



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 05:17 am BST

PDB ID : 4KBL
Title : Structure of HHARI, a RING-IBR-RING ubiquitin ligase: autoinhibition of an Ariadne-family E3 and insights into ligation mechanism
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Deposited on : 2013-04-23
Resolution : 3.30 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

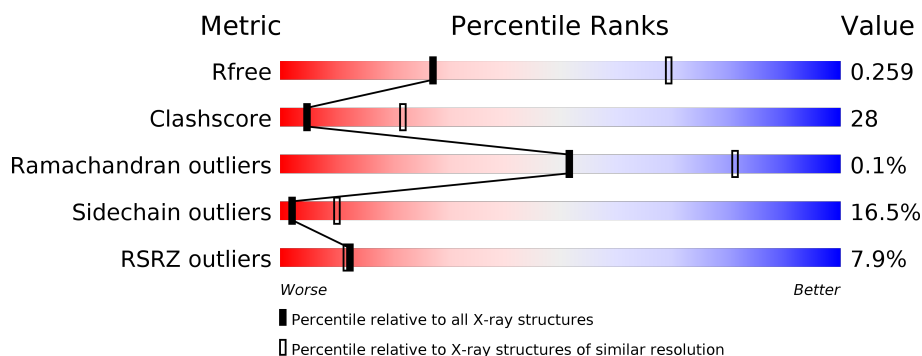
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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 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	559	
1	B	559	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6581 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 E3 ubiquitin-protein ligase ARIH1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	395	Total	C	N	O	S	0	0	0
			3286	2084	579	582	41			
1	B	394	Total	C	N	O	S	0	0	0
			3283	2082	577	584	40			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP Q9Y4X5
A	0	SER	-	EXPRESSION TAG	UNP Q9Y4X5
B	-1	GLY	-	EXPRESSION TAG	UNP Q9Y4X5
B	0	SER	-	EXPRESSION TAG	UNP Q9Y4X5

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	6	Total	Zn	0	0
			6	6		
2	A	6	Total	Zn	0	0
			6	6		



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	147.40 Å 147.40 Å 86.82 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.61 – 3.30 46.61 – 3.28	Depositor EDS
% Data completeness (in resolution range)	92.4 (46.61-3.30) 97.1 (46.61-3.28)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.78 (at 3.25 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.231 , 0.283 0.217 , 0.259	Depositor DCC
R_{free} test set	2162 reflections (7.75%)	wwPDB-VP
Wilson B-factor (Å ²)	125.3	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 100.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.448 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6581	wwPDB-VP
Average B, all atoms (Å ²)	132.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.50% 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	0/3366	0.63	3/4538 (0.1%)
1	B	0.35	0/3362	0.62	0/4531
All	All	0.35	0/6728	0.62	3/9069 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	2
All	All	0	6

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	253	LYS	N-CA-C	-5.44	96.30	111.00
1	A	355	GLY	N-CA-C	-5.36	99.69	113.10
1	A	379	TRP	N-CA-C	-5.04	97.39	111.00

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	193	TYR	Peptide
1	A	312	HIS	Peptide
1	A	378	PRO	Peptide

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Mol	Chain	Res	Type	Group
1	A	456	GLN	Peptide
1	B	312	HIS	Peptide
1	B	552	TRP	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3286	0	3180	185	0
1	B	3283	0	3172	187	0
2	A	6	0	0	0	0
2	B	6	0	0	0	0
All	All	6581	0	6352	359	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 28.

