



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:05 AM GMT

PDB ID : 2FML
Title : Crystal structure of MutT/nudix family protein from *Enterococcus faecalis*
Authors : Chang, C.; Quartey, P.; Moy, S.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2006-01-09
Resolution : 2.26 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

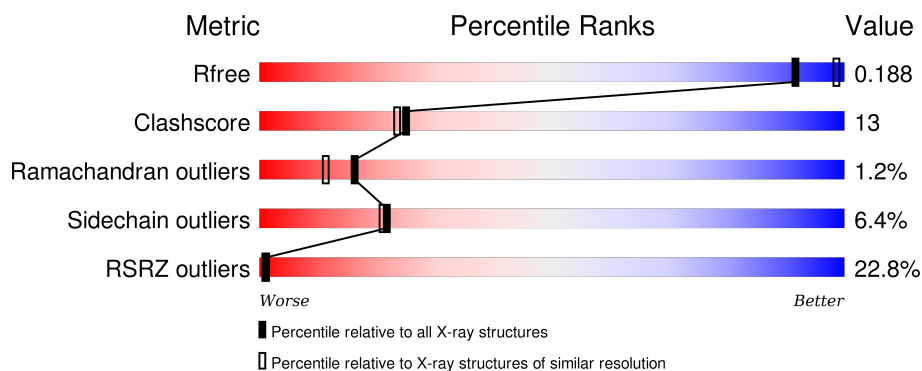
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.26 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}	91344	1640 (2.28-2.24)
Clashscore	102246	1095 (2.26-2.26)
Ramachandran outliers	100387	1063 (2.26-2.26)
Sidechain outliers	100360	1063 (2.26-2.26)
RSRZ outliers	91569	1647 (2.28-2.24)

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	273	
1	B	273	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4466 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 MutT/nudix family protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	259	Total	C	N	O	S	Se	0	0	0
			2104	1340	359	401	1	3			
1	B	256	Total	C	N	O	S	Se	0	2	0
			2092	1333	358	397	1	3			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	GB 29344646
A	44	MSE	MET	MODIFIED RESIDUE	GB 29344646
A	201	MSE	MET	MODIFIED RESIDUE	GB 29344646
A	244	MSE	MET	MODIFIED RESIDUE	GB 29344646
B	1	MSE	MET	MODIFIED RESIDUE	GB 29344646
B	44	MSE	MET	MODIFIED RESIDUE	GB 29344646
B	201	MSE	MET	MODIFIED RESIDUE	GB 29344646
B	244	MSE	MET	MODIFIED RESIDUE	GB 29344646

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

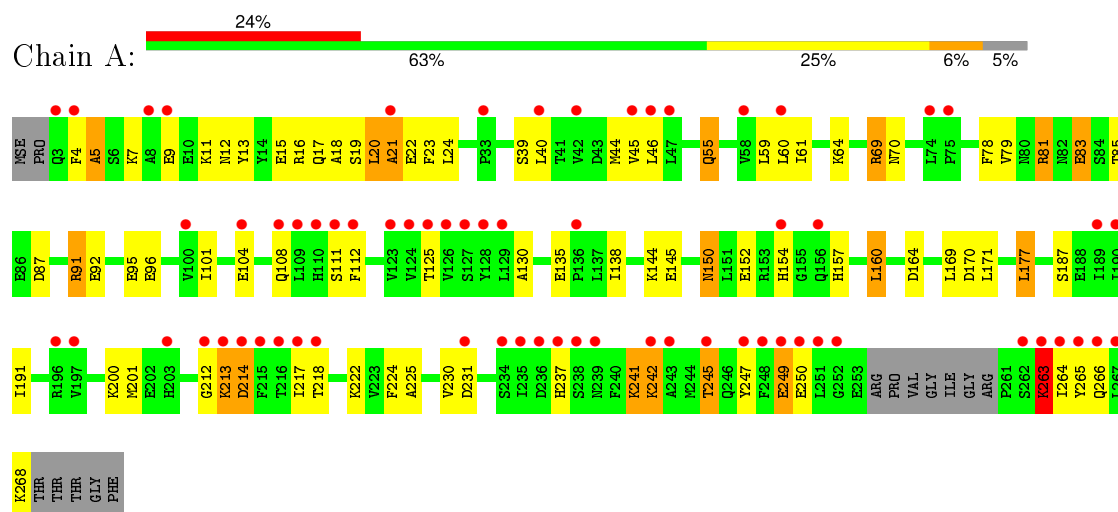
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	101	Total	O	0	0
			101	101		
3	B	163	Total	O	0	0
			163	163		

