



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 12, 2024 – 11:33 PM EDT

PDB ID : 3HPA
Title : Crystal structure of an amidohydrolase gi:44264246 from an environmental sample of sargasso sea
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Deposited on : 2009-06-03
Resolution : 2.20 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
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
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)	:	2.36.2

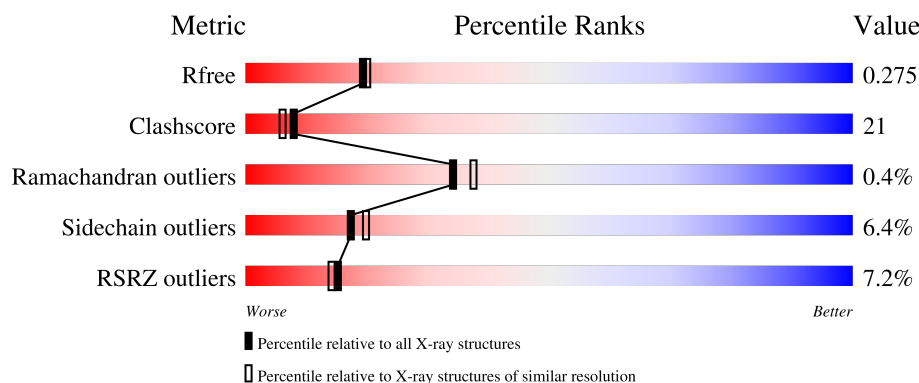
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	479	<div> <div>4%</div> <div>59%</div> <div>27%</div> <div>•</div> <div>11%</div> </div>
1	B	479	<div> <div>9%</div> <div>56%</div> <div>30%</div> <div>•</div> <div>11%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6625 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 AMIDOHYDROLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	428	Total	C	N	O	S	0	0	0
			3247	2035	586	607	19			
1	B	428	Total	C	N	O	S	0	0	0
			3247	2035	586	607	19			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

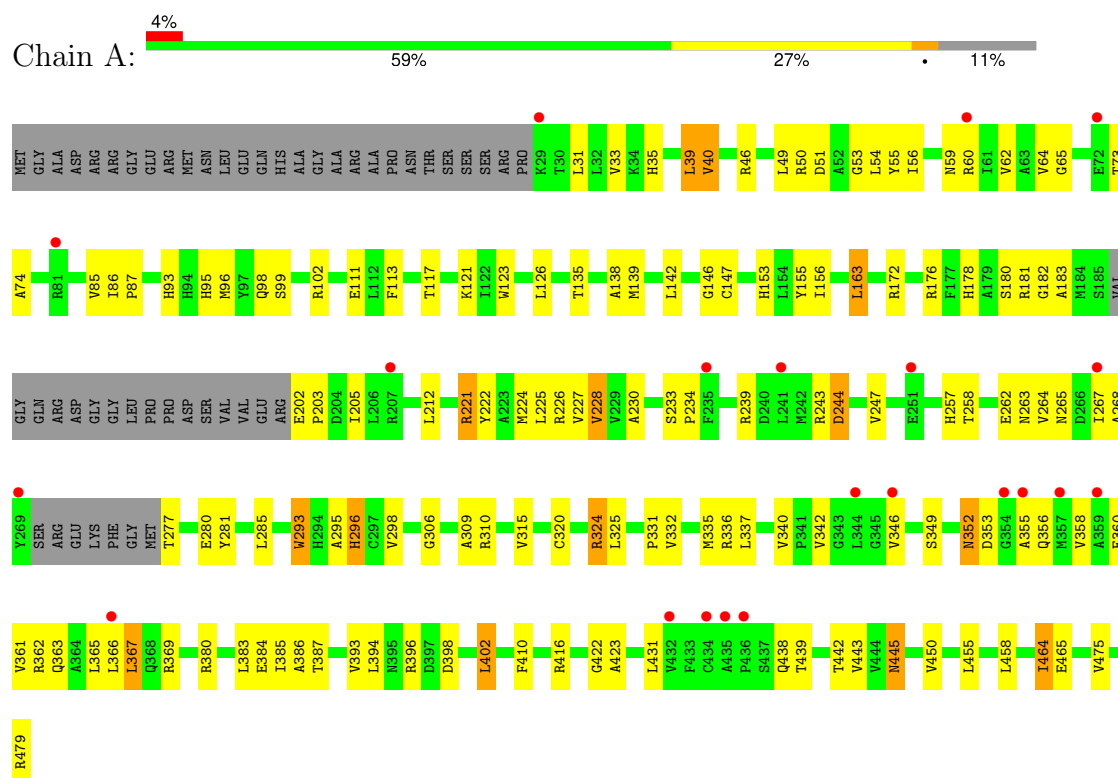
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	73	Total	O	0	0
			73	73		
3	B	56	Total	O	0	0
			56	56		