All (359) 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:B:220:ILE:HD11	1:B:254:VAL:HG13	1.30	1.05
1:A:441:LYS:NZ	1:A:514:SER:OG	1.91	1.03
1:A:116:CYS:SG	1:A:142:LYS:NZ	2.36	0.98
1:B:213:SER:O	1:B:217:THR:OG1	1.83	0.96
1:B:100:ARG:HE	1:B:288:GLN:HG3	1.27	0.95
1:A:213:SER:O	1:A:217:THR:OG1	1.84	0.95
1:B:124:ILE:HG23	1:B:149:TYR:HE1	1.33	0.93
1:B:381:PRO:HB2	1:B:387:TYR:HD2	1.31	0.93
1:A:498:LEU:HD22	1:A:536:ARG:HA	1.52	0.92
1:B:482:LEU:HD21	1:B:552:TRP:HB3	1.50	0.92
1:B:392:TYR:CD2	1:B:413:ARG:HG3	2.07	0.90
1:B:315:VAL:HG21	1:B:477:VAL:HG12	1.55	0.88
1:B:113:MET:HE2	1:B:263:THR:HG22	1.57	0.87
1:A:299:CYS:N	1:A:300:GLY:HA2	1.92	0.82
1:A:129:THR:HG21	1:A:241:ASP:HA	1.59	0.82
1:A:549:LYS:HB3	1:A:551:LEU:CD1	2.11	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:LYS:C	1:A:207:PHE:HD1	1.86	0.79
1:B:129:THR:HG21	1:B:241:ASP:HA	1.65	0.78
1:A:190:TYR:O	1:B:530:ARG:NH1	2.18	0.77
1:A:425:MET:HG2	1:A:473:MET:SD	2.24	0.77
1:A:189:CYS:O	1:B:529:TYR:OH	2.02	0.76
1:A:549:LYS:HB3	1:A:551:LEU:HD13	1.67	0.75
1:B:299:CYS:N	1:B:300:GLY:HA2	2.00	0.75
1:A:220:ILE:HD11	1:A:254:VAL:HG22	1.69	0.75
1:B:100:ARG:NE	1:B:288:GLN:HG3	2.01	0.75
1:A:130:ILE:HA	1:A:133:ILE:HD12	1.69	0.75
1:A:103:VAL:HG11	1:A:298:LYS:HE2	1.69	0.75
1:B:113:MET:O	1:B:117:ILE:HG12	1.87	0.74
1:A:125:GLN:O	1:A:125:GLN:HG2	1.86	0.74
1:B:299:CYS:HB3	1:B:301:ARG:H	1.53	0.73
1:A:249:ILE:O	1:A:249:ILE:HD13	1.89	0.73
1:B:438:VAL:O	1:B:442:MET:HG2	1.90	0.71
1:B:372:CYS:HB3	1:B:382:HIS:CE1	2.26	0.71
1:A:109:ILE:HD11	1:A:273:LEU:HD13	1.73	0.70
1:B:361:VAL:HG12	1:B:370:GLU:HG2	1.71	0.70
1:B:479:ALA:HA	1:B:482:LEU:HB2	1.73	0.70
1:B:233:ALA:C	1:B:235:GLY:HA3	2.11	0.70
1:B:472:LEU:HD21	1:B:498:LEU:HG	1.74	0.70
1:A:149:TYR:HD2	1:A:150:PHE:CD1	2.09	0.70
1:B:359:HIS:O	1:B:511:ARG:NH2	2.24	0.70
1:A:424:HIS:CE1	1:A:472:LEU:HD23	2.27	0.70
1:A:508:TYR:HE2	1:A:525:VAL:HG23	1.58	0.69
1:A:516:ASP:OD2	1:A:524:LYS:NZ	2.20	0.69
1:B:116:CYS:SG	1:B:142:LYS:NZ	2.59	0.69
1:A:189:CYS:O	1:A:190:TYR:HB2	1.92	0.69
1:A:431:GLU:HG2	1:A:465:LEU:HG	1.74	0.68
1:A:315:VAL:HG21	1:A:477:VAL:HG12	1.75	0.68
1:A:214:GLU:O	1:A:218:THR:HG23	1.92	0.68
1:B:287:VAL:HG12	1:B:288:GLN:N	2.08	0.68
1:B:110:LEU:HD22	1:B:259:GLN:HG2	1.74	0.68
1:B:297:CYS:O	1:B:298:LYS:HB2	1.94	0.67
1:A:472:LEU:HD11	1:A:498:LEU:HG	1.77	0.67
1:B:316:LYS:HB2	1:B:319:TRP:HD1	1.58	0.67
1:A:482:LEU:HD11	1:A:552:TRP:HB3	1.77	0.67
1:A:120:VAL:HG12	1:A:120:VAL:O	1.95	0.67
1:A:452:TRP:N	1:A:454:GLU:OE2	2.28	0.67
1:B:197:TYR:O	1:B:209:MET:N	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:TYR:O	1:A:209:MET:N	2.27	0.66
1:A:379:TRP:CD1	1:A:380:GLU:HB3	2.30	0.66
1:A:337:ILE:HG22	1:A:338:ALA:H	1.60	0.66
1:A:425:MET:HG2	1:A:473:MET:CE	2.26	0.65
1:A:191:LEU:HB2	1:A:193:TYR:CE2	2.32	0.65
1:B:220:ILE:CD1	1:B:254:VAL:HG13	2.18	0.65
1:A:315:VAL:HG21	1:A:477:VAL:CG1	2.27	0.64
1:B:407:SER:O	1:B:407:SER:OG	2.14	0.64
1:B:299:CYS:HB3	1:B:301:ARG:N	2.11	0.64
1:A:110:LEU:HD22	1:A:259:GLN:HG2	1.79	0.63
1:B:381:PRO:HB2	1:B:387:TYR:CD2	2.24	0.63
1:B:323:TRP:HZ3	1:B:421:TYR:CE1	2.17	0.62
1:A:109:ILE:HD11	1:A:273:LEU:CD1	2.29	0.62
1:B:149:TYR:HD2	1:B:150:PHE:CD1	2.15	0.62