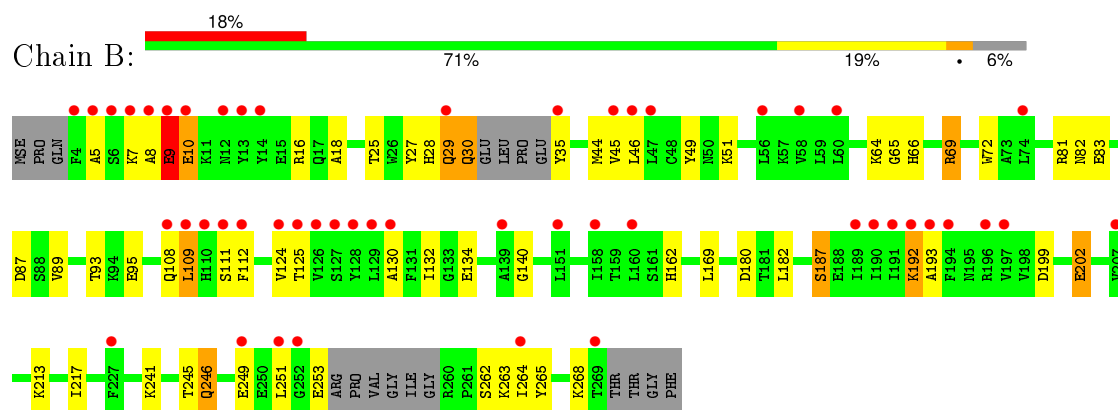
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: MutT/nudix family protein



• Molecule 1: MutT/nudix family protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	86.39 Å 132.03 Å 64.02 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.26 34.56 – 2.26	Depositor EDS
% Data completeness (in resolution range)	99.2 (50.00-2.26) 99.2 (34.56-2.26)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.16 (at 2.27 Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.192 , 0.241 0.191 , 0.188	Depositor DCC
R_{free} test set	1732 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	39.9	Xtriage
Anisotropy	0.580	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 42.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 34753 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4466	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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, 0.375 respectively for untwinned datasets, and 0.333, 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

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	1.32	10/2149 (0.5%)	1.07	19/2899 (0.7%)
1	B	1.29	11/2141 (0.5%)	1.07	9/2886 (0.3%)
All	All	1.30	21/4290 (0.5%)	1.07	28/5785 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	1
All	All	0	4

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	263	LYS	CE-NZ	14.35	1.84	1.49
1	A	237	HIS	CE1-NE2	14.11	1.65	1.32
1	A	247	TYR	CE2-CZ	13.74	1.56	1.38
1	A	247	TYR	CG-CD1	13.43	1.56	1.39
1	A	237	HIS	CG-CD2	12.00	1.56	1.35
1	A	268	LYS	C-O	11.29	1.44	1.23
1	A	237	HIS	CG-ND1	10.98	1.62	1.38
1	A	247	TYR	CE1-CZ	10.46	1.52	1.38
1	A	247	TYR	CG-CD2	9.87	1.51	1.39
1	B	9	GLU	CG-CD	9.68	1.66	1.51
1	B	9	GLU	CD-OE1	8.61	1.35	1.25
1	B	9	GLU	CD-OE2	6.85	1.33	1.25
1	B	49	TYR	CD2-CE2	6.72	1.49	1.39
1	A	241	LYS	C-O	6.68	1.36	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	10	GLU	CG-CD	6.05	1.61	1.51
1	B	187	SER	CB-OG	-6.02	1.34	1.42
1	B	45	VAL	CB-CG1	6.00	1.65	1.52
1	B	27	TYR	CD2-CE2	5.80	1.48	1.39
1	B	192	LYS	CD-CE	5.51	1.65	1.51
1	B	10	GLU	CB-CG	5.10	1.61	1.52
1	B	10	GLU	CD-OE2	5.01	1.31	1.25