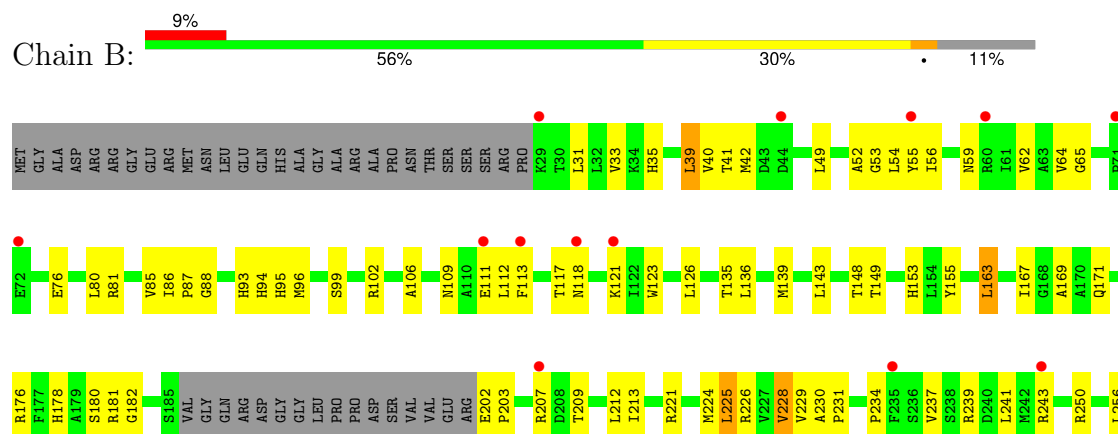
3 Residue-property plots

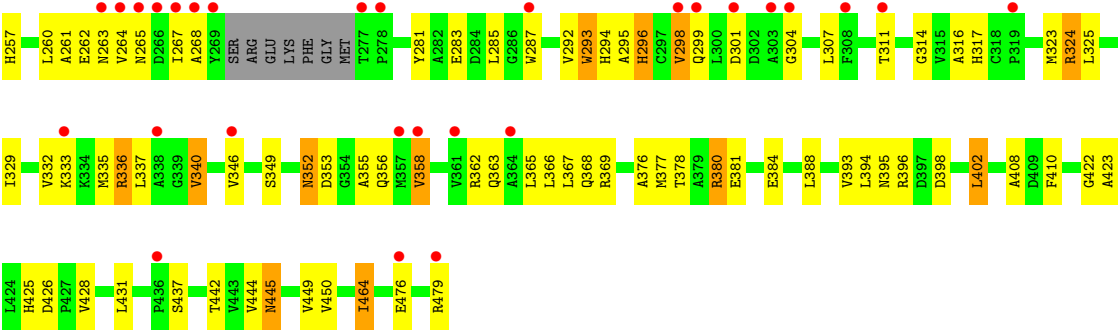
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: AMIDOHYDROLASE



• Molecule 1: AMIDOHYDROLASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	83.30Å 83.30Å 229.12Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.62 – 2.20 39.15 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.7 (24.62-2.20) 99.9 (39.15-2.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.232 , 0.276 0.232 , 0.275	Depositor DCC
R_{free} test set	2407 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	39.6	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.038 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6625	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.35	0/3310	0.63	0/4502
1	B	0.34	0/3310	0.62	0/4502
All	All	0.35	0/6620	0.62	0/9004

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

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	3247	0	3221	128	0
1	B	3247	0	3221	159	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	73	0	0	2	0
3	B	56	0	0	5	1
All	All	6625	0	6442	278	1

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 21.

