



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 10:30 pm GMT

PDB ID : 4AC8
Title : R2-like ligand binding Mn-Fe oxidase from *M. tuberculosis* with an organized C-terminal helix
Authors : Andersson, C.S.; Berthold, C.L.; Hogbom, M.
Deposited on : 2011-12-14
Resolution : 2.75 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

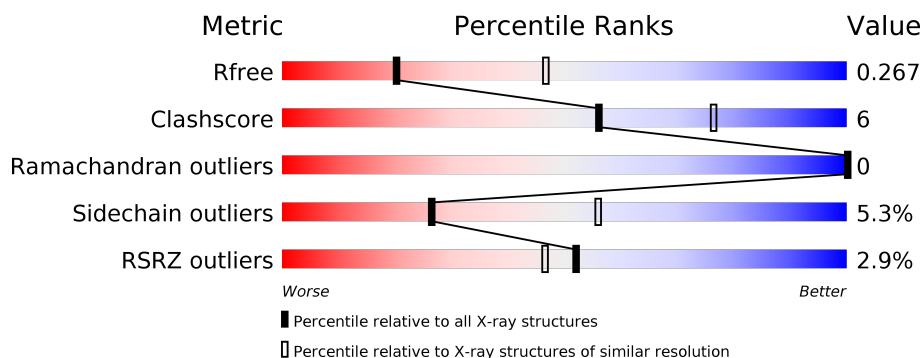
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	3666 (2.80-2.72)
Clashscore	112137	4174 (2.80-2.72)
Ramachandran outliers	110173	4103 (2.80-2.72)
Sidechain outliers	110143	4106 (2.80-2.72)
RSRZ outliers	101464	3697 (2.80-2.72)

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	323	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 15%, green 79%, grey 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 79% 15% • • </div> </div>
1	B	323	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 14%, green 80%, grey 4%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 80% 14% • • </div> </div>
1	C	323	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 5%, orange 1%, yellow 12%, green 82%, grey 3%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 5% 82% 12% • • </div> </div>
1	D	323	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 4%, orange 1%, yellow 14%, green 81%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 4% 81% 14% • • </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MYR	A	600	-	-	-	X
4	MYR	B	600	-	-	-	X
4	MYR	C	600	-	-	-	X
4	MYR	D	600	-	-	-	X
6	GOL	A	1314	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 10107 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 R2-LIKE LIGAND BINDING OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	311	Total	C	N	O	S	0	0	0
			2491	1569	437	472	13			
1	B	309	Total	C	N	O	S	0	0	0
			2481	1563	435	470	13			
1	C	309	Total	C	N	O	S	0	0	0
			2481	1563	435	470	13			
1	D	310	Total	C	N	O	S	0	0	0
			2486	1566	436	471	13			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	EXPRESSION TAG	UNP P96416
A	-7	ALA	-	EXPRESSION TAG	UNP P96416
A	-6	HIS	-	EXPRESSION TAG	UNP P96416
A	-5	HIS	-	EXPRESSION TAG	UNP P96416
A	-4	HIS	-	EXPRESSION TAG	UNP P96416
A	-3	HIS	-	EXPRESSION TAG	UNP P96416
A	-2	HIS	-	EXPRESSION TAG	UNP P96416
A	-1	HIS	-	EXPRESSION TAG	UNP P96416
A	0	GLY	-	EXPRESSION TAG	UNP P96416
B	-8	MET	-	EXPRESSION TAG	UNP P96416
B	-7	ALA	-	EXPRESSION TAG	UNP P96416
B	-6	HIS	-	EXPRESSION TAG	UNP P96416
B	-5	HIS	-	EXPRESSION TAG	UNP P96416
B	-4	HIS	-	EXPRESSION TAG	UNP P96416
B	-3	HIS	-	EXPRESSION TAG	UNP P96416
B	-2	HIS	-	EXPRESSION TAG	UNP P96416
B	-1	HIS	-	EXPRESSION TAG	UNP P96416
B	0	GLY	-	EXPRESSION TAG	UNP P96416
C	-8	MET	-	EXPRESSION TAG	UNP P96416
C	-7	ALA	-	EXPRESSION TAG	UNP P96416
C	-6	HIS	-	EXPRESSION TAG	UNP P96416