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	69	ARG	NE-CZ-NH2	-11.81	114.39	120.30
1	A	91	ARG	NE-CZ-NH2	-10.43	115.08	120.30
1	A	91	ARG	NE-CZ-NH1	9.39	125.00	120.30
1	B	69	ARG	NE-CZ-NH1	9.01	124.80	120.30
1	A	81	ARG	NE-CZ-NH2	-7.43	116.59	120.30
1	B	64	LYS	N-CA-C	6.55	128.69	111.00
1	A	268	LYS	CA-C-O	-6.42	106.62	120.10
1	B	51	LYS	CD-CE-NZ	6.42	126.46	111.70
1	A	237	HIS	CG-CD2-NE2	-6.37	97.09	109.20
1	A	247	TYR	CB-CG-CD2	-6.34	117.20	121.00
1	A	20	LEU	N-CA-C	6.18	127.69	111.00
1	B	64	LYS	CA-C-N	5.84	127.87	116.20
1	A	177	LEU	CA-CB-CG	5.79	128.60	115.30
1	B	109	LEU	CA-CB-CG	5.77	128.57	115.30
1	A	69	ARG	NE-CZ-NH2	-5.74	117.43	120.30
1	B	180	ASP	CB-CG-OD2	5.58	123.32	118.30
1	A	83	GLU	CB-CA-C	-5.51	99.37	110.40
1	A	247	TYR	CD1-CG-CD2	5.43	123.87	117.90
1	A	237	HIS	ND1-CG-CD2	5.29	116.20	108.80
1	A	24	LEU	N-CA-C	-5.26	96.80	111.00
1	A	247	TYR	CG-CD2-CE2	-5.14	117.18	121.30
1	B	64	LYS	C-N-CA	5.14	133.10	122.30
1	A	247	TYR	CD1-CE1-CZ	-5.11	115.20	119.80
1	A	81	ARG	NE-CZ-NH1	5.10	122.85	120.30
1	A	69	ARG	NE-CZ-NH1	5.10	122.85	120.30
1	A	231	ASP	CB-CG-OD2	5.08	122.88	118.30
1	A	177	LEU	CB-CG-CD1	-5.07	102.38	111.00
1	B	199	ASP	CB-CG-OD2	-5.02	113.78	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	20	LEU	Peptide
1	A	23	PHE	Peptide
1	A	249	GLU	Peptide
1	B	9	GLU	Peptide

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	2104	0	2038	71	0
1	B	2092	0	2032	42	0
2	A	6	0	8	0	0
3	A	101	0	0	6	0
3	B	163	0	0	7	0
All	All	4466	0	4078	105	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 13.

