



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 01:04 am GMT

PDB ID : 4Q3Q
Title : Crystal structure of Schistosoma mansoni arginase in complex with inhibitor ABH
Authors : Hai, Y.; Edwards, J.E.; Van Zandt, M.C.; Hoffmann, K.F.; Christianson, D.W.
Deposited on : 2014-04-12
Resolution : 2.00 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

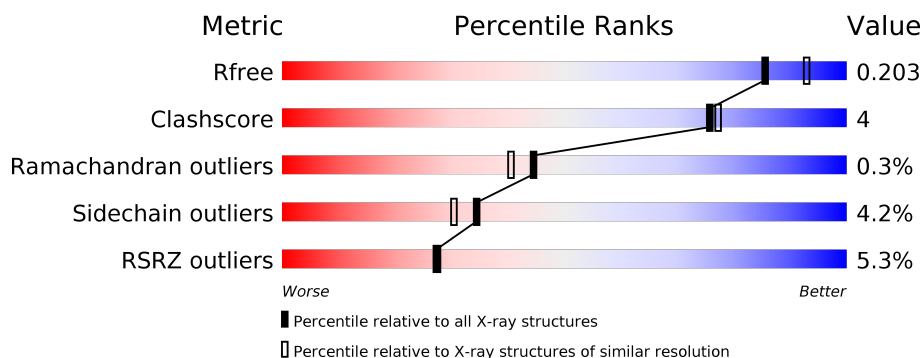
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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	385	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 1%, green 82%, yellow 6%, orange 2%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 82% • • 13% </div> </div>
1	B	385	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, green 1%, green 79%, yellow 6%, orange 2%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> 2% 79% 6% • 13% </div> </div>
1	C	385	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 1%, green 78%, yellow 8%, orange 2%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 78% 8% • 13% </div> </div>
1	D	385	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 15%, green 1%, green 74%, yellow 10%, orange 2%, grey 14%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> 15% 74% 10% • 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
2	MN	A	401	-	-	-	X
3	GOL	B	403	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11232 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 Arginase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	335	Total	C	N	O	S	0	0	0
			2571	1619	450	487	15			
1	B	335	Total	C	N	O	S	0	0	0
			2571	1619	450	487	15			
1	C	335	Total	C	N	O	S	0	0	0
			2569	1617	449	488	15			
1	D	330	Total	C	N	O	S	0	0	0
			2530	1595	441	479	15			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	EXPRESSION TAG	UNP Q6WVP6
A	-19	GLY	-	EXPRESSION TAG	UNP Q6WVP6
A	-18	SER	-	EXPRESSION TAG	UNP Q6WVP6
A	-17	SER	-	EXPRESSION TAG	UNP Q6WVP6
A	-16	HIS	-	EXPRESSION TAG	UNP Q6WVP6
A	-15	HIS	-	EXPRESSION TAG	UNP Q6WVP6
A	-14	HIS	-	EXPRESSION TAG	UNP Q6WVP6
A	-13	HIS	-	EXPRESSION TAG	UNP Q6WVP6
A	-12	HIS	-	EXPRESSION TAG	UNP Q6WVP6
A	-11	HIS	-	EXPRESSION TAG	UNP Q6WVP6
A	-10	SER	-	EXPRESSION TAG	UNP Q6WVP6
A	-9	SER	-	EXPRESSION TAG	UNP Q6WVP6
A	-8	GLY	-	EXPRESSION TAG	UNP Q6WVP6
A	-7	LEU	-	EXPRESSION TAG	UNP Q6WVP6
A	-6	VAL	-	EXPRESSION TAG	UNP Q6WVP6
A	-5	PRO	-	EXPRESSION TAG	UNP Q6WVP6
A	-4	ARG	-	EXPRESSION TAG	UNP Q6WVP6
A	-3	GLY	-	EXPRESSION TAG	UNP Q6WVP6
A	-2	SER	-	EXPRESSION TAG	UNP Q6WVP6
A	-1	HIS	-	EXPRESSION TAG	UNP Q6WVP6
