



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 23, 2023 – 12:12 pm GMT

PDB ID : 8OY0
Title : ATP phosphoribosyltransferase (HisZG ATPPRT) from *Acinetobacter baumannii*
Authors : Alpey, M.S.; Read, B.; da Silva, R.G.
Deposited on : 2023-05-03
Resolution : 2.40 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

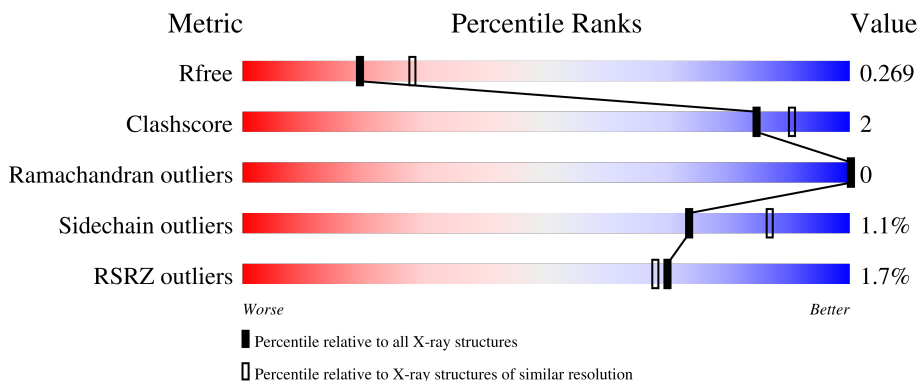
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



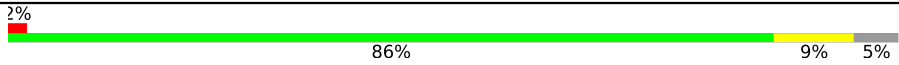


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	389	 2% 91% 5%
1	B	389	 2% 87% 6% 7%
1	C	389	 2% 91% 5%
1	D	389	 2% 91% 5%
2	E	228	 % 90% 6%

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Mol	Chain	Length	Quality of chain
2	F	228	 2% 86% 9% 5%
2	G	228	 % 86% 10% •
2	H	228	 % 89% 7% •

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 18247 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 ATP phosphoribosyltransferase regulatory subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	370	Total 2863	C 1825	N 491	O 540	S 7	0	0	0
1	B	361	Total 2775	C 1765	N 478	O 525	S 7	0	0	0
1	C	370	Total 2865	C 1822	N 494	O 542	S 7	0	0	0
1	D	373	Total 2864	C 1824	N 489	O 544	S 7	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP A0A059ZNW9
B	0	GLY	-	expression tag	UNP A0A059ZNW9
C	0	GLY	-	expression tag	UNP A0A059ZNW9
D	0	GLY	-	expression tag	UNP A0A059ZNW9

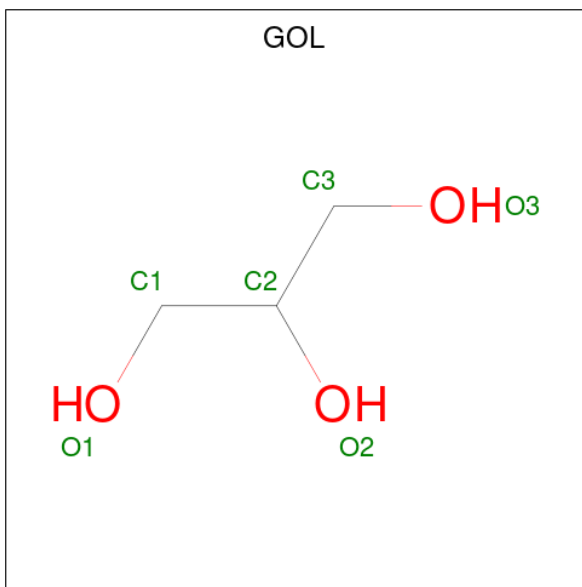
- Molecule 2 is a protein called ATP phosphoribosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	E	219	Total 1662	C 1059	N 286	O 310	S 7	0	0	0
2	F	217	Total 1639	C 1044	N 282	O 307	S 6	0	0	0
2	G	218	Total 1649	C 1051	N 283	O 309	S 6	0	0	0
2	H	219	Total 1663	C 1058	N 284	O 314	S 7	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	0	GLY	-	expression tag	UNP V5VGC6
F	0	GLY	-	expression tag	UNP V5VGC6
G	0	GLY	-	expression tag	UNP V5VGC6
H	0	GLY	-	expression tag	UNP V5VGC6

