG23	5:H:432:HOH:O	2.19	0.42
1:F:158:THR:O	1:F:162:ILE:HG13	2.20	0.42
1:A:201:ILE:CD1	1:C:256:ILE:HG23	2.44	0.42
1:F:173:TYR:HH	1:G:100:THR:H	1.66	0.42
1:A:142:SER:HB3	1:A:159:LYS:HG3	2.02	0.42
1:A:113:VAL:HG13	2:A:270:GOL:H2	2.00	0.42
1:H:29:ARG:NH1	5:H:336:HOH:O	2.51	0.42
1:B:253:LEU:HB3	1:B:254:PRO:HD3	2.02	0.41
1:F:147:ALA:HB3	1:H:250:LEU:HD23	2.01	0.41
1:F:10:ALA:HB2	1:F:84:ILE:HB	2.02	0.41
1:G:70:ALA:HB3	5:G:285:HOH:O	2.19	0.41
1:D:187:LEU:HA	1:D:187:LEU:HD12	1.93	0.41
1:E:190:THR:HB	1:E:191:PRO:HD2	2.02	0.41
1:G:188:VAL:O	1:G:190:THR:HG23	2.20	0.41
1:A:99:VAL:HG22	1:A:153:THR:HG21	2.03	0.41
1:G:12:ILE:HD13	1:G:34:VAL:CG1	2.50	0.41
1:B:58:HIS:NE2	5:B:295:HOH:O	2.37	0.41
1:E:202:VAL:HG12	1:E:203:ASP:N	2.34	0.41
1:H:94:PRO:O	1:H:97:MET:CE	2.69	0.41
1:C:12:ILE:HD12	1:C:34:VAL:HG13	2.02	0.41
1:E:160:ALA:HB2	1:H:164:THR:OG1	2.20	0.41
1:E:8:LYS:HE3	5:E:568:HOH:O	2.21	0.41
1:B:12:ILE:HD13	1:B:24:SER:HA	2.02	0.41
1:A:253:LEU:N	1:A:254:PRO:CD	2.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:187:LEU:HD23	1:B:214:ILE:HG22	2.02	0.41
1:C:97:MET:CE	1:C:151:MET:HB2	2.47	0.41
1:H:141:SER:OG	1:H:142:SER:N	2.54	0.41
1:B:146:HIS:HE1	1:B:163:GLU:OE2	2.04	0.40
1:B:84:ILE:HD13	1:B:228:ALA:HB1	2.03	0.40
1:C:209:HIS:CE1	1:C:246:LEU:HD13	2.56	0.40
1:D:199:GLN:HE21	1:D:203:ASP:CG	2.24	0.40
1:F:160:ALA:HB2	1:G:164:THR:OG1	2.21	0.40
1:F:187:LEU:HD13	4:F:268:PEG:C4	2.52	0.40
1:B:97:MET:CE	5:B:671:HOH:O	2.70	0.40
1:C:122:CYS:O	1:C:126:ILE:HD12	2.20	0.40
1:F:154:ALA:O	1:F:158:THR:HG23	2.21	0.40
4:E:268:PEG:H22	1:G:247:LEU:HB3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	256/271 (94%)	244 (95%)	12 (5%)	0	100	100
1	B	254/271 (94%)	244 (96%)	10 (4%)	0	100	100
1	C	259/271 (96%)	251 (97%)	8 (3%)	0	100	100
1	D	257/271 (95%)	247 (96%)	10 (4%)	0	100	100
1	E	259/271 (96%)	251 (97%)	8 (3%)	0	100	100
1	F	259/271 (96%)	249 (96%)	10 (4%)	0	100	100
1	G	258/271 (95%)	245 (95%)	13 (5%)	0	100	100
1	H	259/271 (96%)	248 (96%)	11 (4%)	0	100	100
All	All	2061/2168 (95%)	1979 (96%)	82 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	192/205 (94%)	190 (99%)	2 (1%)	80	93
1	B	189/205 (92%)	185 (98%)	4 (2%)	59	83
1	C	189/205 (92%)	187 (99%)	2 (1%)	78	92
1	D	190/205 (93%)	184 (97%)	6 (3%)	44	71
1	E	196/205 (96%)	193 (98%)	3 (2%)	70	89