A	0	MET	-	EXPRESSION TAG	UNP Q6WVP6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	MET	-	EXPRESSION TAG	UNP Q6WVP6
B	-19	GLY	-	EXPRESSION TAG	UNP Q6WVP6
B	-18	SER	-	EXPRESSION TAG	UNP Q6WVP6
B	-17	SER	-	EXPRESSION TAG	UNP Q6WVP6
B	-16	HIS	-	EXPRESSION TAG	UNP Q6WVP6
B	-15	HIS	-	EXPRESSION TAG	UNP Q6WVP6
B	-14	HIS	-	EXPRESSION TAG	UNP Q6WVP6
B	-13	HIS	-	EXPRESSION TAG	UNP Q6WVP6
B	-12	HIS	-	EXPRESSION TAG	UNP Q6WVP6
B	-11	HIS	-	EXPRESSION TAG	UNP Q6WVP6
B	-10	SER	-	EXPRESSION TAG	UNP Q6WVP6
B	-9	SER	-	EXPRESSION TAG	UNP Q6WVP6
B	-8	GLY	-	EXPRESSION TAG	UNP Q6WVP6
B	-7	LEU	-	EXPRESSION TAG	UNP Q6WVP6
B	-6	VAL	-	EXPRESSION TAG	UNP Q6WVP6
B	-5	PRO	-	EXPRESSION TAG	UNP Q6WVP6
B	-4	ARG	-	EXPRESSION TAG	UNP Q6WVP6
B	-3	GLY	-	EXPRESSION TAG	UNP Q6WVP6
B	-2	SER	-	EXPRESSION TAG	UNP Q6WVP6
B	-1	HIS	-	EXPRESSION TAG	UNP Q6WVP6
B	0	MET	-	EXPRESSION TAG	UNP Q6WVP6
C	-20	MET	-	EXPRESSION TAG	UNP Q6WVP6
C	-19	GLY	-	EXPRESSION TAG	UNP Q6WVP6
C	-18	SER	-	EXPRESSION TAG	UNP Q6WVP6
C	-17	SER	-	EXPRESSION TAG	UNP Q6WVP6
C	-16	HIS	-	EXPRESSION TAG	UNP Q6WVP6
C	-15	HIS	-	EXPRESSION TAG	UNP Q6WVP6
C	-14	HIS	-	EXPRESSION TAG	UNP Q6WVP6
C	-13	HIS	-	EXPRESSION TAG	UNP Q6WVP6
C	-12	HIS	-	EXPRESSION TAG	UNP Q6WVP6
C	-11	HIS	-	EXPRESSION TAG	UNP Q6WVP6
C	-10	SER	-	EXPRESSION TAG	UNP Q6WVP6
C	-9	SER	-	EXPRESSION TAG	UNP Q6WVP6
C	-8	GLY	-	EXPRESSION TAG	UNP Q6WVP6
C	-7	LEU	-	EXPRESSION TAG	UNP Q6WVP6
C	-6	VAL	-	EXPRESSION TAG	UNP Q6WVP6
C	-5	PRO	-	EXPRESSION TAG	UNP Q6WVP6
C	-4	ARG	-	EXPRESSION TAG	UNP Q6WVP6
C	-3	GLY	-	EXPRESSION TAG	UNP Q6WVP6
C	-2	SER	-	EXPRESSION TAG	UNP Q6WVP6
C	-1	HIS	-	EXPRESSION TAG	UNP Q6WVP6
C	0	MET	-	EXPRESSION TAG	UNP Q6WVP6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-20	MET	-	EXPRESSION TAG	UNP Q6WVP6
D	-19	GLY	-	EXPRESSION TAG	UNP Q6WVP6
D	-18	SER	-	EXPRESSION TAG	UNP Q6WVP6
D	-17	SER	-	EXPRESSION TAG	UNP Q6WVP6
D	-16	HIS	-	EXPRESSION TAG	UNP Q6WVP6
D	-15	HIS	-	EXPRESSION TAG	UNP Q6WVP6
D	-14	HIS	-	EXPRESSION TAG	UNP Q6WVP6
D	-13	HIS	-	EXPRESSION TAG	UNP Q6WVP6
D	-12	HIS	-	EXPRESSION TAG	UNP Q6WVP6
D	-11	HIS	-	EXPRESSION TAG	UNP Q6WVP6
D	-10	SER	-	EXPRESSION TAG	UNP Q6WVP6
D	-9	SER	-	EXPRESSION TAG	UNP Q6WVP6
D	-8	GLY	-	EXPRESSION TAG	UNP Q6WVP6
D	-7	LEU	-	EXPRESSION TAG	UNP Q6WVP6
D	-6	VAL	-	EXPRESSION TAG	UNP Q6WVP6
D	-5	PRO	-	EXPRESSION TAG	UNP Q6WVP6
D	-4	ARG	-	EXPRESSION TAG	UNP Q6WVP6
D	-3	GLY	-	EXPRESSION TAG	UNP Q6WVP6
D	-2	SER	-	EXPRESSION TAG	UNP Q6WVP6
D	-1	HIS	-	EXPRESSION TAG	UNP Q6WVP6
D	0	MET	-	EXPRESSION TAG	UNP Q6WVP6