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



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

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0
4	B	1	Total Na 1 1	0	0
4	C	1	Total Na 1 1	0	0
4	D	1	Total Na 1 1	0	0

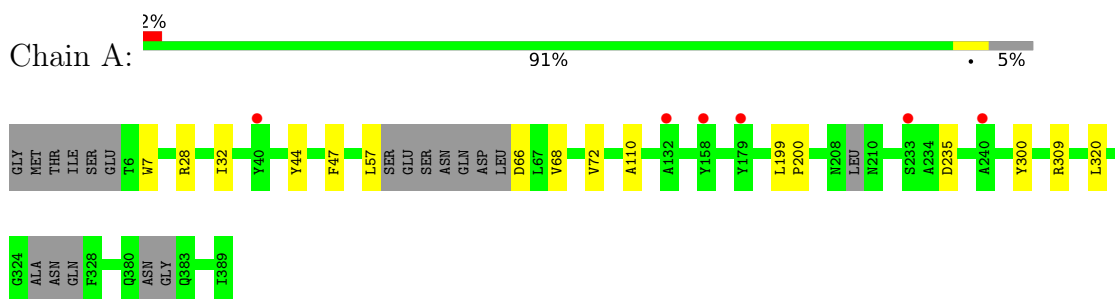
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	58	Total O 58 58	0	0
5	B	44	Total O 44 44	0	0
5	C	47	Total O 47 47	0	0
5	D	37	Total O 37 37	0	0
5	E	25	Total O 25 25	0	0
5	F	18	Total O 18 18	0	0
5	G	12	Total O 12 12	0	0
5	H	16	Total O 16 16	0	0

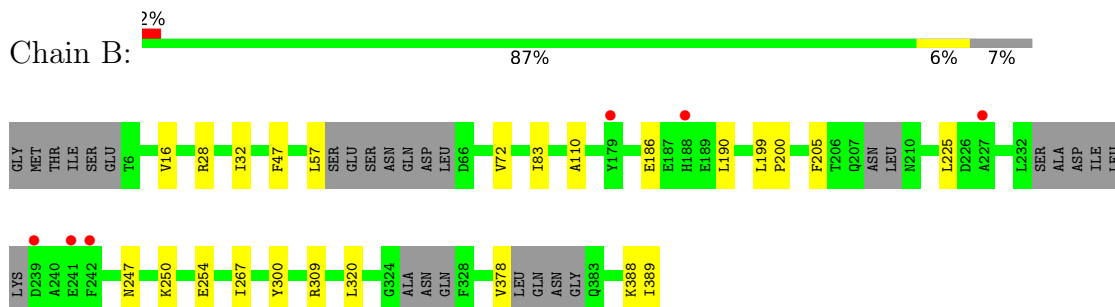
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

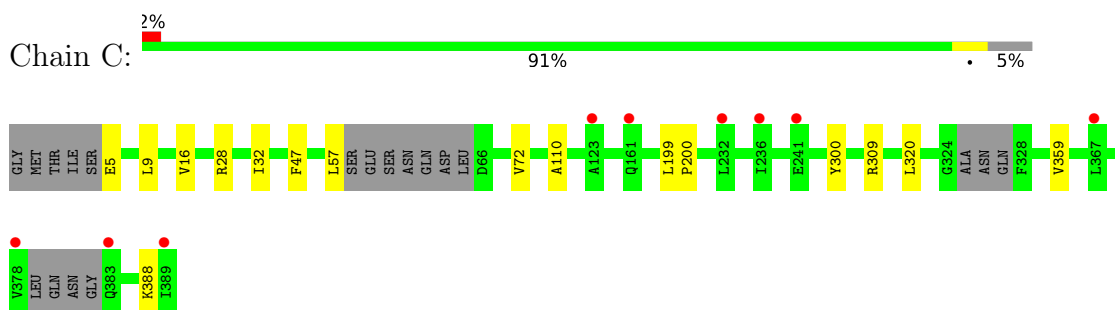
- Molecule 1: ATP phosphoribosyltransferase regulatory subunit