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	HIS	-	EXPRESSION TAG	UNP P96416
C	-4	HIS	-	EXPRESSION TAG	UNP P96416
C	-3	HIS	-	EXPRESSION TAG	UNP P96416
C	-2	HIS	-	EXPRESSION TAG	UNP P96416
C	-1	HIS	-	EXPRESSION TAG	UNP P96416
C	0	GLY	-	EXPRESSION TAG	UNP P96416
D	-8	MET	-	EXPRESSION TAG	UNP P96416
D	-7	ALA	-	EXPRESSION TAG	UNP P96416
D	-6	HIS	-	EXPRESSION TAG	UNP P96416
D	-5	HIS	-	EXPRESSION TAG	UNP P96416
D	-4	HIS	-	EXPRESSION TAG	UNP P96416
D	-3	HIS	-	EXPRESSION TAG	UNP P96416
D	-2	HIS	-	EXPRESSION TAG	UNP P96416
D	-1	HIS	-	EXPRESSION TAG	UNP P96416
D	0	GLY	-	EXPRESSION TAG	UNP P96416

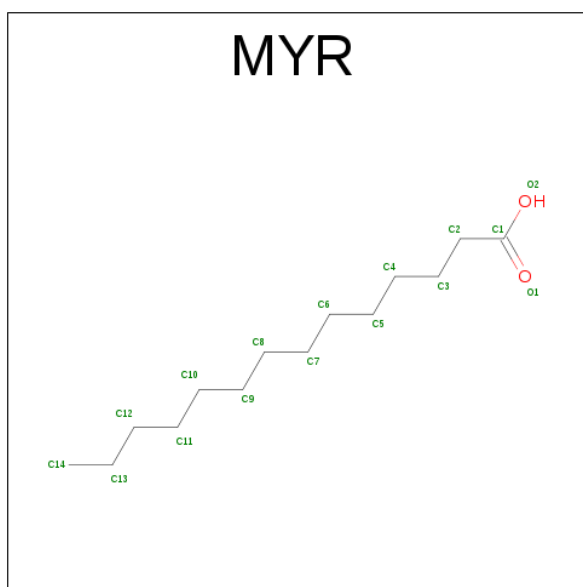
- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Fe 1 1	0	0
2	A	1	Total Fe 1 1	0	0
2	D	1	Total Fe 1 1	0	0
2	C	1	Total Fe 1 1	0	0

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mn 1 1	0	0
3	A	1	Total Mn 1 1	0	0
3	D	1	Total Mn 1 1	0	0
3	C	1	Total Mn 1 1	0	0

- Molecule 4 is MYRISTIC ACID (three-letter code: MYR) (formula: C₁₄H₂₈O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			16	14	2		
4	B	1	Total	C	O	0	0
			16	14	2		
4	C	1	Total	C	O	0	0
			16	14	2		
4	D	1	Total	C	O	0	0
			16	14	2		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Ca	0	0
			1	1		
5	A	1	Total	Ca	0	0
			1	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

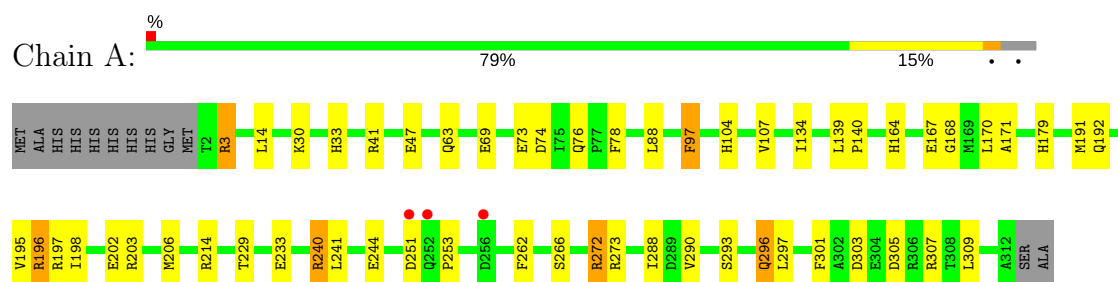
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	33	Total	O	0	0
			33	33		
7	B	26	Total	O	0	0
			26	26		
7	C	9	Total	O	0	0
			9	9		
7	D	20	Total	O	0	0
			20	20		