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

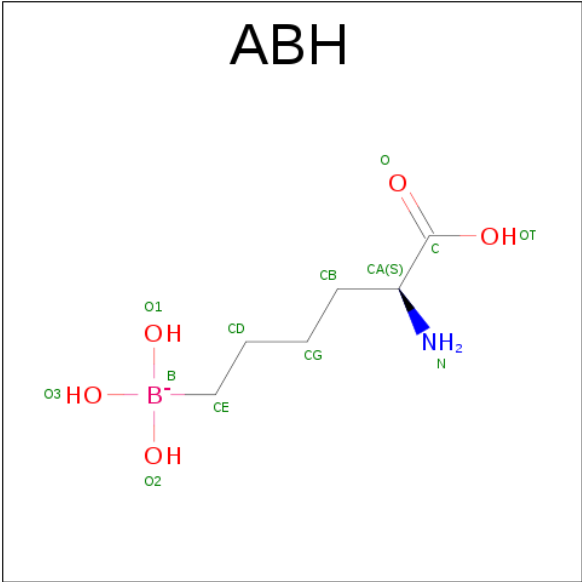
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Mn 2 2	0	0
2	A	2	Total Mn 2 2	0	0
2	D	2	Total Mn 2 2	0	0
2	C	2	Total Mn 2 2	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is 2(S)-AMINO-6-BORONOHEXOIC ACID (three-letter code: ABH) (formula: C₆H₁₅BNO₅).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	B	C	N	O	0	0
			13	1	6	1	5		
4	B	1	Total	B	C	N	O	0	0
			13	1	6	1	5		
4	C	1	Total	B	C	N	O	0	0
			13	1	6	1	5		
4	D	1	Total	B	C	N	O	0	0
			13	1	6	1	5		

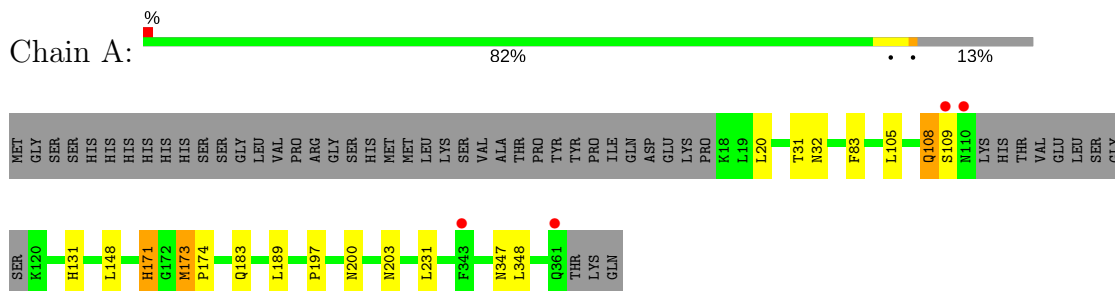
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	299	Total	O	0	0
			299	299		
5	B	285	Total	O	0	0
			285	285		
5	C	229	Total	O	0	0
			229	229		
5	D	82	Total	O	0	0
			82	82		

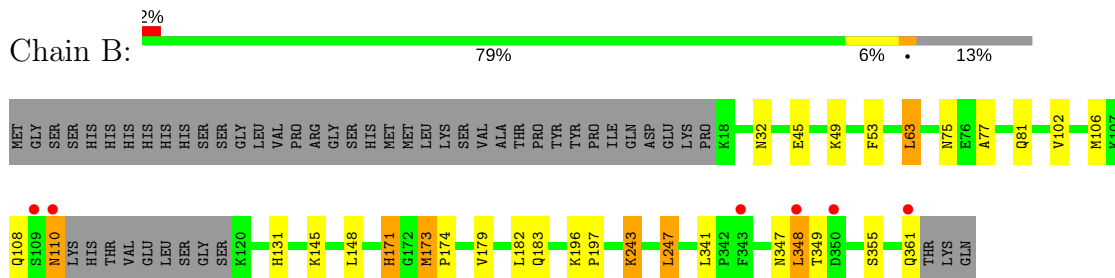
3 Residue-property plots

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 ($\text{RSRZ} > 2$). 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.