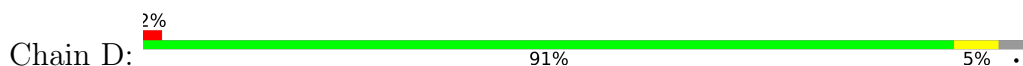
- Molecule 1: ATP phosphoribosyltransferase regulatory subunit

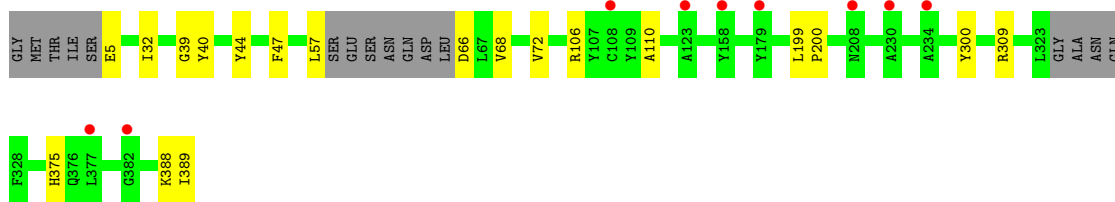


- Molecule 1: ATP phosphoribosyltransferase regulatory subunit

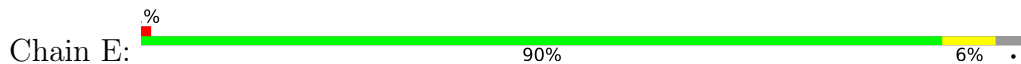


- Molecule 1: ATP phosphoribosyltransferase regulatory subunit

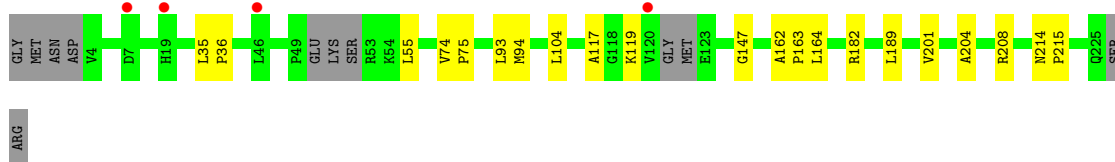
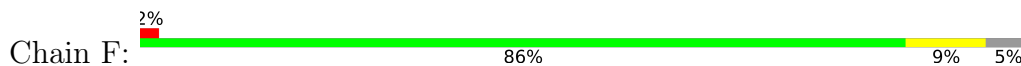




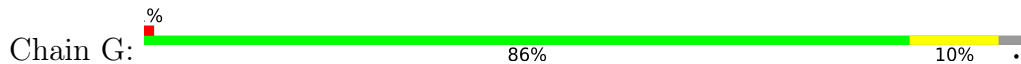
• Molecule 2: ATP phosphoribosyltransferase



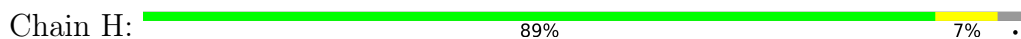
• Molecule 2: ATP phosphoribosyltransferase



• Molecule 2: ATP phosphoribosyltransferase



• Molecule 2: ATP phosphoribosyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	80.27Å 172.82Å 98.11Å 90.00° 90.97° 90.00°	Depositor
Resolution (Å)	30.82 – 2.40 30.82 – 2.40	Depositor EDS
% Data completeness (in resolution range)	95.3 (30.82-2.40) 95.3 (30.82-2.40)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.8.0405	Depositor
R, R_{free}	0.238 , 0.264 0.242 , 0.269	Depositor DCC
R_{free} test set	5033 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	41.5	Xtrriage
Anisotropy	0.424	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 32.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	0.045 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18247	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% 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: GOL, NA

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	0.30	0/2918	0.54	0/3965
1	B	0.30	0/2828	0.54	0/3845
1	C	0.29	0/2920	0.53	0/3968
1	D	0.28	0/2920	0.52	0/3974
2	E	0.29	0/1682	0.52	0/2274
2	F	0.30	0/1660	0.53	0/2251
2	G	0.30	0/1670	0.52	0/2262
2	H	0.29	0/1686	0.53	0/2285
All	All	0.29	0/18284	0.53	0/24824