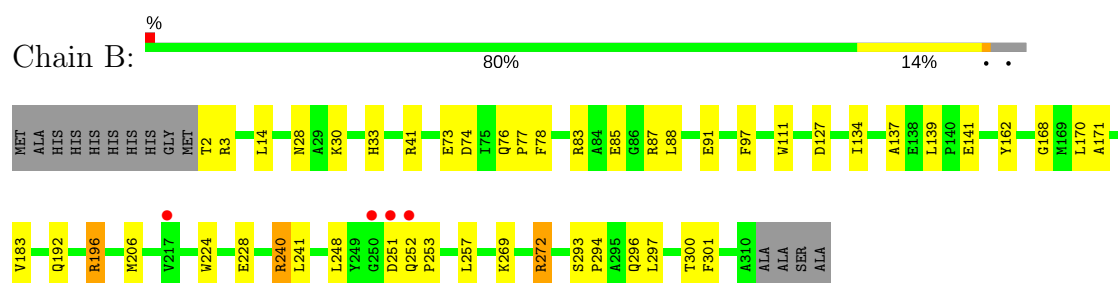
3 Residue-property plots

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

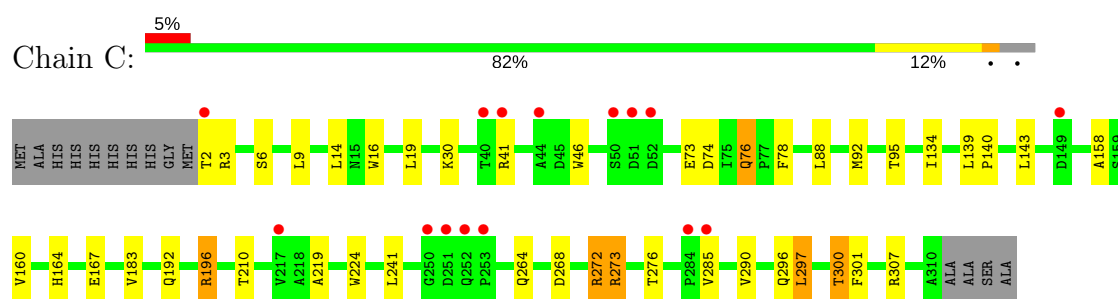
• Molecule 1: R2-LIKE LIGAND BINDING OXIDASE



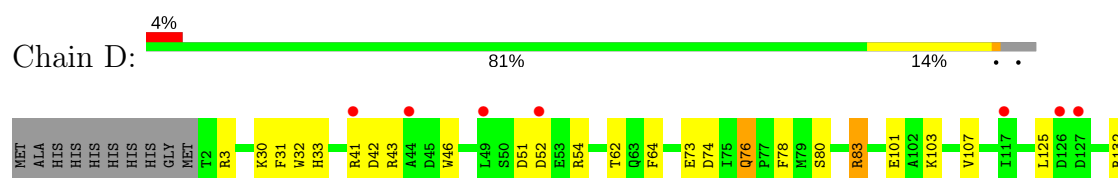
• Molecule 1: R2-LIKE LIGAND BINDING OXIDASE

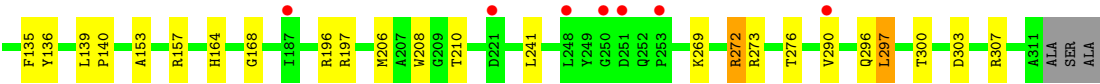


• Molecule 1: R2-LIKE LIGAND BINDING OXIDASE



• Molecule 1: R2-LIKE LIGAND BINDING OXIDASE





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	109.99Å 210.85Å 139.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.72 – 2.75 36.72 – 2.75	Depositor EDS
% Data completeness (in resolution range)	92.1 (36.72-2.75) 92.1 (36.72-2.75)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.22 (at 2.77Å)	Xtrriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.220 , 0.268 0.220 , 0.267	Depositor DCC
R_{free} test set	1963 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	32.8	Xtrriage
Anisotropy	0.335	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.36$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10107	wwPDB-VP
Average B, all atoms (Å ²)	31.0	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 55.97 % 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 2.9298e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: MYR, GOL, CA, MN, FE

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	0.53	0/2551	0.59	0/3460
1	B	0.54	2/2541 (0.1%)	0.59	0/3446
1	C	0.53	3/2541 (0.1%)	0.57	0/3446
1	D	0.53	3/2546 (0.1%)	0.58	0/3453
All	All	0.53	8/10179 (0.1%)	0.58	0/13805

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	208	TRP	CD2-CE2	5.22	1.47	1.41
1	B	224	TRP	CD2-CE2	5.15	1.47	1.41
1	D	46	TRP	CD2-CE2	5.14	1.47	1.41
1	C	224	TRP	CD2-CE2	5.11	1.47	1.41
1	D	32	TRP	CD2-CE2	5.07	1.47	1.41
1	C	46	TRP	CD2-CE2	5.04	1.47	1.41
1	C	16	TRP	CD2-CE2	5.01	1.47	1.41
1	B	111	TRP	CD2-CE2	5.01	1.47	1.41

There are no bond angle outliers.