All (105) 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:A:263:LYS:CE	1:A:263:LYS:NZ	1.84	1.40
1:B:44:MSE:CE	3:B:356:HOH:O	1.69	1.34
1:B:44:MSE:HE1	3:B:356:HOH:O	1.36	1.04
1:B:9:GLU:HB3	1:B:10:GLU:HB2	1.40	1.02
1:A:18:ALA:HB1	1:A:22:GLU:HG3	1.39	1.00
1:A:108:GLN:HE22	1:B:111:SER:H	1.02	0.99
1:A:55:GLN:HG2	1:A:150:ASN:HD21	1.29	0.97
1:A:111:SER:H	1:B:108:GLN:HE22	1.19	0.88
1:B:44:MSE:HE2	3:B:356:HOH:O	1.46	0.86
1:A:18:ALA:O	1:B:69:ARG:NH2	2.09	0.85
1:A:55:GLN:HG2	1:A:150:ASN:ND2	1.98	0.79
1:B:162:HIS:HD2	3:B:297:HOH:O	1.66	0.78
1:A:95:GLU:HG2	3:A:387:HOH:O	1.83	0.77
1:A:18:ALA:HB1	1:A:22:GLU:CG	2.14	0.76
1:A:4:PHE:HA	1:A:5:ALA:CB	2.16	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:GLN:NE2	1:B:111:SER:H	1.84	0.75
1:A:91:ARG:O	1:A:95:GLU:HG3	1.87	0.74
1:A:250:GLU:H	1:A:265:TYR:HA	1.50	0.73
1:B:217:ILE:HD11	1:B:265:TYR:CE1	2.23	0.73
1:A:249:GLU:HB3	1:A:266:GLN:HG2	1.72	0.72
1:B:25:THR:O	1:B:29:GLN:HG3	1.92	0.70
1:A:152:GLU:HG2	1:A:154:HIS:CE1	2.28	0.68
1:A:4:PHE:HA	1:A:5:ALA:HB2	1.76	0.67
1:B:217:ILE:CD1	1:B:265:TYR:CE1	2.78	0.66
1:A:249:GLU:CG	1:A:250:GLU:HA	2.29	0.62
1:A:44:MSE:HE2	1:A:46:LEU:HD23	1.82	0.60
1:A:44:MSE:HE3	1:A:45:VAL:N	2.16	0.60
1:A:249:GLU:CB	1:A:250:GLU:HA	2.32	0.59
1:B:169:LEU:HD22	1:B:187:SER:HB2	1.83	0.59
1:A:59:LEU:HD23	1:A:59:LEU:C	2.24	0.58
1:A:13:TYR:HA	1:A:17:GLN:HE21	1.68	0.58
1:A:249:GLU:HB3	1:A:250:GLU:HA	1.86	0.57
1:A:150:ASN:ND2	3:A:394:HOH:O	2.36	0.57
1:A:91:ARG:NH2	1:A:92:GLU:OE2	2.38	0.57
1:A:87:ASP:OD2	3:A:370:HOH:O	2.18	0.56
1:A:263:LYS:CD	1:A:263:LYS:NZ	2.66	0.55
1:A:55:GLN:CG	1:A:150:ASN:HD21	2.13	0.54
1:A:44:MSE:HE1	1:A:130:ALA:N	2.22	0.54
1:A:4:PHE:CA	1:A:5:ALA:CB	2.86	0.53
1:B:44:MSE:HE3	1:B:93:THR:OG1	2.08	0.53
1:B:217:ILE:HD11	1:B:265:TYR:CZ	2.43	0.53
1:A:201:MSE:HE3	1:A:224:PHE:CD2	2.45	0.52
3:A:385:HOH:O	1:B:35:TYR:CB	2.57	0.52
1:A:157:HIS:HD2	1:A:170:ASP:HA	1.76	0.51
1:A:214:ASP:HB2	1:A:264:ILE:CG2	2.40	0.51
1:A:59:LEU:HD23	1:A:60:LEU:N	2.25	0.51
1:B:83:GLU:HB2	1:B:87:ASP:HB2	1.92	0.51
1:A:46:LEU:HD12	1:A:59:LEU:HD13	1.92	0.51
1:B:5:ALA:HB3	1:B:9:GLU:OE1	2.11	0.50
1:B:46:LEU:HD23	1:B:130:ALA:HB3	1.93	0.50
1:B:249:GLU:CG	1:B:268:LYS:HB3	2.42	0.50
1:A:171:LEU:HA	1:A:191:ILE:HD12	1.93	0.50
1:A:44:MSE:CE	1:A:45:VAL:O	2.60	0.50
1:A:225:ALA:HB1	1:A:230:VAL:O	2.12	0.50
1:A:242:LYS:HE2	3:A:400:HOH:O	2.11	0.50
1:B:246:GLN:O	1:B:268:LYS:HE2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:LYS:HD2	1:B:16:ARG:CZ	2.43	0.49
1:A:5:ALA:CB	1:A:9:GLU:OE2	2.60	0.48
1:A:40:LEU:HD22	1:B:124:VAL:HG21	1.95	0.48
1:A:4:PHE:HA	1:A:5:ALA:HB3	1.92	0.48
1:B:7:LYS:O	1:B:10:GLU:HB3	2.14	0.48
1:B:182:LEU:HD12	1:B:187:SER:HB3	1.94	0.48
1:A:169:LEU:HD22	1:A:187:SER:HB2	1.95	0.48
1:A:249:GLU:HB3	1:A:250:GLU:CA	2.44	0.47
1:A:69:ARG:NH2	1:B:18:ALA:O	2.38	0.47
1:B:134:GLU:HG2	3:B:377:HOH:O	2.14	0.47
1:B:109:LEU:HD11	1:B:193:ALA:HA	1.97	0.47
1:A:171:LEU:HD23	1:A:191:ILE:CD1	2.45	0.47
1:B:202:GLU:HB2	3:B:296:HOH:O	2.14	0.46
1:A:150:ASN:O	1:A:160:LEU:HA	2.15	0.46
1:B:217:ILE:HD12	1:B:265:TYR:CE1	2.49	0.46
1:A:214:ASP:HB2	1:A:264:ILE:HG23	1.96	0.46
1:A:83:GLU:OE2	1:A:91:ARG:HD3	2.16	0.46
1:A:12:ASN:HB2	1:A:16:ARG:HD2	1.96	0.46
1:A:39:SER:HB3	1:A:78:PHE:HE1	1.81	0.45
1:A:108:GLN:HE22	1:B:111:SER:N	1.87	0.45
1:A:69:ARG:O	1:A:70:ASN:HB2	2.17	0.45
1:A:171:LEU:HD23	1:A:191:ILE:HD12	1.98	0.45
1:A:112:PHE:HB2	1:A:125:THR:HG22	1.99	0.44
1:B:241:LYS:O	1:B:245:THR:HB	2.18	0.44
1:B:72:TRP:O	1:B:182:LEU:HA	2.18	0.43
1:A:92:GLU:O	1:A:96:GLU:HG3	2.18	0.43
1:A:44:MSE:HE3	1:A:45:VAL:H	1.82	0.43
1:A:218:THR:O	1:A:222:LYS:HG3	2.18	0.43
1:A:13:TYR:HA	1:A:17:GLN:NE2	2.34	0.43
1:A:19:SER:OG	1:A:21:ALA:HB3	2.18	0.43
1:B:251:LEU:HB2	1:B:264:ILE:HG13	2.01	0.43
1:A:61:ILE:O	1:A:61:ILE:HG13	2.19	0.43
1:B:29:GLN:O	1:B:30:GLN:HB3	2.18	0.43
1:B:8:ALA:N	1:B:9:GLU:HB2	2.34	0.42
1:A:11:LYS:O	1:A:15:GLU:HG3	2.19	0.42
1:A:79:VAL:HG11	1:A:85:THR:HG22	2.02	0.42
1:B:95:GLU:HG3	3:B:387:HOH:O	2.18	0.42
3:A:336:HOH:O	1:B:28:HIS:HE1	2.03	0.42
1:B:246:GLN:O	1:B:268:LYS:CE	2.68	0.42
1:A:249:GLU:CB	1:A:266:GLN:HG2	2.47	0.41
1:A:144:LYS:O	1:A:145:GLU:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:HIS:CD2	1:B:69:ARG:HB2	2.55	0.41
1:A:39:SER:HB3	1:A:78:PHE:CE1	2.56	0.41
1:A:217:ILE:HG13	1:A:241:LYS:HG3	2.01	0.41
1:B:112:PHE:HB2	1:B:125:THR:HG22	2.03	0.41
1:A:212:GLY:O	1:A:213:LYS:HB2	2.21	0.41
1:A:241:LYS:O	1:A:245:THR:HB	2.20	0.40
1:B:44:MSE:HG2	1:B:89:VAL:HG13	2.04	0.40
1:A:4:PHE:CA	1:A:5:ALA:HB3	2.51	0.40