All (278) 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:39:LEU:HD13	1:A:85:VAL:HG23	1.36	1.03
1:B:346:VAL:HG21	1:B:355:ALA:HA	1.49	0.94
1:A:39:LEU:HD11	1:A:402:LEU:HD23	1.49	0.92
1:B:224:MET:HE3	1:B:445:ASN:HB2	1.51	0.89
1:B:239:ARG:HH21	1:B:243:ARG:HH22	1.17	0.89
1:B:239:ARG:NH2	1:B:243:ARG:HH22	1.70	0.88
1:B:106:ALA:HB1	1:B:118:ASN:HD22	1.37	0.86
1:A:346:VAL:HG21	1:A:355:ALA:HA	1.55	0.85
1:B:178:HIS:HE1	1:B:396:ARG:HH11	1.24	0.83
1:B:329:ILE:HG23	1:B:367:LEU:CD1	2.09	0.81
1:A:356:GLN:OE1	1:A:358:VAL:HG22	1.81	0.81
1:B:86:ILE:HG23	1:B:87:PRO:HD2	1.62	0.80
1:B:180:SER:HA	1:B:228:VAL:HG13	1.63	0.80
1:B:323:MET:HE3	1:B:363:GLN:HG3	1.66	0.78
1:B:39:LEU:HD13	1:B:85:VAL:HG23	1.63	0.78
1:B:239:ARG:HE	1:B:243:ARG:HH12	1.29	0.78
1:A:336:ARG:HD2	1:A:385:ILE:HD11	1.67	0.77
1:B:336:ARG:HG2	1:B:336:ARG:HH11	1.50	0.77
1:B:163:LEU:HD12	1:B:212:LEU:HD13	1.65	0.76
1:B:176:ARG:CZ	1:B:224:MET:HE1	2.16	0.76
1:B:231:PRO:HD2	1:B:287:TRP:HH2	1.51	0.75
1:B:264:VAL:HG22	1:B:299:GLN:HE22	1.52	0.74
1:B:135:THR:HG22	1:B:139:MET:CE	2.17	0.73
1:B:178:HIS:CE1	1:B:396:ARG:HD2	2.23	0.73
1:B:113:PHE:O	1:B:117:THR:HG23	1.89	0.73
1:B:93:HIS:HD1	1:B:257:HIS:HE1	1.38	0.72
1:B:224:MET:HE3	1:B:445:ASN:CB	2.19	0.72
1:B:118:ASN:HA	1:B:121:LYS:NZ	2.05	0.71
1:A:281:TYR:O	1:A:285:LEU:HD23	1.90	0.71
1:A:221:ARG:HG2	1:A:221:ARG:HH11	1.55	0.70
1:A:475:VAL:HG21	1:B:425:HIS:CD2	2.26	0.70
1:A:60:ARG:NH1	1:A:62:VAL:HG12	2.05	0.70
1:A:182:GLY:HA2	1:A:230:ALA:O	1.90	0.70
1:B:203:PRO:O	1:B:207:ARG:HG3	1.90	0.70
1:A:40:VAL:CG1	1:A:86:ILE:HG12	2.21	0.70
1:B:87:PRO:HG3	1:B:402:LEU:HD22	1.74	0.70
1:B:237:VAL:HG21	1:B:241:LEU:HD12	1.72	0.70
1:B:307:LEU:O	1:B:311:THR:HG22	1.91	0.69
1:A:176:ARG:HH22	1:A:445:ASN:ND2	1.91	0.69
1:B:239:ARG:HH21	1:B:243:ARG:NH2	1.90	0.69
1:B:239:ARG:HB3	1:B:281:TYR:OH	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:HIS:HD1	1:A:257:HIS:HE1	1.41	0.68
1:A:225:LEU:HD23	1:A:226:ARG:N	2.09	0.68
1:A:96:MET:HE1	1:A:139:MET:HG3	1.74	0.68
1:B:178:HIS:CE1	1:B:396:ARG:HH11	2.11	0.68
1:B:106:ALA:HB1	1:B:118:ASN:ND2	2.06	0.68
1:B:264:VAL:CG2	1:B:299:GLN:HE22	2.07	0.68
1:B:54:LEU:HD22	1:B:64:VAL:HG22	1.77	0.67
1:A:86:ILE:HG23	1:A:87:PRO:HD2	1.75	0.67
1:B:298:VAL:O	1:B:299:GLN:HB2	1.94	0.67
1:B:329:ILE:HG23	1:B:367:LEU:HD13	1.75	0.67
1:B:281:TYR:O	1:B:285:LEU:HD23	1.94	0.67
1:B:135:THR:HG22	1:B:139:MET:HE2	1.77	0.67
1:A:352:ASN:HD22	1:A:352:ASN:C	1.99	0.66