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	2863	0	2809	12	0
1	B	2775	0	2696	16	0
1	C	2865	0	2816	12	0
1	D	2864	0	2794	13	0
2	E	1662	0	1705	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1639	0	1668	13	0
2	G	1649	0	1688	17	0
2	H	1663	0	1709	10	0
3	A	6	0	8	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	58	0	0	0	0
5	B	44	0	0	0	0
5	C	47	0	0	0	0
5	D	37	0	0	0	0
5	E	25	0	0	0	0
5	F	18	0	0	0	0
5	G	12	0	0	0	0
5	H	16	0	0	0	0
All	All	18247	0	17893	81	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 2.

All (81) 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)
2:F:93:LEU:HG	2:F:94:MET:HE2	1.71	0.72
2:G:93:LEU:HG	2:G:94:MET:HE2	1.73	0.71
1:B:225:LEU:CD1	1:B:267:ILE:HG21	2.22	0.69
2:E:204:ALA:O	2:E:208:ARG:HG2	1.93	0.68
2:H:204:ALA:O	2:H:208:ARG:HG2	1.93	0.68
2:F:204:ALA:O	2:F:208:ARG:HG2	1.93	0.68
2:G:204:ALA:O	2:G:208:ARG:HG2	1.93	0.67
1:C:72:VAL:CG1	1:D:72:VAL:CG1	2.79	0.59
2:F:117:ALA:HA	2:F:189:LEU:HD23	1.85	0.58
1:A:72:VAL:CG1	1:B:72:VAL:CG1	2.81	0.57
2:G:27:LYS:HE3	2:G:70:ARG:HG2	1.87	0.57
2:E:184:ASN:ND2	2:F:55:LEU:HD12	2.21	0.56
2:G:161:LEU:HD21	2:H:56:ILE:HG12	1.90	0.54
1:B:186:GLU:O	1:B:190:LEU:HD23	2.08	0.54
2:G:41:ALA:HA	2:G:219:GLN:HG2	1.89	0.54
1:B:250:LYS:O	1:B:254:GLU:HG2	2.09	0.53
2:E:162:ALA:HB3	2:E:163:PRO:HD3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:162:ALA:HB3	2:H:163:PRO:HD3	1.92	0.52
2:G:23:LEU:C	2:G:23:LEU:HD23	2.30	0.51
2:F:162:ALA:HB3	2:F:163:PRO:HD3	1.93	0.51
1:D:40:TYR:CD1	1:D:106:ARG:HB3	2.46	0.51
2:G:23:LEU:HD21	2:G:25:LEU:HD21	1.92	0.51
2:G:162:ALA:HB3	2:G:163:PRO:HD3	1.93	0.51
1:C:72:VAL:HG13	1:D:72:VAL:CG1	2.42	0.50
2:E:184:ASN:ND2	2:F:55:LEU:CD1	2.74	0.50
2:G:70:ARG:HD3	2:H:157:GLY:HA3	1.92	0.50
1:B:32:ILE:HD11	1:B:110:ALA:HB2	1.94	0.49
2:G:55:LEU:HD22	2:H:184:ASN:ND2	2.27	0.49
1:D:388:LYS:O	1:D:389:ILE:CB	2.61	0.48
2:G:23:LEU:HD23	2:G:24:ALA:N	2.28	0.48
2:F:214:ASN:HB3	2:F:215:PRO:HD3	1.95	0.48
1:B:388:LYS:O	1:B:389:ILE:CB	2.62	0.48
1:D:32:ILE:HD11	1:D:110:ALA:HB2	1.94	0.47
1:A:32:ILE:HD11	1:A:110:ALA:HB2	1.95	0.47
1:C:47:PHE:CZ	1:D:47:PHE:CD1	3.02	0.47
1:C:32:ILE:HD11	1:C:110:ALA:HB2	1.97	0.46
1:C:72:VAL:CG1	1:D:72:VAL:HG13	2.45	0.46
2:G:6:ASN:HB2	2:G:62:LYS:HG2	1.97	0.46
2:G:23:LEU:HD22	2:G:25:LEU:HG	1.97	0.45
2:F:119:LYS:HE2	2:F:164:LEU:HD23	1.98	0.44
1:D:199:LEU:N	1:D:200:PRO:CD	2.81	0.44
2:F:74:VAL:HB	2:F:75:PRO:HD3	2.00	0.44
2:E:104:LEU:HD12	2:E:201:VAL:HG21	2.00	0.44
2:G:23:LEU:HD21	2:G:25:LEU:CD2	2.46	0.44