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	255/273 (93%)	239 (94%)	14 (6%)	2 (1%)	24	21
1	B	252/273 (92%)	236 (94%)	12 (5%)	4 (2%)	12	7
All	All	507/546 (93%)	475 (94%)	26 (5%)	6 (1%)	16	11

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	ALA
1	A	21	ALA
1	B	9	GLU
1	B	65	GLY
1	B	140	GLY
1	B	246	GLN

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	227/238 (95%)	210 (92%)	17 (8%)	17	16
1	B	226/238 (95%)	214 (95%)	12 (5%)	28	30
All	All	453/476 (95%)	424 (94%)	29 (6%)	22	21

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LYS
1	A	55	GLN
1	A	81	ARG
1	A	101	ILE
1	A	104	GLU
1	A	135	GLU
1	A	138	ILE
1	A	150	ASN
1	A	160	LEU
1	A	164	ASP
1	A	177	LEU
1	A	200	LYS
1	A	213	LYS
1	A	214	ASP
1	A	242	LYS
1	A	245	THR
1	A	263	LYS
1	B	9	GLU
1	B	29	GLN
1	B	30	GLN
1	B	81	ARG
1	B	82	ASN
1	B	132	ILE
1	B	192	LYS
1	B	202	GLU
1	B	213	LYS
1	B	253	GLU

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Mol	Chain	Res	Type
1	B	262	SER
1	B	263	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	17	GLN
1	A	62	GLN
1	A	80	ASN
1	A	108	GLN
1	A	147	HIS
1	A	150	ASN
1	A	154	HIS
1	A	157	HIS
1	A	206	GLN
1	A	266	GLN
1	B	66	HIS
1	B	70	ASN
1	B	82	ASN
1	B	108	GLN
1	B	162	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 [i](#)

1 ligand is 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	GOL	A	301	-	5,5,5	0.55	0	5,5,5	1.21	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
2	GOL	A	301	-	-	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.