1:A:233:SER:HA	1:A:258:THR:OG1	1.95	0.66
1:A:176:ARG:HH22	1:A:445:ASN:HD22	1.44	0.66
1:B:479:ARG:HH11	1:B:479:ARG:HG3	1.61	0.65
1:B:329:ILE:HG23	1:B:367:LEU:HD11	1.78	0.65
1:B:93:HIS:HD1	1:B:257:HIS:CE1	2.14	0.65
1:A:234:PRO:HB2	1:A:281:TYR:HE2	1.62	0.64
1:A:96:MET:HE2	1:A:138:ALA:HB3	1.79	0.64
1:B:123:TRP:HA	1:B:126:LEU:HD13	1.78	0.64
1:B:349:SER:O	1:B:353:ASP:HB3	1.97	0.64
1:A:39:LEU:HD13	1:A:85:VAL:CG2	2.20	0.64
1:A:50:ARG:HG3	1:A:50:ARG:HH11	1.63	0.64
1:B:40:VAL:HG22	1:B:86:ILE:HG12	1.79	0.64
1:B:239:ARG:HE	1:B:243:ARG:NH1	1.94	0.64
1:A:172:ARG:HH11	1:A:172:ARG:HB2	1.63	0.63
1:B:356:GLN:OE1	1:B:358:VAL:HG13	1.98	0.63
1:A:46:ARG:NH1	1:A:384:GLU:OE1	2.32	0.63
1:A:335:MET:HB3	1:A:340:VAL:CG2	2.29	0.63
1:A:96:MET:CE	1:A:138:ALA:HB3	2.28	0.63
1:A:96:MET:CE	1:A:139:MET:HG3	2.29	0.62
1:A:40:VAL:HG13	1:A:86:ILE:HG12	1.81	0.62
1:B:118:ASN:HA	1:B:121:LYS:HZ1	1.64	0.62
1:B:323:MET:HE1	1:B:367:LEU:HB2	1.81	0.61
1:B:35:HIS:O	1:B:81:ARG:HA	2.00	0.61
1:B:59:ASN:HB2	1:B:445:ASN:ND2	2.15	0.61
1:B:135:THR:HG22	1:B:139:MET:HE1	1.81	0.61
1:A:180:SER:HA	1:A:228:VAL:HG13	1.81	0.61
1:A:332:VAL:O	1:A:336:ARG:HG3	2.00	0.61
1:B:86:ILE:HG23	1:B:87:PRO:CD	2.31	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:293:TRP:HB2	1:B:393:VAL:HG13	1.83	0.60
1:B:40:VAL:CG2	1:B:86:ILE:HG12	2.32	0.60
1:B:167:ILE:O	1:B:171:GLN:HG3	2.01	0.60
1:A:178:HIS:HE1	1:A:396:ARG:HH11	1.50	0.59
1:A:55:TYR:O	1:A:62:VAL:HG22	2.02	0.59
1:A:73:THR:HG22	1:A:74:ALA:N	2.17	0.59
1:B:263:ASN:ND2	1:B:265:ASN:HB2	2.18	0.59
1:B:336:ARG:HG2	1:B:336:ARG:NH1	2.17	0.59
1:A:422:GLY:HA3	1:B:99:SER:O	2.03	0.59
1:A:475:VAL:O	1:A:479:ARG:HG2	2.03	0.59
1:A:54:LEU:HD23	1:A:64:VAL:HG13	1.85	0.59
1:A:33:VAL:O	1:A:53:GLY:HA3	2.03	0.58
1:B:221:ARG:HG2	1:B:221:ARG:HH11	1.67	0.58
1:A:335:MET:HB3	1:A:340:VAL:HG22	1.86	0.58
1:B:180:SER:CA	1:B:228:VAL:HG13	2.32	0.58
1:A:234:PRO:HB2	1:A:281:TYR:CE2	2.38	0.58
1:A:367:LEU:HB3	3:A:484:HOH:O	2.03	0.58
1:A:86:ILE:HG22	1:A:87:PRO:O	2.04	0.57
1:B:182:GLY:HA2	1:B:230:ALA:O	2.04	0.57
1:B:293:TRP:CB	1:B:393:VAL:HG13	2.35	0.57
1:B:324:ARG:HG2	1:B:324:ARG:HH11	1.69	0.57
1:B:295:ALA:HA	1:B:316:ALA:HB3	1.85	0.57
1:B:33:VAL:O	1:B:53:GLY:HA3	2.04	0.57
1:A:331:PRO:O	1:A:335:MET:HG3	2.05	0.57
1:A:315:VAL:CG2	1:A:342:VAL:HG22	2.34	0.57
1:A:356:GLN:HE21	1:A:438:GLN:NE2	2.03	0.57
1:A:39:LEU:CD1	1:A:402:LEU:HD23	2.31	0.56
1:A:221:ARG:HG2	1:A:221:ARG:NH1	2.21	0.56
1:A:336:ARG:CD	1:A:385:ILE:HD11	2.33	0.56