1:A:222:GLU:OE2	1:A:223:GLU:HA	1.99	0.62
1:B:427:SER:HB3	1:B:469:ARG:HD2	1.82	0.62
1:A:105:THR:N	1:A:108:GLN:OE1	2.22	0.62
1:B:470:ALA:HA	1:B:473:MET:HE3	1.81	0.62
1:A:353:LYS:HG2	1:A:355:GLY:O	2.00	0.61
1:B:464:VAL:HG11	1:B:529:TYR:HB2	1.83	0.61
1:B:297:CYS:O	1:B:298:LYS:CB	2.49	0.61
1:A:120:VAL:CG2	1:A:142:LYS:HD3	2.30	0.61
1:B:392:TYR:CE2	1:B:413:ARG:HG3	2.35	0.61
1:A:428:LEU:O	1:A:428:LEU:HD12	2.00	0.61
1:B:206:LYS:C	1:B:207:PHE:CD1	2.74	0.61
1:B:431:GLU:OE2	1:B:465:LEU:HD21	2.01	0.61
1:A:309:GLU:OE1	1:A:321:LYS:HE3	2.00	0.61
1:A:539:LEU:O	1:A:543:VAL:HG13	2.01	0.60
1:A:191:LEU:HD13	1:B:533:GLU:HG3	1.82	0.60
1:B:149:TYR:CD2	1:B:150:PHE:CD1	2.89	0.60
1:A:110:LEU:O	1:A:114:VAL:HG23	2.01	0.60
1:A:153:ASN:ND2	1:A:153:ASN:O	2.34	0.60
1:A:184:MET:N	1:A:185:PRO:HD3	2.16	0.60
1:A:270:ASN:OD1	1:A:271:ARG:N	2.35	0.59
1:B:285:VAL:HG21	1:B:295:VAL:HG11	1.84	0.59
1:B:353:LYS:HE2	1:B:355:GLY:O	2.02	0.59
1:A:530:ARG:NH1	1:B:190:TYR:O	2.36	0.59
1:B:452:TRP:N	1:B:454:GLU:OE1	2.35	0.59
1:B:113:MET:CE	1:B:263:THR:HG22	2.28	0.59
1:B:323:TRP:HZ3	1:B:421:TYR:CZ	2.20	0.59
1:B:425:MET:HB2	1:B:473:MET:SD	2.43	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:PHE:N	1:A:207:PHE:CD1	2.71	0.59
1:A:516:ASP:OD1	1:A:517:SER:N	2.35	0.59
1:B:250:THR:OG1	1:B:251:ASP:N	2.34	0.59
1:A:349:VAL:CG1	1:A:350:THR:N	2.66	0.58
1:A:293:LYS:HB3	1:A:294:PRO:CD	2.32	0.58
1:A:379:TRP:HD1	1:A:380:GLU:HB3	1.67	0.58
1:B:355:GLY:HA2	1:B:430:PHE:HB3	1.86	0.58
1:A:250:THR:OG1	1:A:251:ASP:N	2.36	0.58
1:A:549:LYS:HB3	1:A:551:LEU:HD11	1.84	0.57
1:B:511:ARG:HG3	1:B:512:ASP:N	2.19	0.57
1:A:244:THR:HG22	1:A:247:ARG:NH1	2.19	0.57
1:B:323:TRP:CH2	1:B:421:TYR:CG	2.92	0.57
1:B:539:LEU:HD13	1:B:539:LEU:C	2.24	0.57
1:B:101:TYR:CD1	1:B:295:VAL:HG22	2.39	0.57
1:B:287:VAL:HG12	1:B:289:TYR:H	1.70	0.57
1:A:539:LEU:HD13	1:A:539:LEU:C	2.25	0.57
1:A:381:PRO:HG2	1:A:387:TYR:HD1	1.70	0.56
1:B:241:ASP:OD1	1:B:244:THR:HG23	2.06	0.56
1:B:316:LYS:HB2	1:B:319:TRP:CD1	2.40	0.56
1:B:134:LEU:HD22	1:B:145:LEU:HD11	1.87	0.56
1:A:127:PRO:HG2	1:A:130:ILE:CG1	2.36	0.56
1:B:186:CYS:HB2	1:B:198:PHE:HE1	1.70	0.56
1:B:238:ILE:HD12	1:B:239:LEU:N	2.21	0.56
1:A:207:PHE:N	1:A:207:PHE:HD1	2.04	0.55
1:B:124:ILE:HG23	1:B:149:TYR:CE1	2.26	0.55
1:B:285:VAL:HG21	1:B:295:VAL:CG1	2.35	0.55
1:A:411:LEU:HD13	1:A:411:LEU:O	2.07	0.55
1:B:478:PHE:O	1:B:479:ALA:HB3	2.07	0.55
1:B:311:TRP:CE3	1:B:311:TRP:HA	2.42	0.55
1:B:278:ALA:HB3	1:B:281:CYS:HB3	1.87	0.55
1:B:234:HIS:N	1:B:235:GLY:HA3	2.22	0.55
1:B:287:VAL:HG23	1:B:305:PHE:CE1	2.42	0.55
1:A:208:CYS:SG	1:A:211:CYS:HB2	2.46	0.54
1:B:413:ARG:NH2	1:B:480:PHE:O	2.39	0.54
1:B:236:CYS:SG	1:B:238:ILE:HG23	2.48	0.54
1:B:312:HIS:HE1	1:B:317:CYS:SG	2.29	0.54
1:A:316:LYS:HB2	1:A:319:TRP:HD1	1.71	0.54
1:B:461:ALA:HB1	1:B:509:LEU:HD21	1.89	0.54
1:A:371:PHE:CD1	1:A:371:PHE:N	2.76	0.53
1:B:100:ARG:HB2	1:B:288:GLN:HG3	1.90	0.53
1:A:350:THR:O	1:A:351:ILE:HD13	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:539:LEU:O	1:B:543:VAL:HG23	2.08	0.53
1:A:126:ASN:HB3	1:A:127:PRO:HD2	1.92	0.52
1:A:392:TYR:CE2	1:A:413:ARG:HB2	2.43	0.52
1:B:319:TRP:CZ3	1:B:322:LYS:HE3	2.44	0.52
1:B:327:CYS:O	1:B:328:ASP:HB2	2.08	0.52
1:B:504:VAL:HG12	1:B:505:LEU:N	2.23	0.52