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	2491	0	2376	35	0
1	B	2481	0	2366	26	0
1	C	2481	0	2366	29	0
1	D	2486	0	2371	32	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
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
4	A	16	0	27	3	0
4	B	16	0	27	1	0
4	C	16	0	27	1	0
4	D	16	0	27	2	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	6	0	8	0	0
7	A	33	0	0	1	0
7	B	26	0	0	1	0
7	C	9	0	0	0	0
7	D	20	0	0	2	0
All	All	10107	0	9595	114	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 6.

All (114) 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:D:83:ARG:HG3	1:D:83:ARG:HH11	1.07	1.11
1:C:192:GLN:O	1:C:196:ARG:HG2	1.74	0.86
1:D:83:ARG:HG3	1:D:83:ARG:NH1	1.87	0.86
1:C:73:GLU:O	1:C:76:GLN:HG2	1.83	0.79
1:C:276:THR:HG23	1:C:297:LEU:HD12	1.66	0.78
1:D:73:GLU:O	1:D:76:GLN:HG2	1.85	0.77
1:B:192:GLN:O	1:B:196:ARG:HG2	1.86	0.76
1:A:139:LEU:HB3	1:A:140:PRO:HD3	1.68	0.75
1:D:83:ARG:HH11	1:D:83:ARG:CG	1.94	0.74
1:A:179:HIS:CE1	1:A:309:LEU:HD12	2.26	0.70
1:C:297:LEU:HD13	1:C:301:PHE:CE2	2.26	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:LEU:HD21	1:A:88:LEU:HD23	1.74	0.69
1:A:192:GLN:O	1:A:196:ARG:HG2	1.93	0.67
1:B:85:GLU:HB3	1:B:87:ARG:HG3	1.78	0.66
1:C:210:THR:CG2	1:C:276:THR:HG22	2.27	0.65
1:A:3:ARG:HD3	7:A:2001:HOH:O	1.96	0.65
1:C:167:GLU:HG2	4:C:600:MYR:O2	1.95	0.64
1:D:51:ASP:OD1	1:D:54:ARG:NH2	2.32	0.62
1:C:74:ASP:OD2	1:D:3:ARG:NH2	2.33	0.61
1:C:290:VAL:O	1:C:290:VAL:HG12	2.00	0.61
1:C:219:ALA:HB2	1:C:285:VAL:HG11	1.82	0.61
1:C:290:VAL:O	1:C:290:VAL:CG1	2.50	0.59
1:C:210:THR:HG23	1:C:276:THR:HG22	1.85	0.58
1:A:134:ILE:HD13	1:A:170:LEU:HD11	1.85	0.57
1:A:191:MET:O	1:A:195:VAL:HG23	2.05	0.57
1:C:14:LEU:HD21	1:C:88:LEU:HD23	1.87	0.57
1:A:251:ASP:O	1:A:253:PRO:HD3	2.06	0.56
1:C:164:HIS:ND1	1:C:273:ARG:HD3	2.21	0.56
1:D:153:ALA:O	1:D:157:ARG:HG3	2.07	0.55
1:B:171:ALA:HB2	4:B:600:MYR:H22	1.87	0.55
1:A:171:ALA:HB2	4:A:600:MYR:H22	1.89	0.54
1:B:73:GLU:O	1:B:76:GLN:HG2	2.08	0.54
1:C:74:ASP:CG	1:D:3:ARG:HH22	2.12	0.53
1:B:127:ASP:HB3	1:B:248:LEU:HD21	1.89	0.53
1:A:240:ARG:O	1:A:244:GLU:HG3	2.09	0.53
1:A:290:VAL:O	1:A:290:VAL:HG12	2.09	0.52
1:A:168:GLY:HA2	1:A:206:MET:CE	2.40	0.52
1:C:92:MET:O	1:C:95:THR:OG1	2.22	0.52
1:D:164:HIS:ND1	1:D:273:ARG:HD3	2.25	0.52
1:A:305:ASP:O	1:A:309:LEU:HD23	2.09	0.51
1:A:167:GLU:HG2	4:A:600:MYR:O2	2.11	0.51
1:A:63:GLN:OE1	1:A:241:LEU:HD21	2.10	0.51
1:D:276:THR:HG23	1:D:297:LEU:HD12	1.93	0.51
1:B:168:GLY:HA2	1:B:206:MET:HE3	1.92	0.51
1:B:14:LEU:HD21	1:B:88:LEU:HD23	1.93	0.50
1:D:135:PHE:CZ	4:D:600:MYR:H62	2.47	0.50
1:B:293:SER:HA	1:B:296:GLN:HB2	1.94	0.50
1:C:210:THR:HG21	1:C:276:THR:HG22	1.93	0.50
1:C:19:LEU:C	1:C:19:LEU:HD13	2.32	0.50
1:A:293:SER:HA	1:A:296:GLN:CG	2.42	0.49
1:B:183:VAL:HG22	1:B:192:GLN:NE2	2.28	0.49
1:A:69:GLU:O	1:A:73:GLU:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:HIS:O	1:A:107:VAL:HG12	2.13	0.49
1:D:303:ASP:OD2	1:D:307:ARG:NH1	2.46	0.48
1:D:290:VAL:O	1:D:290:VAL:CG1	2.61	0.48
1:C:134:ILE:HD12	1:C:241:LEU:HD12	1.96	0.48