1:B:352:ASN:C	1:B:352:ASN:HD22	2.08	0.56
1:B:378:THR:OG1	1:B:381:GLU:HG3	2.05	0.56
1:B:56:ILE:HD13	1:B:408:ALA:HB1	1.86	0.56
1:A:320:CYS:SG	1:A:360:GLU:OE2	2.64	0.56
1:A:360:GLU:HG2	3:A:515:HOH:O	2.06	0.55
1:B:176:ARG:CZ	1:B:224:MET:CE	2.84	0.55
1:B:293:TRP:HA	1:B:314:GLY:O	2.07	0.55
1:A:416:ARG:HB2	1:A:416:ARG:NH1	2.23	0.54
1:A:257:HIS:HD2	1:A:293:TRP:O	1.90	0.54
1:B:225:LEU:HD23	1:B:226:ARG:N	2.21	0.54
1:B:96:MET:CE	1:B:135:THR:HG23	2.38	0.54
1:B:323:MET:CE	1:B:363:GLN:HG3	2.34	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:LEU:CD1	1:A:85:VAL:HG23	2.25	0.54
1:A:86:ILE:HD12	1:A:431:LEU:HD22	1.90	0.54
1:A:233:SER:HB2	1:A:234:PRO:HD2	1.90	0.54
1:A:264:VAL:O	1:A:267:ILE:HG22	2.08	0.54
1:B:265:ASN:O	1:B:268:ALA:HB3	2.07	0.54
1:B:209:THR:O	1:B:213:ILE:HG13	2.07	0.54
1:B:86:ILE:HG22	1:B:87:PRO:O	2.08	0.54
1:A:178:HIS:CE1	1:A:396:ARG:HD2	2.42	0.53
1:B:31:LEU:HD12	1:B:76:GLU:O	2.08	0.53
1:B:292:VAL:HG12	1:B:293:TRP:N	2.24	0.53
1:B:39:LEU:HD13	1:B:85:VAL:CG2	2.36	0.53
1:B:55:TYR:HD2	1:B:62:VAL:CG2	2.22	0.53
1:B:231:PRO:HD2	1:B:287:TRP:CH2	2.39	0.53
1:A:202:GLU:HB3	1:A:203:PRO:HD3	1.91	0.53
1:A:87:PRO:HB3	1:A:402:LEU:HD13	1.91	0.53
1:B:176:ARG:NH2	1:B:224:MET:HE1	2.23	0.53
1:A:293:TRP:CG	1:A:393:VAL:HG13	2.44	0.53
1:B:352:ASN:HB3	1:B:353:ASP:HA	1.91	0.53
1:B:367:LEU:HD12	3:B:490:HOH:O	2.07	0.53
1:A:172:ARG:HB2	1:A:172:ARG:NH1	2.23	0.52
1:B:323:MET:HE3	1:B:363:GLN:CG	2.39	0.52
1:A:102:ARG:HB2	1:B:423:ALA:HB2	1.92	0.51
1:B:317:HIS:HD2	3:B:497:HOH:O	1.92	0.51
1:A:267:ILE:HG23	1:A:268:ALA:N	2.25	0.51
1:A:263:ASN:HD22	1:A:265:ASN:H	1.58	0.51
1:B:323:MET:HE2	1:B:367:LEU:HG	1.91	0.51
1:A:59:ASN:HB2	1:A:445:ASN:ND2	2.26	0.51
1:A:263:ASN:ND2	1:A:265:ASN:HB2	2.26	0.51
1:A:363:GLN:HE22	1:B:363:GLN:HE22	1.59	0.51
1:B:283:GLU:HB2	1:B:307:LEU:HD21	1.92	0.51
1:A:73:THR:HG22	1:A:74:ALA:H	1.76	0.50
1:A:277:THR:OG1	1:A:280:GLU:HG3	2.11	0.50
1:A:113:PHE:O	1:A:117:THR:HG23	2.11	0.50
1:B:224:MET:HE3	1:B:445:ASN:CG	2.31	0.50
1:B:96:MET:HE3	1:B:135:THR:HG23	1.93	0.50
1:A:309:ALA:HB2	1:A:340:VAL:HG12	1.94	0.50
1:B:239:ARG:NE	1:B:243:ARG:HH12	2.05	0.50
1:A:59:ASN:HD22	1:A:445:ASN:HD21	1.58	0.49
1:B:324:ARG:HG2	1:B:324:ARG:NH1	2.26	0.49
1:B:143:LEU:HD13	1:B:449:VAL:HG11	1.94	0.49
1:B:260:LEU:HD22	1:B:294:HIS:CD2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:ARG:NE	1:A:398:ASP:HB3	2.27	0.49
1:A:362:ARG:O	1:A:366:LEU:HD13	2.12	0.49
1:B:335:MET:O	1:B:340:VAL:HG13	2.12	0.49