1:B:312:HIS:HB2	1:B:315:VAL:HG12	1.92	0.52
1:A:457:PHE:CE2	1:A:522:LYS:HD3	2.45	0.52
1:A:549:LYS:O	1:A:550:ASP:HB2	2.10	0.52
1:A:244:THR:HG22	1:A:247:ARG:HH12	1.74	0.52
1:A:254:VAL:HG12	1:A:255:LYS:N	2.25	0.52
1:B:249:ILE:HG22	1:B:255:LYS:HB2	1.91	0.52
1:A:125:GLN:O	1:A:125:GLN:CG	2.57	0.51
1:A:297:CYS:C	1:A:298:LYS:HG3	2.30	0.51
1:B:240:VAL:CG1	1:B:245:VAL:HG23	2.40	0.51
1:A:142:LYS:O	1:A:146:MET:HG2	2.10	0.51
1:B:287:VAL:HG12	1:B:288:GLN:H	1.72	0.51
1:B:206:LYS:O	1:B:207:PHE:CD1	2.64	0.51
1:B:233:ALA:O	1:B:235:GLY:HA3	2.10	0.51
1:B:101:TYR:HD1	1:B:295:VAL:HG22	1.76	0.51
1:A:443:GLU:HA	1:A:443:GLU:OE1	2.10	0.51
1:B:482:LEU:CD2	1:B:552:TRP:HB3	2.32	0.51
1:B:287:VAL:CG1	1:B:288:GLN:N	2.74	0.51
1:B:319:TRP:HB3	1:B:481:TYR:CD2	2.46	0.51
1:A:299:CYS:N	1:A:300:GLY:CA	2.71	0.50
1:A:318:LYS:HE3	1:A:319:TRP:CZ2	2.46	0.50
1:B:240:VAL:HG11	1:B:245:VAL:HG23	1.93	0.50
1:B:206:LYS:C	1:B:207:PHE:HD1	2.14	0.50
1:A:189:CYS:HB2	1:B:460:LYS:HG3	1.94	0.50
1:A:312:HIS:HB2	1:A:315:VAL:HG12	1.93	0.50
1:A:465:LEU:HD22	1:A:506:SER:HA	1.93	0.50
1:B:297:CYS:O	1:B:297:CYS:SG	2.70	0.50
1:A:120:VAL:CG1	1:A:120:VAL:O	2.59	0.50
1:B:186:CYS:HB2	1:B:198:PHE:CE1	2.46	0.50
1:B:367:CYS:O	1:B:367:CYS:SG	2.69	0.50
1:A:127:PRO:HG2	1:A:130:ILE:HG12	1.94	0.50
1:A:220:ILE:HD11	1:A:254:VAL:HG13	1.93	0.50
1:A:467:GLN:HG2	1:A:536:ARG:NH1	2.26	0.50
1:B:431:GLU:OE2	1:B:465:LEU:HD11	2.11	0.50
1:B:217:THR:HG23	1:B:254:VAL:HG11	1.94	0.50
1:B:552:TRP:O	1:B:553:GLU:HB2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:323:TRP:CG	1:A:477:VAL:HG22	2.47	0.49
1:A:391:ARG:HD2	1:A:492:GLU:HB3	1.93	0.49
1:B:216:LEU:O	1:B:220:ILE:HG23	2.11	0.49
1:A:189:CYS:CB	1:B:460:LYS:HG3	2.42	0.49
1:A:103:VAL:HG11	1:A:298:LYS:CE	2.39	0.49
1:B:100:ARG:HB2	1:B:288:GLN:CG	2.41	0.49
1:A:109:ILE:HG21	1:A:263:THR:HG21	1.92	0.49
1:A:530:ARG:HH22	1:B:192:ASN:HD21	1.61	0.49
1:A:139:ASN:O	1:A:140:TRP:HB2	2.13	0.49
1:A:191:LEU:HB2	1:A:193:TYR:HE2	1.76	0.49
1:B:382:HIS:CD2	1:B:389:CYS:HB2	2.47	0.49
1:A:315:VAL:HG22	1:A:316:LYS:N	2.27	0.49
1:A:201:LEU:HD11	1:A:240:VAL:HA	1.93	0.49
1:A:317:CYS:O	1:A:321:LYS:HG2	2.13	0.49
1:A:135:LEU:HD13	1:A:140:TRP:CZ3	2.47	0.48
1:B:100:ARG:HD3	1:B:100:ARG:H	1.78	0.48
1:B:201:LEU:HD22	1:B:240:VAL:HG22	1.95	0.48
1:B:323:TRP:CZ3	1:B:421:TYR:CZ	3.01	0.48
1:B:545:GLU:O	1:B:548:GLU:HB2	2.13	0.48
1:A:149:TYR:CD2	1:A:150:PHE:CD1	2.97	0.48
1:A:316:LYS:HB2	1:A:319:TRP:CD1	2.49	0.48
1:B:130:ILE:HA	1:B:133:ILE:HD11	1.95	0.48
1:A:220:ILE:HG22	1:A:229:ILE:HD11	1.95	0.48
1:A:392:TYR:CD2	1:A:413:ARG:HG3	2.49	0.48
1:A:457:PHE:CZ	1:A:522:LYS:HD3	2.48	0.48
1:A:529:TYR:HE1	1:B:191:LEU:HD13	1.78	0.48
1:B:138:PHE:CD2	1:B:145:LEU:HD13	2.49	0.48
1:B:472:LEU:HA	1:B:475:THR:OG1	2.14	0.48
1:A:233:ALA:C	1:A:235:GLY:H	2.17	0.47
1:A:292:ALA:HB2	1:A:306:ASN:HB2	1.95	0.47
1:A:381:PRO:HG2	1:A:387:TYR:CD1	2.49	0.47
1:A:517:SER:O	1:A:521:ILE:HG23	2.14	0.47
1:A:322:LYS:HE3	1:A:322:LYS:HB2	1.58	0.47
1:B:121:ASN:ND2	1:B:128:ALA:HA	2.29	0.47
1:B:201:LEU:CD2	1:B:240:VAL:HG22	2.44	0.47
1:B:460:LYS:HA	1:B:463:ASP:HB2	1.96	0.47
1:B:295:VAL:O	1:B:302:GLN:HA	2.14	0.47
1:B:215:TYR:CE1	1:B:219:LYS:HD3	2.50	0.47