No monomer is involved in short contacts.

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	256/273 (93%)	1.28	66 (25%)  	43, 59, 70, 75	0
1	B	253/273 (92%)	1.21	50 (19%)  	35, 49, 63, 92	0
All	All	509/546 (93%)	1.25	116 (22%)  	35, 54, 68, 92	0

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	5	ALA	10.9
1	B	35	TYR	8.8
1	B	6	SER	8.1
1	A	265	TYR	8.1
1	A	248	PHE	7.3
1	A	238	SER	6.5
1	A	213	LYS	6.3
1	B	13	TYR	5.2
1	A	251	LEU	5.1
1	B	251	LEU	5.0
1	B	45	VAL	5.0
1	A	4	PHE	4.8
1	B	190	ILE	4.8
1	B	47	LEU	4.6
1	B	109	LEU	4.6
1	A	109	LEU	4.6
1	B	7	LYS	4.4
1	A	243	ALA	4.3
1	A	249	GLU	4.3
1	B	189	ILE	4.3
1	B	4	PHE	4.3
1	A	267	LEU	4.2
1	B	129	LEU	4.1
1	A	235	ILE	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	252	GLY	4.0
1	A	3	GLN	4.0
1	B	126	VAL	4.0
1	A	126	VAL	4.0
1	B	269	THR	4.0
1	A	245	THR	4.0
1	B	193	ALA	4.0
1	B	112	PHE	3.9
1	A	189	ILE	3.9
1	A	250	GLU	3.8
1	A	264	ILE	3.8
1	B	74	LEU	3.6
1	A	129	LEU	3.6
1	B	46	LEU	3.6
1	B	128	TYR	3.6
1	A	212	GLY	3.5
1	B	194	PHE	3.5
1	A	242	LYS	3.4
1	A	111	SER	3.4
1	B	227	PHE	3.4
1	A	237	HIS	3.4
1	A	74	LEU	3.4
1	B	196	ARG	3.4
1	B	252	GLY	3.3
1	A	127	SER	3.3
1	B	127	SER	3.3
1	A	217	ILE	3.2
1	B	8	ALA	3.2
1	B	197	VAL	3.2
1	B	58	VAL	3.1
1	A	247	TYR	3.1
1	A	45	VAL	3.1
1	A	190	ILE	3.1
1	A	40	LEU	3.0
1	B	110	HIS	3.0
1	A	266	GLN	3.0
1	B	158	ILE	3.0
1	A	262	SER	3.0
1	A	112	PHE	2.9
1	A	218	THR	2.9
1	B	130	ALA	2.9
1	A	128	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	108	GLN	2.8
1	A	136	PRO	2.8
1	A	104	GLU	2.8
1	A	125	THR	2.7
1	B	111	SER	2.7
1	B	124	VAL	2.7
1	B	207	VAL	2.7
1	A	8	ALA	2.7
1	A	239	ASN	2.7
1	B	125	THR	2.7
1	A	47	LEU	2.7
1	B	192	LYS	2.7
1	A	124	VAL	2.7
1	A	263	LYS	2.6
1	A	9	GLU	2.6
1	B	14	TYR	2.5
1	A	75	PRO	2.5
1	A	100	VAL	2.5
1	A	196	ARG	2.5
1	B	12	ASN	2.5
1	B	108	GLN	2.5
1	A	123	VAL	2.4
1	B	10	GLU	2.4
1	A	203	HIS	2.4
1	A	46	LEU	2.4
1	B	160	LEU	2.4
1	A	42	VAL	2.4
1	B	249	GLU	2.3
1	B	139	ALA	2.3
1	A	110	HIS	2.3
1	A	236	ASP	2.3
1	A	60	LEU	2.3
1	B	191	ILE	2.3
1	B	60	LEU	2.3
1	A	197	VAL	2.2
1	A	154	HIS	2.2
1	B	151	LEU	2.2
1	B	9	GLU	2.2
1	B	29	GLN	2.2
1	A	214	ASP	2.2
1	A	234	SER	2.1
1	A	231	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	215	PHE	2.1
1	B	56	LEU	2.1
1	A	156	GLN	2.1
1	A	33	PRO	2.1
1	A	21	ALA	2.1
1	B	264	ILE	2.1
1	A	58	VAL	2.1
1	A	216	THR	2.1

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	A	301	6/6	0.92	0.20	-0.60	39,40,45,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.