1:A:74:ASP:OD2	1:B:3:ARG:NH2	2.46	0.47
1:A:33:HIS:CD2	1:B:28:ASN:O	2.67	0.47
1:C:183:VAL:HG22	1:C:192:GLN:NE2	2.30	0.47
1:A:3:ARG:NH2	1:B:74:ASP:OD2	2.48	0.47
1:D:168:GLY:HA2	1:D:206:MET:HE3	1.95	0.47
1:A:168:GLY:HA2	1:A:206:MET:HE3	1.98	0.46
1:A:229:THR:O	1:A:233:GLU:HG3	2.16	0.46
1:A:296:GLN:H	1:A:296:GLN:HG2	1.62	0.45
1:B:240:ARG:HH11	1:B:240:ARG:HG3	1.81	0.45
1:D:210:THR:CG2	1:D:276:THR:HG22	2.47	0.45
1:C:297:LEU:HD13	1:C:301:PHE:CZ	2.52	0.45
1:D:296:GLN:O	1:D:300:THR:HG23	2.17	0.44
1:B:253:PRO:HG2	1:B:257:LEU:HB2	1.98	0.44
1:A:293:SER:HA	1:A:296:GLN:HG3	1.98	0.44
1:B:134:ILE:HD13	1:B:170:LEU:HD11	1.99	0.44
1:D:101:GLU:OE1	1:D:101:GLU:HA	2.18	0.44
1:B:33:HIS:HB3	7:B:2006:HOH:O	2.17	0.44
1:D:31:PHE:CE1	1:D:103:LYS:HE2	2.52	0.44
1:D:269:LYS:HA	1:D:272:ARG:HD2	2.00	0.44
1:B:74:ASP:O	1:B:77:PRO:HD2	2.18	0.44
1:D:269:LYS:HA	1:D:269:LYS:HD3	1.88	0.44
1:D:290:VAL:O	1:D:290:VAL:HG12	2.17	0.43
1:B:139:LEU:HD11	1:B:162:TYR:CD2	2.54	0.43
1:A:73:GLU:HG2	1:B:91:GLU:OE2	2.19	0.43
1:C:139:LEU:HB3	1:C:140:PRO:HD3	2.01	0.43
1:D:139:LEU:HB3	1:D:140:PRO:CD	2.48	0.43
1:D:241:LEU:HA	7:D:2012:HOH:O	2.18	0.43
1:D:62:THR:HG22	1:D:125:LEU:HD21	2.00	0.43
1:B:251:ASP:O	1:B:253:PRO:HD3	2.18	0.43
1:D:33:HIS:HB3	7:D:2002:HOH:O	2.18	0.43
1:B:272:ARG:HG3	1:B:301:PHE:CZ	2.54	0.43
1:A:104:HIS:CD2	1:A:198:ILE:HG22	2.54	0.42
1:D:135:PHE:HZ	4:D:600:MYR:H62	1.84	0.42
1:B:137:ALA:O	1:B:141:GLU:HB2	2.20	0.42
1:B:293:SER:N	1:B:294:PRO:CD	2.83	0.42
1:D:132:ARG:O	1:D:136:TYR:HB2	2.20	0.42
1:C:143:LEU:HD13	1:C:158:ALA:HB1	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:6:SER:HB2	1:C:9:LEU:HG	2.02	0.41
1:C:3:ARG:NH2	1:D:74:ASP:OD2	2.51	0.41
1:D:139:LEU:HB3	1:D:140:PRO:HD3	2.02	0.41
1:A:196:ARG:H	1:A:196:ARG:HG2	1.72	0.41
1:B:269:LYS:HA	1:B:269:LYS:HD3	1.93	0.41
1:B:228:GLU:OE2	1:C:307:ARG:NH2	2.54	0.41
1:B:196:ARG:HG2	1:B:196:ARG:H	1.77	0.41
1:C:268:ASP:O	1:C:272:ARG:HB3	2.21	0.41
1:C:296:GLN:O	1:C:300:THR:HG23	2.20	0.41
1:D:210:THR:HG23	1:D:276:THR:HG22	2.03	0.41
1:A:97:PHE:CD1	1:A:97:PHE:C	2.93	0.41
1:A:164:HIS:HD1	1:A:273:ARG:HD3	1.85	0.41
1:A:272:ARG:HG3	1:A:301:PHE:CZ	2.56	0.41
1:D:276:THR:HG23	1:D:297:LEU:CD1	2.50	0.41
1:A:303:ASP:OD1	1:A:307:ARG:NH1	2.53	0.40
1:A:76:GLN:HG2	1:A:76:GLN:H	1.72	0.40
1:A:262:PHE:CD2	4:A:600:MYR:H143	2.56	0.40
1:C:160:VAL:HA	1:C:164:HIS:HD2	1.87	0.40
1:C:19:LEU:O	1:C:19:LEU:HD13	2.22	0.40
1:A:214:ARG:HB3	1:A:288:ILE:HD13	2.03	0.40
1:D:168:GLY:HA2	1:D:206:MET:CE	2.52	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	309/323 (96%)	300 (97%)	9 (3%)	0	100	100
1	B	307/323 (95%)	295 (96%)	12 (4%)	0	100	100
1	C	307/323 (95%)	300 (98%)	7 (2%)	0	100	100
1	D	308/323 (95%)	300 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1231/1292 (95%)	1195 (97%)	36 (3%)	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	254/263 (97%)	239 (94%)	15 (6%)	23	51
1	B	254/263 (97%)	241 (95%)	13 (5%)	28	58
1	C	254/263 (97%)	243 (96%)	11 (4%)	33	64
1	D	254/263 (97%)	239 (94%)	15 (6%)	23	51
All	All	1016/1052 (97%)	962 (95%)	54 (5%)	26	56