1:A:295:ALA:O	1:A:296:HIS:HB2	2.12	0.49
1:B:380:ARG:NH2	1:B:426:ASP:OD2	2.42	0.49
1:B:256:LEU:HB3	1:B:287:TRP:CZ3	2.48	0.49
1:A:464:ILE:HG13	1:A:465:GLU:N	2.28	0.49
1:A:93:HIS:HD1	1:A:257:HIS:CE1	2.27	0.48
1:A:324:ARG:HG2	1:A:324:ARG:HH11	1.77	0.48
1:B:365:LEU:O	1:B:369:ARG:HG3	2.13	0.48
1:B:86:ILE:HD12	1:B:431:LEU:HD22	1.95	0.48
1:B:118:ASN:HA	1:B:121:LYS:HZ3	1.75	0.48
1:B:263:ASN:HD21	1:B:265:ASN:HB2	1.78	0.48
1:B:202:GLU:N	1:B:203:PRO:CD	2.77	0.48
1:B:178:HIS:NE2	1:B:396:ARG:HD2	2.29	0.48
1:A:96:MET:HE2	1:A:135:THR:HA	1.96	0.48
1:A:423:ALA:HB2	1:B:102:ARG:HB2	1.94	0.48
1:B:49:LEU:HD13	1:B:65:GLY:HA2	1.96	0.47
1:B:153:HIS:HE1	1:B:230:ALA:O	1.96	0.47
1:B:329:ILE:HG12	1:B:367:LEU:HD21	1.95	0.47
1:B:352:ASN:HB3	1:B:353:ASP:CA	2.44	0.47
1:B:464:ILE:C	1:B:464:ILE:HD12	2.35	0.47
1:A:178:HIS:CE1	1:A:396:ARG:HH11	2.30	0.47
1:A:410:PHE:CZ	1:A:443:VAL:HG21	2.50	0.47
1:B:167:ILE:CG2	1:B:225:LEU:HD11	2.45	0.47
1:B:229:VAL:HB	1:B:256:LEU:HD23	1.96	0.47
1:B:333:LYS:HG2	1:B:376:ALA:O	2.14	0.47
1:A:180:SER:CA	1:A:228:VAL:HG13	2.45	0.47
1:A:365:LEU:HD23	1:A:366:LEU:HD12	1.97	0.47
1:A:243:ARG:O	1:A:247:VAL:HG12	2.14	0.47
1:B:40:VAL:O	1:B:87:PRO:HD3	2.15	0.46
1:A:442:THR:HB	1:A:450:VAL:HB	1.96	0.46
1:A:117:THR:O	1:A:121:LYS:HG3	2.15	0.46
1:B:87:PRO:CG	1:B:402:LEU:HD22	2.44	0.46
1:A:87:PRO:HG2	1:A:387:THR:HG21	1.97	0.46
1:B:176:ARG:NH1	1:B:224:MET:HE2	2.31	0.46
1:A:40:VAL:HG11	1:A:86:ILE:HG12	1.96	0.46
1:A:99:SER:O	1:B:422:GLY:HA3	2.16	0.46
1:A:263:ASN:HD21	1:A:265:ASN:HB2	1.81	0.46
1:B:88:GLY:HA3	1:B:148:THR:OG1	2.17	0.45
1:B:264:VAL:O	1:B:267:ILE:HG22	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:LEU:HB3	1:A:56:ILE:HB	1.97	0.45
1:B:52:ALA:HB1	1:B:65:GLY:O	2.16	0.45
1:B:155:TYR:HA	1:B:182:GLY:HA3	1.99	0.45
1:B:293:TRP:CG	1:B:393:VAL:HG13	2.52	0.45
1:B:368:GLN:HG3	1:B:377:MET:CE	2.46	0.45
1:B:384:GLU:HG3	1:B:388:LEU:HD12	1.98	0.45
1:A:98:GLN:HG2	1:A:123:TRP:CZ2	2.51	0.45
1:B:176:ARG:NH1	1:B:224:MET:CE	2.79	0.45
1:A:349:SER:O	1:A:353:ASP:HB3	2.17	0.45
1:B:176:ARG:NH2	1:B:224:MET:CE	2.80	0.45
1:B:442:THR:HB	1:B:450:VAL:HB	1.99	0.45
1:A:352:ASN:HB3	1:A:353:ASP:CA	2.47	0.44
1:B:33:VAL:HG13	1:B:80:LEU:HD12	1.99	0.44
1:B:234:PRO:HB3	1:B:281:TYR:HE2	1.82	0.44
1:A:155:TYR:CD1	1:A:156:ILE:HG23	2.52	0.44
1:B:358:VAL:HG11	1:B:437:SER:O	2.17	0.44
1:B:261:ALA:O	1:B:298:VAL:O	2.35	0.44
1:A:49:LEU:HD13	1:A:65:GLY:HA2	1.98	0.44