1:B:129:THR:O	1:B:133:ILE:HG12	2.14	0.47
1:B:452:TRP:CE3	1:B:453:ILE:HD13	2.50	0.47
1:B:327:CYS:O	1:B:328:ASP:CB	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:452:TRP:CZ3	1:B:453:ILE:HD13	2.49	0.47
1:B:505:LEU:HD11	1:B:509:LEU:HD22	1.96	0.47
1:B:234:HIS:N	1:B:235:GLY:CA	2.78	0.47
1:B:311:TRP:HA	1:B:311:TRP:HE3	1.80	0.47
1:B:323:TRP:CH2	1:B:421:TYR:CD1	3.03	0.47
1:B:420:ARG:HD3	1:B:476:TYR:CZ	2.50	0.47
1:A:297:CYS:O	1:A:297:CYS:SG	2.73	0.46
1:A:289:TYR:HA	1:A:290:PRO:HD3	1.68	0.46
1:A:367:CYS:SG	1:A:367:CYS:O	2.73	0.46
1:A:296:ARG:NH1	1:A:300:GLY:O	2.48	0.46
1:B:103:VAL:HG11	1:B:298:LYS:HD2	1.97	0.46
1:B:323:TRP:CZ3	1:B:421:TYR:CE1	3.02	0.46
1:A:361:VAL:HG22	1:A:361:VAL:O	2.15	0.46
1:A:431:GLU:OE1	1:A:469:ARG:HD2	2.15	0.46
1:B:217:THR:CG2	1:B:254:VAL:HG11	2.45	0.46
1:B:217:THR:HG22	1:B:254:VAL:HG21	1.98	0.46
1:A:210:GLN:N	1:A:210:GLN:OE1	2.41	0.46
1:A:480:PHE:CE2	1:A:481:TYR:CE1	3.04	0.46
1:A:427:SER:HB3	1:A:469:ARG:CD	2.46	0.46
1:A:349:VAL:HG12	1:A:350:THR:N	2.29	0.46
1:A:109:ILE:CG2	1:A:263:THR:HG21	2.45	0.46
1:A:299:CYS:HB3	1:A:301:ARG:H	1.81	0.46
1:A:120:VAL:HG21	1:A:142:LYS:HD3	1.98	0.46
1:A:327:CYS:HB3	1:A:422:MET:CE	2.46	0.46
1:B:312:HIS:O	1:B:314:PRO:HD2	2.16	0.45
1:B:539:LEU:CD1	1:B:539:LEU:C	2.84	0.45
1:A:312:HIS:O	1:A:314:PRO:HD2	2.16	0.45
1:A:431:GLU:HG2	1:A:465:LEU:CG	2.44	0.45
1:A:231:CYS:SG	1:A:232:PRO:HD2	2.57	0.45
1:A:371:PHE:HA	1:A:379:TRP:H	1.81	0.45
1:B:323:TRP:CD2	1:B:477:VAL:HG22	2.51	0.45
1:B:345:PRO:HG3	1:B:376:LEU:O	2.16	0.45
1:A:240:VAL:HG12	1:A:245:VAL:HG23	1.98	0.45
1:A:551:LEU:HD13	1:A:551:LEU:N	2.31	0.45
1:A:460:LYS:HE2	1:B:189:CYS:HB2	1.98	0.45
1:A:190:TYR:CE1	1:B:526:GLN:NE2	2.85	0.45
1:A:101:TYR:CD2	1:A:295:VAL:HB	2.52	0.45
1:B:482:LEU:HD11	1:B:552:TRP:CE3	2.52	0.45
1:B:356:GLY:O	1:B:469:ARG:NH1	2.50	0.45
1:B:513:ILE:C	1:B:515:GLN:N	2.70	0.45
1:A:371:PHE:N	1:A:371:PHE:HD1	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:539:LEU:HD13	1:A:539:LEU:O	2.16	0.45
1:A:223:GLU:HG2	1:A:224:GLY:N	2.32	0.44
1:B:135:LEU:HD23	1:B:145:LEU:HD22	1.99	0.44
1:A:482:LEU:CD1	1:A:552:TRP:HB3	2.44	0.44
1:B:420:ARG:HD3	1:B:476:TYR:OH	2.18	0.44
1:A:299:CYS:HB3	1:A:301:ARG:N	2.32	0.44
1:B:205:HIS:HB3	1:B:207:PHE:HE1	1.82	0.44
1:A:539:LEU:C	1:A:539:LEU:CD1	2.85	0.44
1:B:105:THR:CB	1:B:108:GLN:HG3	2.47	0.44
1:B:188:ILE:HB	1:B:211:CYS:SG	2.58	0.44
1:A:190:TYR:CD1	1:B:526:GLN:NE2	2.86	0.44
1:A:193:TYR:N	1:A:193:TYR:CD2	2.85	0.44
1:A:529:TYR:CD1	1:A:529:TYR:C	2.91	0.44
1:A:530:ARG:HH12	1:B:192:ASN:ND2	2.16	0.44
1:B:249:ILE:CG2	1:B:255:LYS:HB2	2.48	0.44
1:B:303:PHE:HA	1:B:310:ASN:HA	1.98	0.44
1:A:276:CYS:HA	1:A:277:PRO:HD3	1.63	0.43
1:A:272:LEU:N	1:A:272:LEU:HD23	2.33	0.43
1:B:216:LEU:HG	1:B:245:VAL:HG22	1.99	0.43
1:A:460:LYS:HE2	1:B:189:CYS:CB	2.48	0.43
1:B:275:TRP:CZ3	1:B:284:VAL:HG12	2.53	0.43
1:A:355:GLY:HA2	1:A:430:PHE:HB3	2.00	0.43
1:A:413:ARG:NH2	1:A:480:PHE:O	2.52	0.43
1:B:392:TYR:HB2	1:B:416:PHE:CD2	2.53	0.43
1:A:124:ILE:HD11	1:A:131:THR:OG1	2.19	0.43
1:B:254:VAL:HG12	1:B:255:LYS:N	2.33	0.43
1:A:278:ALA:HA	1:A:279:PRO:HD3	1.76	0.43
1:B:133:ILE:HG12	1:B:133:ILE:H	1.49	0.43
1:B:146:MET:O	1:B:149:TYR:HB3	2.18	0.43
1:B:245:VAL:HG11	1:B:258:TYR:CZ	2.54	0.43