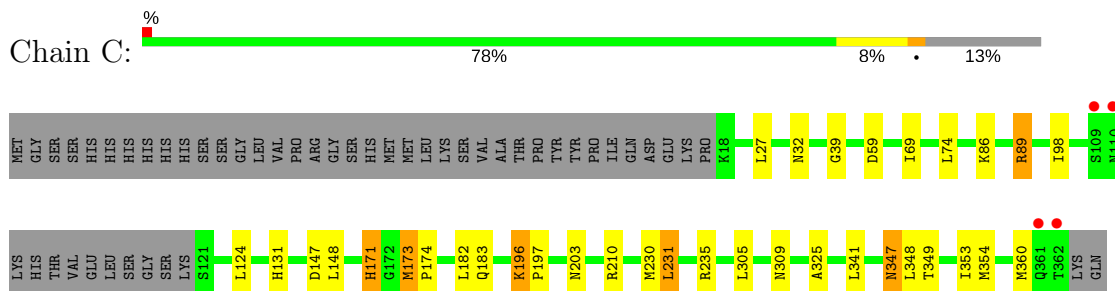
- Molecule 1: Arginase



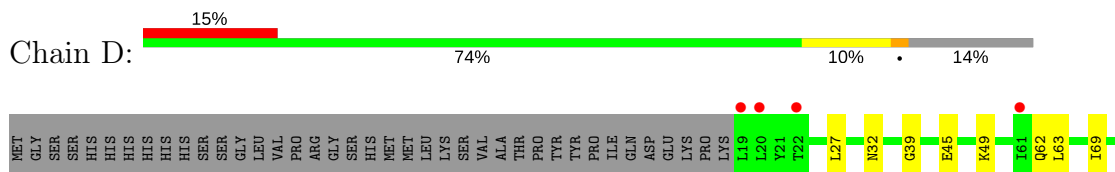
- Molecule 1: Arginase

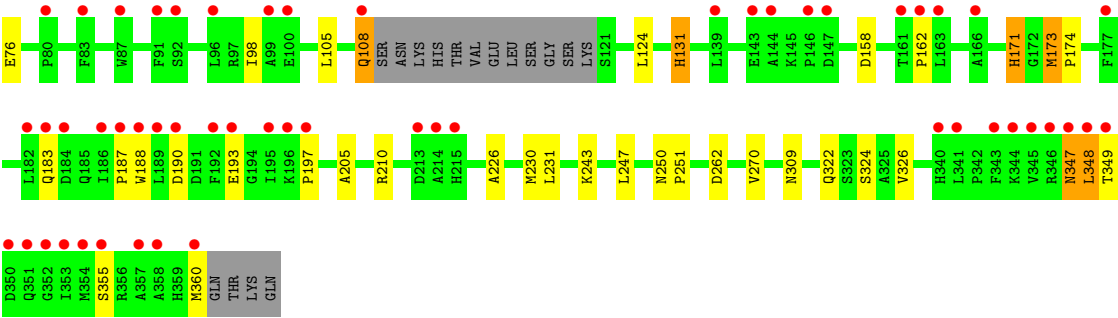


- Molecule 1: Arginase



- Molecule 1: Arginase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	178.22Å 178.22Å 178.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.43 – 2.00 49.43 – 2.00	Depositor EDS
% Data completeness (in resolution range)	93.7 (49.43-2.00) 100.0 (49.43-2.00)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.69 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.168 , 0.202 0.168 , 0.203	Depositor DCC
R_{free} test set	6331 reflections (5.01%)	DCC
Wilson B-factor (Å ²)	24.7	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 58.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.022 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11232	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.73% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.45	0/2618	0.56	0/3547
1	B	0.43	0/2618	0.55	0/3547
1	C	0.37	0/2616	0.54	0/3546
1	D	0.33	0/2577	0.45	0/3494
All	All	0.39	0/10429	0.53	0/14134

There are no bond length outliers.