1:A:352:ASN:N	1:A:353:ASP:HA	2.33	0.44
1:A:352:ASN:HB3	1:A:353:ASP:HA	2.00	0.43
1:B:135:THR:O	1:B:139:MET:HE2	2.19	0.43
1:B:148:THR:HG22	1:B:444:VAL:HG22	2.01	0.43
1:A:46:ARG:HA	1:A:46:ARG:HD3	1.90	0.43
1:A:325:LEU:HD12	1:A:325:LEU:HA	1.78	0.43
1:A:455:LEU:HD23	1:A:458:LEU:CD1	2.49	0.43
1:A:244:ASP:O	1:A:247:VAL:HG13	2.18	0.43
1:B:428:VAL:HG23	3:B:521:HOH:O	2.18	0.43
1:A:225:LEU:HD23	1:A:225:LEU:C	2.38	0.43
1:B:323:MET:HE1	1:B:363:GLN:HE21	1.84	0.43
1:A:352:ASN:C	1:A:352:ASN:ND2	2.71	0.42
1:A:153:HIS:HE1	1:A:230:ALA:O	2.02	0.42
1:A:262:GLU:O	1:A:298:VAL:CG1	2.67	0.42
1:B:317:HIS:ND1	1:B:332:VAL:HG21	2.33	0.42
1:A:183:ALA:HB1	1:A:205:ILE:HD12	2.00	0.42
1:A:59:ASN:ND2	1:A:222:TYR:HB3	2.35	0.42
1:B:479:ARG:HG3	1:B:479:ARG:NH1	2.31	0.42
1:A:176:ARG:HG3	1:A:224:MET:HA	2.01	0.42
1:B:86:ILE:CG2	1:B:87:PRO:N	2.81	0.42
1:B:257:HIS:HD2	1:B:293:TRP:O	2.03	0.42
1:B:368:GLN:HG3	1:B:377:MET:HE2	2.02	0.41
1:B:445:ASN:HD22	1:B:445:ASN:HA	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:ARG:NH1	1:A:172:ARG:CB	2.83	0.41
1:A:306:GLY:O	1:A:310:ARG:HG2	2.20	0.41
1:A:335:MET:HB3	1:A:340:VAL:HG21	2.00	0.41
1:A:363:GLN:HE22	1:B:363:GLN:NE2	2.18	0.41
1:B:41:THR:O	1:B:42:MET:HB2	2.20	0.41
1:B:94:HIS:ND1	1:B:95:HIS:N	2.68	0.41
1:B:136:LEU:HG	1:B:169:ALA:HB1	2.02	0.41
1:A:416:ARG:HB2	1:A:416:ARG:HH11	1.85	0.41
1:B:149:THR:OG1	1:B:176:ARG:HD2	2.21	0.41
1:A:142:LEU:HB3	1:A:147:CYS:HB3	2.02	0.41
1:A:352:ASN:ND2	1:B:362:ARG:NH1	2.67	0.41
1:B:221:ARG:NE	1:B:398:ASP:HB3	2.35	0.41
1:B:337:LEU:HD12	1:B:337:LEU:HA	1.92	0.41
1:A:227:VAL:HG12	1:A:228:VAL:N	2.36	0.41
1:A:73:THR:CG2	1:A:74:ALA:N	2.84	0.41
1:B:167:ILE:HG21	1:B:225:LEU:HD11	2.01	0.41
1:B:221:ARG:HG2	1:B:221:ARG:NH1	2.33	0.41
1:A:50:ARG:HH11	1:A:50:ARG:CG	2.33	0.41
1:A:95:HIS:HE1	1:A:153:HIS:CD2	2.39	0.41
1:A:146:GLY:HA2	1:A:439:THR:HG21	2.02	0.41
1:A:163:LEU:HD12	1:A:212:LEU:HD13	2.02	0.41
1:A:361:VAL:HG22	1:A:386:ALA:HB2	2.03	0.41
1:B:221:ARG:HE	1:B:398:ASP:HB3	1.86	0.41
1:B:262:GLU:HG3	1:B:296:HIS:CG	2.56	0.41
1:A:35:HIS:HD2	1:A:51:ASP:OD1	2.03	0.41
1:A:324:ARG:HG2	1:A:324:ARG:NH1	2.35	0.41
1:B:33:VAL:HG21	1:B:410:PHE:CZ	2.56	0.41
1:B:368:GLN:HG2	3:B:490:HOH:O	2.21	0.41
1:A:239:ARG:HB2	1:A:285:LEU:HD11	2.04	0.40
1:B:317:HIS:HE1	3:B:490:HOH:O	2.04	0.40
1:A:369:ARG:NH2	1:B:109:ASN:OD1	2.53	0.40
1:B:301:ASP:HB3	1:B:304:GLY:H	1.85	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:496:HOH:O	3:B:496:HOH:O[6_554]	1.79	0.41