1	F	193/205 (94%)	192 (100%)	1 (0%)	91	97
1	G	192/205 (94%)	191 (100%)	1 (0%)	91	97
1	H	195/205 (95%)	189 (97%)	6 (3%)	45	73
All	All	1536/1640 (94%)	1511 (98%)	25 (2%)	68	88

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	69	ARG
1	B	149	TYR
1	B	193	LEU
1	B	203	ASP
1	A	25	ARG
1	A	149	TYR
1	D	62	LEU
1	D	88	ASN
1	D	149	TYR
1	D	175	ARG
1	D	193	LEU
1	D	255	GLN
1	C	77	ASP
1	C	149	TYR
1	F	149	TYR
1	E	7	ASN

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Mol	Chain	Res	Type
1	E	149	TYR
1	E	244	SER
1	H	27	LEU
1	H	50	SER
1	H	142	SER
1	H	149	TYR
1	H	234	PHE
1	H	255	GLN
1	G	149	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	146	HIS
1	D	199	GLN
1	C	255	GLN
1	F	208	HIS
1	H	199	GLN

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 [i](#)

18 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	EDO	A	268	-	3,3,3	0.47	0	2,2,2	0.30	0
3	EDO	A	269	-	3,3,3	0.47	0	2,2,2	0.61	0
2	GOL	A	270	-	5,5,5	0.62	0	5,5,5	0.54	0
2	GOL	B	268	-	5,5,5	0.37	0	5,5,5	0.30	0
3	EDO	C	268	-	3,3,3	0.74	0	2,2,2	0.34	0
3	EDO	C	269	-	3,3,3	0.60	0	2,2,2	0.06	0
4	PEG	C	270	-	6,6,6	0.56	0	5,5,5	0.17	0
2	GOL	C	271	-	5,5,5	0.49	0	5,5,5	0.35	0
4	PEG	E	268	-	6,6,6	0.50	0	5,5,5	0.48	0
4	PEG	E	269	-	6,6,6	0.52	0	5,5,5	0.26	0
2	GOL	E	270	-	5,5,5	0.49	0	5,5,5	0.58	0
4	PEG	F	268	-	6,6,6	0.66	0	5,5,5	0.50	0
2	GOL	F	269	-	5,5,5	0.72	0	5,5,5	0.57	0
3	EDO	G	268	-	3,3,3	0.55	0	2,2,2	0.18	0
2	GOL	G	269	-	5,5,5	0.57	0	5,5,5	0.44	0
2	GOL	G	270	-	5,5,5	0.44	0	5,5,5	0.33	0
3	EDO	H	268	-	3,3,3	0.67	0	2,2,2	0.22	0
2	GOL	H	269	-	5,5,5	0.55	0	5,5,5	0.64	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	EDO	A	268	-	-	0/1/1/1	0/0/0/0
3	EDO	A	269	-	-	0/1/1/1	0/0/0/0
2	GOL	A	270	-	-	0/4/4/4	0/0/0/0
2	GOL	B	268	-	-	0/4/4/4	0/0/0/0
3	EDO	C	268	-	-	0/1/1/1	0/0/0/0
3	EDO	C	269	-	-	0/1/1/1	0/0/0/0
4	PEG	C	270	-	-	0/4/4/4	0/0/0/0
2	GOL	C	271	-	-	0/4/4/4	0/0/0/0
4	PEG	E	268	-	-	0/4/4/4	0/0/0/0
4	PEG	E	269	-	-	0/4/4/4	0/0/0/0
2	GOL	E	270	-	-	0/4/4/4	0/0/0/0
4	PEG	F	268	-	-	0/4/4/4	0/0/0/0
2	GOL	F	269	-	-	0/4/4/4	0/0/0/0
3	EDO	G	268	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	G	269	-	-	0/4/4/4	0/0/0/0
2	GOL	G	270	-	-	0/4/4/4	0/0/0/0
3	EDO	H	268	-	-	0/1/1/1	0/0/0/0
2	GOL	H	269	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	270	GOL	1	0