1:A:47:PHE:CD1	1:B:47:PHE:CZ	3.05	0.44
1:A:72:VAL:CG1	1:B:72:VAL:HG13	2.47	0.44
1:A:44:TYR:HB2	1:B:16:VAL:HB	2.00	0.44
2:G:214:ASN:HB3	2:G:215:PRO:HD3	2.00	0.44
2:H:214:ASN:HB3	2:H:215:PRO:HD3	1.99	0.44
1:B:199:LEU:N	1:B:200:PRO:CD	2.81	0.43
2:G:74:VAL:HB	2:G:75:PRO:HD3	2.00	0.43
1:A:199:LEU:N	1:A:200:PRO:CD	2.81	0.43
2:F:117:ALA:HA	2:F:189:LEU:CD2	2.47	0.43
1:D:375:HIS:NE2	1:D:388:LYS:HD3	2.33	0.43
1:B:225:LEU:HD13	1:B:267:ILE:HG21	1.97	0.43
2:E:74:VAL:HB	2:E:75:PRO:HD3	2.01	0.43
2:E:214:ASN:HB3	2:E:215:PRO:HD3	1.99	0.43
2:H:119:LYS:HE2	2:H:164:LEU:HD23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:66:ASP:HB3	1:A:68:VAL:HG22	2.01	0.42
1:A:7:TRP:CZ2	2:F:147:GLY:HA2	2.54	0.42
1:C:199:LEU:N	1:C:200:PRO:CD	2.82	0.42
1:B:190:LEU:CD2	1:B:205:PHE:CE2	3.02	0.42
1:B:28:ARG:HA	1:B:320:LEU:HD21	2.02	0.42
1:B:83:ILE:HD12	1:B:83:ILE:N	2.34	0.42
1:A:72:VAL:HG13	1:B:72:VAL:CG1	2.48	0.42
1:C:9:LEU:HB2	2:E:149:GLN:HE22	1.85	0.41
1:C:72:VAL:CG1	1:D:72:VAL:HG12	2.49	0.41
2:H:74:VAL:HB	2:H:75:PRO:HD3	2.01	0.41
1:C:28:ARG:HA	1:C:320:LEU:HD21	2.02	0.41
1:D:66:ASP:HB3	1:D:68:VAL:HG22	2.02	0.41
2:F:104:LEU:HD12	2:F:201:VAL:HG21	2.01	0.41
1:A:28:ARG:HA	1:A:320:LEU:HD21	2.02	0.41
1:A:28:ARG:O	1:A:32:ILE:HG12	2.21	0.41
1:C:16:VAL:HB	1:D:44:TYR:HB2	2.03	0.41
2:F:35:LEU:N	2:F:36:PRO:CD	2.84	0.41
1:A:72:VAL:HG12	1:B:72:VAL:CG1	2.51	0.41
2:H:104:LEU:HD12	2:H:201:VAL:HG21	2.03	0.41
1:C:359:VAL:CG1	1:D:39:GLY:HA3	2.51	0.40
2:H:27:LYS:HE3	2:H:68:ILE:HG21	2.02	0.40
1:C:32:ILE:HD11	1:C:110:ALA:CB	2.52	0.40
2:G:93:LEU:CG	2:G:94:MET:HE2	2.48	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	360/389 (92%)	351 (98%)	9 (2%)	0	100 100
1	B	349/389 (90%)	339 (97%)	10 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	362/389 (93%)	354 (98%)	8 (2%)	0	100	100
1	D	367/389 (94%)	356 (97%)	11 (3%)	0	100	100
2	E	211/228 (92%)	207 (98%)	4 (2%)	0	100	100
2	F	211/228 (92%)	206 (98%)	5 (2%)	0	100	100
2	G	212/228 (93%)	207 (98%)	5 (2%)	0	100	100
2	H	217/228 (95%)	211 (97%)	6 (3%)	0	100	100
All	All	2289/2468 (93%)	2231 (98%)	58 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	293/316 (93%)	289 (99%)	4 (1%)	67	82
1	B	281/316 (89%)	276 (98%)	5 (2%)	59	76
1	C	294/316 (93%)	289 (98%)	5 (2%)	60	78
1	D	291/316 (92%)	287 (99%)	4 (1%)	67	82
2	E	178/194 (92%)	177 (99%)	1 (1%)	86	94
2	F	174/194 (90%)	173 (99%)	1 (1%)	86	94
2	G	176/194 (91%)	175 (99%)	1 (1%)	86	94
2	H	180/194 (93%)	180 (100%)	0	100	100
All	All	1867/2040 (92%)	1846 (99%)	21 (1%)	73	87