There are no bond angle outliers.

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	2571	0	2585	14	0
1	B	2571	0	2585	18	0
1	C	2569	0	2579	20	0
1	D	2530	0	2540	23	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	12	0	16	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	12	0	16	1	0
3	C	12	0	16	1	0
4	A	13	0	12	1	0
4	B	13	0	12	1	0
4	C	13	0	12	1	0
4	D	13	0	13	1	0
5	A	299	0	0	1	0
5	B	285	0	0	0	0
5	C	229	0	0	1	0
5	D	82	0	0	0	0
All	All	11232	0	10386	75	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 (75) 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:347:ASN:HD22	1:C:349:THR:H	1.31	0.75
1:D:171:HIS:CE1	4:D:403:ABH:HCE1	2.22	0.75
1:D:173:MET:N	1:D:174:PRO:HD3	2.03	0.74
1:D:348:LEU:HD11	1:D:355:SER:HB3	1.71	0.72
1:C:171:HIS:CE1	4:C:405:ABH:HCE1	2.25	0.72
1:C:74:LEU:CD1	1:C:89:ARG:HG2	2.21	0.70
1:B:348:LEU:HD12	1:B:349:THR:N	2.09	0.68
1:C:69:ILE:HD13	1:C:98:ILE:HA	1.78	0.66
1:D:347:ASN:HD22	1:D:349:THR:H	1.44	0.65
1:B:110:ASN:HD21	1:B:145:LYS:HE2	1.65	0.60
1:A:171:HIS:CE1	4:A:405:ABH:HCE1	2.37	0.60
1:D:243:LYS:O	1:D:247:LEU:HD13	2.03	0.58
1:D:69:ILE:HD13	1:D:98:ILE:HA	1.84	0.58
1:B:348:LEU:HD11	1:B:355:SER:HB3	1.87	0.57
1:C:183:GLN:HG3	1:C:197:PRO:HG2	1.86	0.57
1:D:39:GLY:HA3	1:D:309:ASN:OD1	2.05	0.57
1:B:171:HIS:CE1	4:B:405:ABH:HCE1	2.40	0.56
1:D:105:LEU:O	1:D:108:GLN:HG2	2.06	0.56
1:D:173:MET:N	1:D:174:PRO:CD	2.68	0.55
1:C:173:MET:N	1:C:174:PRO:CD	2.69	0.55
1:C:148:LEU:C	1:C:148:LEU:HD12	2.27	0.54
1:A:200:ASN:H	1:A:203:ASN:ND2	2.05	0.54
1:D:158:ASP:HB3	1:D:174:PRO:HD2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:75:ASN:HD22	1:B:77:ALA:H	1.55	0.53
1:C:203:ASN:ND2	5:C:632:HOH:O	2.40	0.53
1:C:74:LEU:HD12	1:C:89:ARG:HG2	1.91	0.52
1:B:183:GLN:HG3	1:B:197:PRO:HG2	1.92	0.51
1:A:173:MET:N	1:A:174:PRO:CD	2.73	0.51
1:A:347:ASN:ND2	1:A:348:LEU:N	2.59	0.51
1:A:200:ASN:H	1:A:203:ASN:HD22	1.60	0.50
1:B:75:ASN:ND2	1:B:77:ALA:H	2.08	0.49
1:B:173:MET:N	1:B:174:PRO:CD	2.75	0.49
1:C:39:GLY:HA3	1:C:309:ASN:OD1	2.13	0.49
1:A:148:LEU:HD12	1:A:148:LEU:C	2.34	0.48