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	30	LYS
1	A	41	ARG
1	A	47	GLU
1	A	78	PHE
1	A	97	PHE
1	A	196	ARG
1	A	197	ARG
1	A	202	GLU
1	A	203	ARG
1	A	240	ARG
1	A	266	SER
1	A	272	ARG
1	A	296	GLN
1	A	297	LEU
1	B	2	THR
1	B	30	LYS

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Mol	Chain	Res	Type
1	B	41	ARG
1	B	78	PHE
1	B	83	ARG
1	B	97	PHE
1	B	196	ARG
1	B	240	ARG
1	B	241	LEU
1	B	252	GLN
1	B	272	ARG
1	B	297	LEU
1	B	300	THR
1	C	2	THR
1	C	30	LYS
1	C	41	ARG
1	C	76	GLN
1	C	78	PHE
1	C	196	ARG
1	C	264	GLN
1	C	272	ARG
1	C	273	ARG
1	C	297	LEU
1	C	300	THR
1	D	30	LYS
1	D	41	ARG
1	D	42	ASP
1	D	43	ARG
1	D	52	ASP
1	D	64	PHE
1	D	76	GLN
1	D	78	PHE
1	D	80	SER
1	D	83	ARG
1	D	107	VAL
1	D	196	ARG
1	D	197	ARG
1	D	272	ARG
1	D	297	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	HIS