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	LEU
1	A	235	ASP
1	A	300	TYR
1	A	309	ARG

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Mol	Chain	Res	Type
1	B	57	LEU
1	B	247	ASN
1	B	300	TYR
1	B	309	ARG
1	B	378	VAL
1	C	5	GLU
1	C	57	LEU
1	C	300	TYR
1	C	309	ARG
1	C	388	LYS
1	D	5	GLU
1	D	57	LEU
1	D	300	TYR
1	D	309	ARG
2	E	226	SER
2	F	182	ARG
2	G	7	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	385	ASN
2	E	184	ASN
2	F	80	ASN
2	H	184	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	401	-	5,5,5	0.22	0	5,5,5	0.51	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	GOL	A	401	-	-	0/4/4/4	-

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	370/389 (95%)	0.04	6 (1%) 72 70	28, 47, 77, 86	0
1	B	361/389 (92%)	0.07	6 (1%) 70 68	30, 48, 84, 96	0
1	C	370/389 (95%)	0.06	9 (2%) 59 57	30, 48, 73, 80	0
1	D	373/389 (95%)	0.19	9 (2%) 59 57	28, 52, 84, 91	0
2	E	219/228 (96%)	-0.06	3 (1%) 75 73	34, 47, 74, 86	0
2	F	217/228 (95%)	-0.03	4 (1%) 68 66	35, 51, 79, 89	0
2	G	218/228 (95%)	0.04	2 (0%) 84 82	36, 56, 88, 100	0
2	H	219/228 (96%)	-0.08	1 (0%) 91 89	33, 51, 75, 88	0
All	All	2347/2468 (95%)	0.04	40 (1%) 70 68	28, 50, 79, 100	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	230	ALA	4.0
1	D	158	TYR	3.9
2	H	179	ASN	3.5
1	D	234	ALA	3.5
1	A	158	TYR	3.3
2	G	121	GLY	3.3
1	D	382	GLY	3.2
1	C	123	ALA	3.2
1	A	240	ALA	3.2
1	C	389	ILE	3.2
2	G	7	ASP	3.1
2	E	49	PRO	3.0
1	D	208	ASN	3.0
2	F	7	ASP	2.8
2	E	53	ARG	2.8
1	B	227	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	179	TYR	2.7
2	F	46	LEU	2.6
1	D	123	ALA	2.6
2	F	120	VAL	2.5
1	B	242	PHE	2.5
1	C	241	GLU	2.5
1	B	239	ASP	2.5
1	C	367	LEU	2.5
1	C	378	VAL	2.4
1	A	179	TYR	2.4
1	B	241	GLU	2.4
1	D	179	TYR	2.4
1	A	233	SER	2.3
2	F	19	HIS	2.3
1	C	161	GLN	2.2
1	D	377	LEU	2.2
1	A	132	ALA	2.2
1	C	236	ILE	2.2
2	E	179	ASN	2.2
1	D	108	CYS	2.2
1	B	188	HIS	2.1
1	C	383	GLN	2.1
1	A	40	TYR	2.1
1	C	232	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 monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	GOL	A	401	6/6	0.77	0.31	43,45,49,49	0
4	NA	D	401	1/1	0.93	0.24	37,37,37,37	0
4	NA	B	401	1/1	0.95	0.22	31,31,31,31	0
4	NA	C	401	1/1	0.95	0.20	45,45,45,45	0
4	NA	A	402	1/1	0.95	0.24	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.