1:B:243:LYS:HE3	1:B:247:LEU:HD13	1.94	0.48
1:D:183:GLN:HG3	1:D:197:PRO:HG2	1.95	0.48
1:B:179:VAL:CG1	1:B:182:LEU:HD13	2.44	0.47
1:D:270:VAL:HG13	1:D:324:SER:OG	2.14	0.47
1:A:105:LEU:O	1:A:108:GLN:HG2	2.14	0.47
1:A:347:ASN:HD22	1:A:348:LEU:H	1.62	0.47
1:D:210:ARG:HD3	1:D:230:MET:HG3	1.96	0.47
1:C:305:LEU:HD21	1:C:325:ALA:HB1	1.95	0.47
1:D:250:ASN:N	1:D:251:PRO:HD3	2.30	0.47
1:C:86:LYS:HA	3:C:403:GOL:H11	1.96	0.47
1:C:348:LEU:HD21	1:C:353:ILE:O	2.15	0.46
1:C:305:LEU:CD2	1:C:325:ALA:HB1	2.47	0.45
1:D:162:PRO:HG2	1:D:187:PRO:HD2	1.98	0.45
1:C:347:ASN:HB3	1:C:349:THR:HG22	1.97	0.45
1:D:348:LEU:C	1:D:348:LEU:HD12	2.37	0.45
1:D:173:MET:H	1:D:174:PRO:HD3	1.77	0.45
1:A:109:SER:HB2	5:A:661:HOH:O	2.16	0.44
1:B:196:LYS:HA	1:B:197:PRO:HD3	1.85	0.44
1:B:53:PHE:CE2	1:B:63:LEU:HD13	2.53	0.44
1:D:347:ASN:ND2	1:D:349:THR:HG22	2.33	0.44
1:B:148:LEU:HD12	1:B:148:LEU:C	2.39	0.43
1:A:347:ASN:HD22	1:A:348:LEU:N	2.15	0.43
1:C:231:LEU:CD1	1:C:235:ARG:HH21	2.32	0.43
1:C:210:ARG:HD3	1:C:230:MET:HG3	2.00	0.43
1:C:347:ASN:ND2	1:C:349:THR:HG22	2.33	0.43
1:C:348:LEU:HD23	1:C:348:LEU:C	2.38	0.43
1:D:131:HIS:CE1	1:D:262:ASP:HB2	2.54	0.42
1:A:20:LEU:HA	1:A:20:LEU:HD12	1.94	0.42
1:D:322:GLN:O	1:D:326:VAL:HG23	2.19	0.42
1:B:45:GLU:HG3	1:B:49:LYS:HD3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:102:VAL:O	1:B:106:MET:HG2	2.19	0.42
1:B:81:GLN:HG2	3:B:403:GOL:H11	2.01	0.42
1:A:183:GLN:HG3	1:A:197:PRO:HG2	2.01	0.42
1:A:83:PHE:HE2	1:A:189:LEU:HD21	1.84	0.42
1:B:348:LEU:HD12	1:B:348:LEU:C	2.40	0.42
1:D:188:TRP:CH2	1:D:193:GLU:HB2	2.55	0.42
1:A:83:PHE:CE2	1:A:189:LEU:HD21	2.56	0.41
1:C:196:LYS:HA	1:C:197:PRO:HD3	1.84	0.41
1:B:45:GLU:OE1	1:B:49:LYS:HG3	2.21	0.40
1:D:205:ALA:HA	1:D:226:ALA:O	2.21	0.40
1:D:45:GLU:OE2	1:D:49:LYS:HE3	2.22	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	331/385 (86%)	324 (98%)	6 (2%)	1 (0%)	44	40
1	B	331/385 (86%)	324 (98%)	6 (2%)	1 (0%)	44	40
1	C	331/385 (86%)	322 (97%)	8 (2%)	1 (0%)	44	40
1	D	326/385 (85%)	318 (98%)	7 (2%)	1 (0%)	44	40
All	All	1319/1540 (86%)	1288 (98%)	27 (2%)	4 (0%)	44	40