2	B	268	GOL	1	0
3	C	269	EDO	1	0
4	E	268	PEG	2	0
4	E	269	PEG	2	0
2	E	270	GOL	1	0
4	F	268	PEG	2	0
2	G	269	GOL	1	0
2	H	269	GOL	1	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	259/271 (95%)	-0.35	5 (1%) 67 69	6, 13, 34, 54	0
1	B	258/271 (95%)	-0.17	8 (3%) 49 52	8, 19, 35, 51	0
1	C	261/271 (96%)	-0.27	3 (1%) 80 81	10, 18, 36, 61	0
1	D	259/271 (95%)	-0.28	5 (1%) 67 69	8, 16, 29, 39	0
1	E	260/271 (95%)	-0.34	5 (1%) 67 69	7, 13, 29, 58	0
1	F	261/271 (96%)	-0.30	5 (1%) 67 69	8, 16, 26, 46	0
1	G	260/271 (95%)	-0.35	3 (1%) 79 80	7, 14, 32, 49	0
1	H	261/271 (96%)	-0.41	1 (0%) 92 92	7, 13, 23, 39	0
All	All	2079/2168 (95%)	-0.31	35 (1%) 70 72	6, 15, 32, 61	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	260	VAL	4.3
1	G	195	VAL	4.0
1	B	7	ASN	3.9
1	E	195	VAL	3.9
1	B	261	ALA	3.5
1	G	261	ALA	3.4
1	E	196	GLY	3.4
1	D	261	ALA	3.3
1	D	3	ALA	3.2
1	G	260	VAL	3.2
1	C	191	PRO	3.2
1	C	195	VAL	2.9
1	B	191	PRO	2.8
1	B	3	ALA	2.7
1	F	195	VAL	2.6
1	F	261	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	263	LEU	2.6
1	B	193	LEU	2.5
1	F	3	ALA	2.5
1	E	262	GLU	2.4
1	H	195	VAL	2.4
1	A	193	LEU	2.4
1	D	195	VAL	2.4
1	C	260	VAL	2.3
1	A	261	ALA	2.3
1	A	194	GLU	2.2
1	E	260	VAL	2.2
1	F	262	GLU	2.2
1	D	53	ARG	2.2
1	B	260	VAL	2.1
1	A	262	GLU	2.1
1	B	200	PRO	2.1
1	E	261	ALA	2.1
1	B	262	GLU	2.1
1	F	263	LEU	2.0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	GOL	G	270	6/6	0.89	0.35	14.16	35,36,38,39	0
3	EDO	C	268	4/4	0.83	0.23	12.61	30,30,31,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	GOL	G	269	6/6	0.84	0.22	8.73	35,36,36,38	0
2	GOL	H	269	6/6	0.73	0.28	8.40	35,35,37,38	0
2	GOL	A	270	6/6	0.92	0.28	7.97	25,26,26,27	0
3	EDO	A	269	4/4	0.85	0.26	7.53	36,37,38,39	0
4	PEG	F	268	7/7	0.80	0.24	6.44	27,29,31,32	0
4	PEG	E	268	7/7	0.90	0.30	5.36	13,13,14,14	7
2	GOL	C	271	6/6	0.81	0.26	4.11	42,43,44,45	0
4	PEG	E	269	7/7	0.94	0.22	3.64	12,13,15,16	0
2	GOL	E	270	6/6	0.86	0.23	2.89	36,36,36,37	0
2	GOL	F	269	6/6	0.89	0.22	2.74	22,24,24,26	0
2	GOL	B	268	6/6	0.91	0.17	2.73	39,41,42,42	0
3	EDO	A	268	4/4	0.90	0.14	0.65	26,26,26,26	0
3	EDO	C	269	4/4	0.87	0.21	-	36,37,38,40	0
3	EDO	H	268	4/4	0.89	0.20	-	41,41,43,43	0
4	PEG	C	270	7/7	0.80	0.27	-	70,74,82,82	0
3	EDO	G	268	4/4	0.87	0.24	-	39,42,45,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.