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Mol	Chain	Res	Type
1	A	179	HIS
1	A	296	GLN
1	B	192	GLN
1	B	252	GLN
1	B	264	GLN
1	C	192	GLN
1	C	264	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](#)

Of 15 ligands modelled in this entry, 10 are monoatomic - leaving 5 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	$\# Z > 2$
6	GOL	A	1314	-	5,5,5	0.37	0	5,5,5	0.12	0
4	MYR	A	600	3,2	12,15,15	0.26	0	11,15,15	0.60	0
4	MYR	B	600	3,2	12,15,15	0.26	0	11,15,15	0.63	0
4	MYR	C	600	3,2	12,15,15	0.24	0	11,15,15	0.55	0
4	MYR	D	600	3,2	12,15,15	0.25	0	11,15,15	0.56	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	GOL	A	1314	-	-	0/4/4/4	0/0/0/0
4	MYR	A	600	3,2	-	0/11/13/13	0/0/0/0
4	MYR	B	600	3,2	-	0/11/13/13	0/0/0/0
4	MYR	C	600	3,2	-	0/11/13/13	0/0/0/0
4	MYR	D	600	3,2	-	0/11/13/13	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.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	600	MYR	3	0
4	B	600	MYR	1	0
4	C	600	MYR	1	0
4	D	600	MYR	2	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	311/323 (96%)	-0.22	3 (0%) 82 80	15, 25, 49, 58	0
1	B	309/323 (95%)	-0.19	4 (1%) 77 74	15, 24, 45, 56	0
1	C	309/323 (95%)	0.22	15 (4%) 30 24	19, 35, 54, 70	0
1	D	310/323 (95%)	0.17	14 (4%) 34 28	18, 32, 55, 69	0
All	All	1239/1292 (95%)	-0.00	36 (2%) 52 46	15, 30, 52, 70	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	251	ASP	4.1
1	A	252	GLN	4.0
1	C	52	ASP	3.9
1	A	251	ASP	3.7
1	D	41	ARG	3.7
1	D	250	GLY	3.7
1	C	250	GLY	3.6
1	D	251	ASP	3.1
1	C	251	ASP	3.1
1	C	2	THR	3.1
1	D	44	ALA	3.1
1	D	127	ASP	3.0
1	C	40	THR	3.0
1	C	41	ARG	2.8
1	C	284	PRO	2.7
1	C	285	VAL	2.6
1	A	256	ASP	2.6
1	D	248	LEU	2.6
1	B	252	GLN	2.6
1	C	252	GLN	2.6
1	D	187	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	51	ASP	2.5
1	B	217	VAL	2.4
1	C	50	SER	2.3
1	C	217	VAL	2.3
1	D	126	ASP	2.3
1	D	253	PRO	2.3
1	C	44	ALA	2.3
1	B	250	GLY	2.1
1	C	149	ASP	2.1
1	C	253	PRO	2.1
1	D	52	ASP	2.1
1	D	49	LEU	2.0
1	D	117	ILE	2.0
1	D	221	ASP	2.0
1	D	290	VAL	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
4	MYR	B	600	16/16	0.89	0.26	4.08	29,32,35,36	0
4	MYR	D	600	16/16	0.94	0.33	3.91	31,34,41,42	0
4	MYR	C	600	16/16	0.95	0.29	3.65	31,36,48,49	0
6	GOL	A	1314	6/6	0.79	0.26	3.52	39,43,43,44	0
4	MYR	A	600	16/16	0.92	0.21	2.28	20,21,23,23	0
2	FE	B	500	1/1	0.93	0.13	-0.49	28,28,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	MN	B	501	1/1	0.96	0.13	-0.95	18,18,18,18	0
2	FE	C	500	1/1	0.97	0.11	-1.51	33,33,33,33	0
3	MN	C	501	1/1	0.99	0.10	-1.61	31,31,31,31	0
3	MN	A	501	1/1	0.99	0.10	-2.11	18,18,18,18	0
2	FE	A	500	1/1	0.99	0.10	-2.27	25,25,25,25	0
2	FE	D	500	1/1	0.98	0.11	-3.22	31,31,31,31	0
3	MN	D	501	1/1	0.98	0.13	-3.75	29,29,29,29	0
5	CA	A	1313	1/1	0.98	0.15	-	29,29,29,29	0
5	CA	B	1311	1/1	0.96	0.09	-	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.