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	173	MET
1	B	173	MET
1	C	173	MET
1	D	173	MET

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	282/327 (86%)	276 (98%)	6 (2%)	59	62
1	B	282/327 (86%)	270 (96%)	12 (4%)	33	29
1	C	282/327 (86%)	267 (95%)	15 (5%)	26	21
1	D	277/327 (85%)	263 (95%)	14 (5%)	28	22
All	All	1123/1308 (86%)	1076 (96%)	47 (4%)	34	30

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	THR
1	A	32	ASN
1	A	108	GLN
1	A	131	HIS
1	A	171	HIS
1	A	231	LEU
1	B	32	ASN
1	B	63	LEU
1	B	108	GLN
1	B	110	ASN
1	B	131	HIS
1	B	171	HIS
1	B	243	LYS
1	B	247	LEU
1	B	341	LEU
1	B	347	ASN
1	B	348	LEU
1	B	361	GLN
1	C	27	LEU
1	C	32	ASN
1	C	59	ASP
1	C	89	ARG
1	C	124	LEU
1	C	131	HIS

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Mol	Chain	Res	Type
1	C	147	ASP
1	C	171	HIS
1	C	182	LEU
1	C	196	LYS
1	C	231	LEU
1	C	341	LEU
1	C	347	ASN
1	C	354	MET
1	C	360	MET
1	D	27	LEU
1	D	32	ASN
1	D	62	GLN
1	D	63	LEU
1	D	76	GLU
1	D	108	GLN
1	D	124	LEU
1	D	131	HIS
1	D	171	HIS
1	D	190	ASP
1	D	231	LEU
1	D	347	ASN
1	D	348	LEU
1	D	360	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	GLN
1	A	110	ASN
1	A	203	ASN
1	A	322	GLN
1	A	347	ASN
1	B	75	ASN
1	B	81	GLN
1	B	110	ASN
1	B	203	ASN
1	B	347	ASN
1	C	108	GLN
1	C	203	ASN
1	C	347	ASN
1	C	351	GLN
1	C	361	GLN

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Mol	Chain	Res	Type
1	D	62	GLN
1	D	81	GLN
1	D	108	GLN
1	D	185	GLN
1	D	218	HIS
1	D	322	GLN
1	D	347	ASN

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 18 ligands modelled in this entry, 8 are monoatomic - leaving 10 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	$\# Z > 2$
3	GOL	A	403	-	5,5,5	0.34	0	5,5,5	0.49	0
3	GOL	A	404	-	5,5,5	0.35	0	5,5,5	0.54	0
4	ABH	A	405	2	4,12,12	0.53	0	6,16,16	1.91	3 (50%)
3	GOL	B	403	-	5,5,5	0.23	0	5,5,5	0.34	0
3	GOL	B	404	-	5,5,5	0.40	0	5,5,5	0.27	0
4	ABH	B	405	2	4,12,12	0.50	0	6,16,16	1.48	2 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	C	403	-	5,5,5	0.26	0	5,5,5	0.44	0
3	GOL	C	404	-	5,5,5	0.34	0	5,5,5	0.23	0
4	ABH	C	405	2	4,12,12	0.53	0	6,16,16	1.64	2 (33%)
4	ABH	D	403	2	4,12,12	0.47	0	6,16,16	1.97	3 (50%)

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	GOL	A	403	-	-	0/4/4/4	0/0/0/0
3	GOL	A	404	-	-	0/4/4/4	0/0/0/0
4	ABH	A	405	2	-	0/5/12/12	0/0/0/0
3	GOL	B	403	-	-	0/4/4/4	0/0/0/0
3	GOL	B	404	-	-	0/4/4/4	0/0/0/0
4	ABH	B	405	2	-	0/5/12/12	0/0/0/0
3	GOL	C	403	-	-	0/4/4/4	0/0/0/0
3	GOL	C	404	-	-	0/4/4/4	0/0/0/0
4	ABH	C	405	2	-	0/5/12/12	0/0/0/0
4	ABH	D	403	2	-	0/5/12/12	0/0/0/0

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	403	ABH	O3-B-O1	-2.84	98.98	109.18
4	A	405	ABH	O3-B-O1	-2.79	99.14	109.18
4	D	403	ABH	O3-B-O2	-2.76	99.27	109.18
4	C	405	ABH	O3-B-O1	-2.75	99.30	109.18
4	A	405	ABH	O3-B-O2	-2.60	99.84	109.18
4	B	405	ABH	O3-B-O1	-2.37	100.67	109.18
4	B	405	ABH	O3-B-O2	-2.12	101.56	109.18
4	C	405	ABH	O3-B-O2	-2.12	101.57	109.18
4	A	405	ABH	O1-B-O2	2.27	117.34	109.18
4	D	403	ABH	O1-B-O2	2.48	118.09	109.18

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	405	ABH	1	0
3	B	403	GOL	1	0
4	B	405	ABH	1	0
3	C	403	GOL	1	0
4	C	405	ABH	1	0
4	D	403	ABH	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	335/385 (87%)	-0.54	4 (1%) 79 78	11, 20, 42, 64	0
1	B	335/385 (87%)	-0.35	6 (1%) 69 68	12, 21, 47, 77	0
1	C	335/385 (87%)	-0.45	4 (1%) 79 78	20, 28, 47, 69	0
1	D	330/385 (85%)	0.82	57 (17%) 2 2	31, 47, 80, 93	10 (3%)
All	All	1335/1540 (86%)	-0.13	71 (5%) 27 27	11, 27, 62, 93	10 (0%)