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	422/479 (88%)	406 (96%)	15 (4%)	1 (0%)	47	55
1	B	422/479 (88%)	399 (94%)	21 (5%)	2 (0%)	29	31
All	All	844/958 (88%)	805 (95%)	36 (4%)	3 (0%)	34	37

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	112	LEU
1	A	296	HIS
1	B	296	HIS

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	337/377 (89%)	317 (94%)	20 (6%)	19	23
1	B	337/377 (89%)	314 (93%)	23 (7%)	16	17
All	All	674/754 (89%)	631 (94%)	43 (6%)	17	20

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	LEU
1	A	40	VAL
1	A	111	GLU

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Mol	Chain	Res	Type
1	A	126	LEU
1	A	163	LEU
1	A	181	ARG
1	A	221	ARG
1	A	228	VAL
1	A	244	ASP
1	A	293	TRP
1	A	324	ARG
1	A	337	LEU
1	A	352	ASN
1	A	367	LEU
1	A	380	ARG
1	A	383	LEU
1	A	394	LEU
1	A	402	LEU
1	A	445	ASN
1	A	464	ILE
1	B	39	LEU
1	B	111	GLU
1	B	163	LEU
1	B	181	ARG
1	B	225	LEU
1	B	228	VAL
1	B	250	ARG
1	B	293	TRP
1	B	298	VAL
1	B	324	ARG
1	B	325	LEU
1	B	336	ARG
1	B	340	VAL
1	B	352	ASN
1	B	358	VAL
1	B	366	LEU
1	B	380	ARG
1	B	394	LEU
1	B	395	ASN
1	B	402	LEU
1	B	445	ASN
1	B	464	ILE
1	B	476	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	HIS
1	A	144	GLN
1	A	153	HIS
1	A	159	ASN
1	A	178	HIS
1	A	210	GLN
1	A	257	HIS
1	A	263	ASN
1	A	317	HIS
1	A	352	ASN
1	A	395	ASN
1	A	425	HIS
1	A	438	GLN
1	A	445	ASN
1	B	118	ASN
1	B	144	GLN
1	B	153	HIS
1	B	178	HIS
1	B	210	GLN
1	B	257	HIS
1	B	265	ASN
1	B	290	HIS
1	B	294	HIS
1	B	317	HIS
1	B	352	ASN
1	B	363	GLN
1	B	395	ASN
1	B	425	HIS
1	B	438	GLN
1	B	445	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	428/479 (89%)	0.22	21 (4%) 29 28	27, 39, 57, 70	0
1	B	428/479 (89%)	0.44	41 (9%) 8 6	29, 44, 66, 79	0
All	All	856/958 (89%)	0.33	62 (7%) 15 14	27, 41, 63, 79	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	113	PHE	6.7
1	B	264	VAL	6.1
1	A	207	ARG	4.7
1	B	303	ALA	4.3
1	B	301	ASP	4.1
1	B	263	ASN	4.0
1	B	269	TYR	3.8
1	A	346	VAL	3.6
1	B	361	VAL	3.5
1	B	265	ASN	3.4
1	B	243	ARG	3.4
1	B	436	PRO	3.3
1	B	235	PHE	3.1
1	B	308	PHE	3.0
1	B	207	ARG	3.0
1	A	359	ALA	2.9
1	A	435	ALA	2.9
1	A	436	PRO	2.9
1	A	269	TYR	2.9
1	B	311	THR	2.9
1	A	354	GLY	2.8
1	B	476	GLU	2.8
1	A	344	LEU	2.8
1	B	358	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	277	THR	2.7
1	B	304	GLY	2.7
1	A	72	GLU	2.6
1	B	29	LYS	2.6
1	B	287	TRP	2.6
1	B	278	PRO	2.6
1	B	44	ASP	2.6
1	A	355	ALA	2.6
1	B	55	TYR	2.5
1	A	432	VAL	2.5
1	A	81	ARG	2.5
1	A	267	ILE	2.5
1	A	251	GLU	2.4
1	B	479	ARG	2.4
1	A	357	MET	2.4
1	A	60	ARG	2.4
1	B	266	ASP	2.3
1	A	241	LEU	2.3
1	A	235	PHE	2.3
1	B	299	GLN	2.3
1	B	346	VAL	2.3
1	A	366	LEU	2.3
1	B	338	ALA	2.3
1	B	121	LYS	2.3
1	A	434	CYS	2.3
1	B	268	ALA	2.3
1	B	72	GLU	2.2
1	B	298	VAL	2.2
1	B	111	GLU	2.2
1	B	357	MET	2.2
1	B	118	ASN	2.1
1	B	319	PRO	2.1
1	B	364	ALA	2.1
1	B	71	PRO	2.1
1	B	60	ARG	2.0
1	A	29	LYS	2.0
1	B	267	ILE	2.0
1	B	333	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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
2	ZN	A	480	1/1	0.98	0.13	43,43,43,43	0
2	ZN	B	480	1/1	0.98	0.13	45,45,45,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.