1:B:99:TYR:OH	1:B:287:VAL:HG11	2.19	0.43
1:A:534:SER:O	1:A:538:VAL:HG23	2.18	0.43
1:B:411:LEU:CD1	1:B:415:LEU:HD22	2.49	0.42
1:A:344:CYS:O	1:A:348:HIS:N	2.51	0.42
1:A:431:GLU:CG	1:A:465:LEU:HD21	2.50	0.42
1:A:549:LYS:O	1:A:550:ASP:CB	2.67	0.42
1:B:287:VAL:CG1	1:B:288:GLN:H	2.33	0.42
1:B:533:GLU:OE1	1:B:536:ARG:NH1	2.52	0.42
1:B:322:LYS:HB2	1:B:322:LYS:HE2	1.94	0.42
1:B:359:HIS:HB2	1:B:379:TRP:CZ2	2.55	0.42
1:B:425:MET:HE2	1:B:429:ARG:HH12	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:ILE:HG12	1:A:238:ILE:O	2.19	0.42
1:B:376:LEU:HD13	1:B:376:LEU:HA	1.55	0.42
1:B:130:ILE:HD13	1:B:133:ILE:HD11	2.02	0.42
1:B:197:TYR:O	1:B:209:MET:HG2	2.19	0.42
1:A:220:ILE:CD1	1:A:254:VAL:HG13	2.49	0.42
1:A:499:GLU:O	1:A:503:GLU:HG2	2.19	0.42
1:B:421:TYR:C	1:B:421:TYR:CD1	2.92	0.42
1:B:393:ASN:O	1:B:394:GLU:HB3	2.20	0.42
1:B:508:TYR:HA	1:B:512:ASP:HB2	2.02	0.42
1:A:222:GLU:HG3	1:A:223:GLU:HB2	2.02	0.42
1:A:469:ARG:O	1:A:473:MET:HG3	2.20	0.42
1:A:323:TRP:HZ3	1:A:421:TYR:CD1	2.38	0.42
1:A:457:PHE:CD2	1:A:457:PHE:N	2.86	0.42
1:B:323:TRP:CZ3	1:B:421:TYR:CD1	3.08	0.42
1:A:431:GLU:O	1:A:434:LEU:HB2	2.19	0.41
1:B:220:ILE:HA	1:B:225:MET:SD	2.60	0.41
1:B:534:SER:O	1:B:538:VAL:HG23	2.20	0.41
1:A:299:CYS:H	1:A:300:GLY:HA2	1.80	0.41
1:A:551:LEU:CD1	1:A:551:LEU:N	2.84	0.41
1:B:201:LEU:HD23	1:B:231:CYS:HB2	2.03	0.41
1:A:319:TRP:HB3	1:A:481:TYR:HD2	1.86	0.41
1:B:104:LEU:HB3	1:B:108:GLN:HB2	2.01	0.41
1:B:482:LEU:HA	1:B:482:LEU:HD23	1.63	0.41
1:A:348:HIS:ND1	1:A:348:HIS:N	2.67	0.41
1:A:315:VAL:CG2	1:A:477:VAL:HG12	2.48	0.41
1:B:208:CYS:SG	1:B:211:CYS:HB2	2.60	0.41
1:A:222:GLU:HA	1:A:223:GLU:HA	1.74	0.41
1:A:380:GLU:N	1:A:381:PRO:CD	2.84	0.41
1:A:416:PHE:CE1	1:A:420:ARG:CZ	3.03	0.41
1:A:457:PHE:CD2	1:A:522:LYS:HE2	2.56	0.41
1:B:231:CYS:HA	1:B:232:PRO:HD3	1.68	0.41
1:B:275:TRP:CE3	1:B:284:VAL:HG12	2.56	0.41
1:B:499:GLU:O	1:B:503:GLU:HG2	2.19	0.41
1:A:222:GLU:HG3	1:A:223:GLU:CB	2.51	0.41
1:A:135:LEU:HD23	1:A:145:LEU:HD22	2.02	0.41
1:A:297:CYS:C	1:A:299:CYS:N	2.70	0.41
1:B:201:LEU:HD12	1:B:201:LEU:HA	1.79	0.41
1:B:217:THR:HG1	1:B:217:THR:H	1.57	0.41
1:B:323:TRP:CZ3	1:B:421:TYR:CE2	3.08	0.41
1:A:110:LEU:CD2	1:A:246:MET:HE3	2.50	0.41
1:B:186:CYS:N	1:B:198:PHE:HZ	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:TRP:CZ3	1:A:284:VAL:HG12	2.55	0.41
1:A:360:MET:HB2	1:A:371:PHE:CE1	2.55	0.41
1:A:392:TYR:CZ	1:A:413:ARG:HB2	2.57	0.41
1:A:323:TRP:CZ3	1:A:421:TYR:CD1	3.08	0.41
1:B:472:LEU:O	1:B:473:MET:C	2.60	0.41
1:A:312:HIS:HE1	1:A:317:CYS:SG	2.44	0.40
1:A:498:LEU:HD12	1:A:498:LEU:O	2.21	0.40
1:A:475:THR:HG21	1:A:539:LEU:HD11	2.03	0.40
1:A:472:LEU:CD1	1:A:498:LEU:HG	2.47	0.40
1:B:270:ASN:OD1	1:B:271:ARG:N	2.54	0.40
1:B:113:MET:HB3	1:B:113:MET:HE2	1.91	0.40
1:A:193:TYR:O	1:A:194:PRO:C	2.59	0.40
1:A:498:LEU:HD21	1:A:536:ARG:HG3	2.03	0.40
1:B:216:LEU:HD12	1:B:229:ILE:HG21	2.04	0.40
1:B:287:VAL:CG2	1:B:305:PHE:CE1	3.05	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	385/559 (69%)	363 (94%)	21 (6%)	1 (0%)	41	71
1	B	382/559 (68%)	361 (94%)	21 (6%)	0	100	100
All	All	767/1118 (69%)	724 (94%)	42 (6%)	1 (0%)	51	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	194	PRO