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	350	ASP	6.7
1	D	345	VAL	5.4
1	D	357	ALA	5.3
1	D	343	PHE	5.3
1	D	353	ILE	4.8
1	D	188	TRP	4.5
1	C	362	THR	4.5
1	D	346	ARG	4.3
1	D	358	ALA	4.3
1	D	190	ASP	4.3
1	D	344	LYS	4.2
1	B	110	ASN	4.1
1	B	343	PHE	4.1
1	D	196	LYS	4.0
1	D	184	ASP	3.9
1	C	361	GLN	3.8
1	D	91	PHE	3.8
1	D	360	MET	3.7
1	B	361	GLN	3.5
1	B	109	SER	3.5
1	D	96	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	352	GLY	3.2
1	D	146	PRO	3.2
1	D	193	GLU	3.2
1	D	147	ASP	3.2
1	D	197	PRO	3.2
1	C	110	ASN	3.1
1	D	347	ASN	3.0
1	D	139	LEU	3.0
1	D	189	LEU	3.0
1	D	87	TRP	3.0
1	D	214	ALA	2.9
1	D	163	LEU	2.9
1	D	166	ALA	2.8
1	D	92	SER	2.8
1	D	192	PHE	2.8
1	D	351	GLN	2.8
1	D	341	LEU	2.8
1	D	144	ALA	2.7
1	D	354	MET	2.7
1	B	348	LEU	2.7
1	D	182	LEU	2.7
1	C	109	SER	2.7
1	D	161	THR	2.7
1	D	61	ILE	2.6
1	D	22	THR	2.6
1	B	350	ASP	2.6
1	D	108	GLN	2.6
1	A	343	PHE	2.6
1	D	162	PRO	2.6
1	D	340	HIS	2.5
1	D	213	ASP	2.5
1	D	355	SER	2.5
1	A	110	ASN	2.5
1	D	349	THR	2.5
1	D	187	PRO	2.4
1	D	186	ILE	2.4
1	D	83	PHE	2.4
1	D	183	GLN	2.4
1	D	215	HIS	2.3
1	D	348	LEU	2.2
1	D	19	LEU	2.2
1	D	100	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	143	GLU	2.2
1	D	177	PHE	2.1
1	D	195	ILE	2.1
1	D	20	LEU	2.1
1	D	99	ALA	2.1
1	D	80	PRO	2.1
1	A	109	SER	2.0
1	A	361	GLN	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	MN	A	401	1/1	1.00	0.11	8.77	16,16,16,16	0
3	GOL	B	403	6/6	0.93	0.17	3.10	25,36,43,55	1
2	MN	B	401	1/1	1.00	0.12	1.93	17,17,17,17	0
2	MN	B	402	1/1	1.00	0.13	1.85	15,15,15,15	0
3	GOL	A	403	6/6	0.94	0.13	1.35	22,32,45,53	1
3	GOL	C	403	6/6	0.93	0.12	1.34	28,37,47,58	1
4	ABH	C	405	13/13	0.93	0.10	1.31	19,28,33,34	0
4	ABH	D	403	13/13	0.85	0.22	1.29	34,45,54,55	0
2	MN	A	402	1/1	1.00	0.10	1.04	15,15,15,15	0
2	MN	C	402	1/1	1.00	0.11	0.84	22,22,22,22	0
2	MN	C	401	1/1	1.00	0.09	0.38	23,23,23,23	0
4	ABH	B	405	13/13	0.94	0.10	0.22	17,23,30,30	0
4	ABH	A	405	13/13	0.96	0.08	-0.36	18,24,27,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	MN	D	402	1/1	0.99	0.05	-2.03	29,29,29,29	1
2	MN	D	401	1/1	0.99	0.04	-3.82	29,29,29,29	1
3	GOL	A	404	6/6	0.94	0.09	-	28,35,36,41	0
3	GOL	C	404	6/6	0.93	0.15	-	37,42,43,47	1
3	GOL	B	404	6/6	0.95	0.13	-	27,38,39,41	1

6.5 Other polymers [i](#)

There are no such residues in this entry.