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	364/489 (74%)	305 (84%)	59 (16%)	2	10
1	B	364/489 (74%)	303 (83%)	61 (17%)	2	9
All	All	728/978 (74%)	608 (84%)	120 (16%)	2	10

All (120) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	TYR
1	A	121	ASN
1	A	124	ILE
1	A	125	GLN
1	A	129	THR
1	A	134	LEU
1	A	153	ASN
1	A	186	CYS
1	A	198	PHE
1	A	201	LEU
1	A	207	PHE
1	A	211	CYS
1	A	213	SER
1	A	216	LEU
1	A	217	THR
1	A	222	GLU
1	A	238	ILE
1	A	239	LEU
1	A	249	ILE
1	A	254	VAL
1	A	271	ARG
1	A	276	CYS
1	A	284	VAL
1	A	289	TYR
1	A	297	CYS
1	A	301	ARG
1	A	323	TRP

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Mol	Chain	Res	Type
1	A	340	ASN
1	A	343	GLU
1	A	348	HIS
1	A	350	THR
1	A	359	HIS
1	A	360	MET
1	A	361	VAL
1	A	362	CYS
1	A	363	ARG
1	A	367	CYS
1	A	370	GLU
1	A	371	PHE
1	A	372	CYS
1	A	376	LEU
1	A	387	TYR
1	A	389	CYS
1	A	415	LEU
1	A	420	ARG
1	A	421	TYR
1	A	425	MET
1	A	427	SER
1	A	431	GLU
1	A	454	GLU
1	A	455	VAL
1	A	472	LEU
1	A	477	VAL
1	A	491	PHE
1	A	504	VAL
1	A	518	LEU
1	A	529	TYR
1	A	549	LYS
1	A	551	LEU
1	B	100	ARG
1	B	101	TYR
1	B	109	ILE
1	B	118	ARG
1	B	124	ILE
1	B	129	THR
1	B	133	ILE
1	B	134	LEU
1	B	136	SER
1	B	151	ASP

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Mol	Chain	Res	Type
1	B	191	LEU
1	B	198	PHE
1	B	202	GLU
1	B	210	GLN
1	B	216	LEU
1	B	217	THR
1	B	231	CYS
1	B	234	HIS
1	B	237	ASP
1	B	238	ILE
1	B	248	LEU
1	B	256	LEU
1	B	261	LEU
1	B	268	GLU
1	B	271	ARG
1	B	293	LYS
1	B	297	CYS
1	B	301	ARG
1	B	309	GLU
1	B	310	ASN
1	B	318	LYS
1	B	325	LYS
1	B	328	ASP
1	B	341	THR
1	B	347	CYS
1	B	350	THR
1	B	359	HIS
1	B	367	CYS
1	B	372	CYS
1	B	376	LEU
1	B	380	GLU
1	B	406	ARG
1	B	407	SER
1	B	415	LEU
1	B	420	ARG
1	B	421	TYR
1	B	427	SER
1	B	430	PHE
1	B	438	VAL
1	B	443	GLU
1	B	454	GLU
1	B	491	PHE

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Mol	Chain	Res	Type
1	B	499	GLU
1	B	504	VAL
1	B	505	LEU
1	B	509	LEU
1	B	511	ARG
1	B	515	GLN
1	B	516	ASP
1	B	529	TYR
1	B	534	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	121	ASN
1	B	192	ASN
1	B	526	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 12 ligands modelled in this entry, 12 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	395/559 (70%)	0.78	27 (6%)	17 17	84, 129, 186, 249	0
1	B	394/559 (70%)	0.80	35 (8%)	9 10	83, 127, 181, 265	0
All	All	789/1118 (70%)	0.79	62 (7%)	12 12	83, 128, 183, 265	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	366	ASN	7.4
1	A	386	TRP	5.5
1	B	206	LYS	3.6
1	B	319	TRP	3.5
1	A	411	LEU	3.3
1	B	227	GLN	3.3
1	B	365	GLN	3.3
1	A	220	ILE	3.1
1	A	478	PHE	3.0
1	B	477	VAL	3.0
1	A	227	GLN	3.0
1	A	498	LEU	2.9
1	B	187	GLN	2.9
1	B	145	LEU	2.9
1	A	351	ILE	2.8
1	A	431	GLU	2.8
1	A	248	LEU	2.8
1	B	136	SER	2.7
1	A	346	LYS	2.7
1	B	311	TRP	2.6
1	A	475	THR	2.6
1	A	455	VAL	2.6
1	B	456	GLN	2.6
1	A	120	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	431	GLU	2.5
1	B	225	MET	2.5
1	B	527	ASP	2.5
1	B	134	LEU	2.5
1	B	327	CYS	2.5
1	A	226	GLY	2.5
1	A	552	TRP	2.4
1	B	315	VAL	2.4
1	B	540	LEU	2.4
1	B	434	LEU	2.4
1	B	125	GLN	2.3
1	A	352	GLU	2.3
1	A	458	LEU	2.3
1	B	188	ILE	2.2
1	A	323	TRP	2.2
1	A	539	LEU	2.2
1	B	267	VAL	2.2
1	B	412	GLN	2.2
1	A	373	TRP	2.2
1	B	473	MET	2.2
1	B	525	VAL	2.2
1	B	552	TRP	2.1
1	A	106	ALA	2.1
1	A	131	THR	2.1
1	B	103	VAL	2.1
1	A	254	VAL	2.1
1	A	132	ARG	2.1
1	A	461	ALA	2.1
1	B	249	ILE	2.1
1	B	386	TRP	2.1
1	B	290	PRO	2.1
1	B	475	THR	2.1
1	A	428	LEU	2.1
1	B	387	TYR	2.1
1	B	539	LEU	2.0
1	B	523	GLN	2.0
1	A	374	VAL	2.0
1	B	482	LEU	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 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. 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(Å ²)	Q<0.9
2	ZN	A	606	1/1	0.92	0.26	159,159,159,159	0
2	ZN	A	603	1/1	0.95	0.30	136,136,136,136	0
2	ZN	A	601	1/1	0.96	0.22	157,157,157,157	0
2	ZN	B	605	1/1	0.96	0.29	139,139,139,139	0
2	ZN	B	604	1/1	0.96	0.24	120,120,120,120	0
2	ZN	A	605	1/1	0.98	0.28	136,136,136,136	0
2	ZN	B	606	1/1	0.98	0.22	163,163,163,163	0
2	ZN	A	604	1/1	0.98	0.27	115,115,115,115	0
2	ZN	B	603	1/1	0.98	0.28	138,138,138,138	0
2	ZN	B	602	1/1	0.99	0.32	109,109,109,109	0
2	ZN	A	602	1/1	0.99	0.27	108,108,108,108	0
2	ZN	B	601	1/1	0.99	0.24	163,163,163,163	0

6.5 Other polymers [i](#)

There are no such residues in this entry.