



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 08:40 PM UTC

PDB ID : 1XA6 / pdb_00001xa6
Title : Crystal Structure of the Human Beta2-Chimaerin
Authors : Canagarajah, B.; Leskow, F.C.; Ho, J.Y.; Mischak, H.; Saidi, L.F.; Kazanietz, M.G.; Hurley, J.H.
Deposited on : 2004-08-25
Resolution : 3.20 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

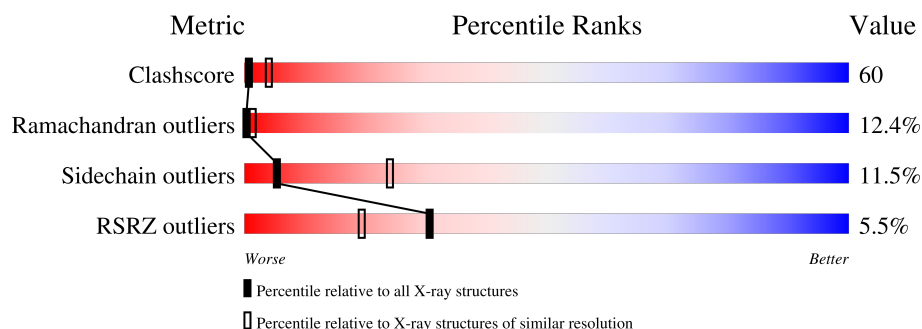
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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))
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	466	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3256 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 Beta2-chimaerin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	399	Total	C	N	O	S	0	0	0
			3254	2078	564	591	21			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	131.09Å 131.09Å 288.75Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.20 20.00 – 3.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-3.20) 99.1 (20.00-3.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 3.11Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.252 , 0.298 0.239 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	105.7	Xtriage
Anisotropy	0.192	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 96.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3256	wwPDB-VP
Average B, all atoms (Å ²)	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% 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	0.51	0/3331	1.12	36/4506 (0.8%)

There are no bond length outliers.

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	157	ALA	N-CA-C	-10.11	99.84	112.88
1	A	41	ILE	N-CA-C	-9.79	99.75	113.07
1	A	139	ALA	N-CA-C	-9.77	101.12	113.23
1	A	336	SER	N-CA-C	8.95	129.86	110.80
1	A	286	THR	N-CA-C	8.71	125.40	113.21
1	A	123	ASP	N-CA-C	-8.63	100.88	111.33
1	A	410	LYS	N-CA-C	-8.27	102.64	112.89
1	A	304	LEU	N-CA-C	-8.17	103.10	113.23
1	A	56	ARG	N-CA-C	-7.63	102.27	114.09
1	A	359	ILE	CA-C-N	6.82	126.81	119.78
1	A	359	ILE	C-N-CA	6.82	126.81	119.78
1	A	57	GLU	N-CA-C	-6.80	104.55	112.92
1	A	335	ILE	N-CA-C	6.77	123.43	109.34
1	A	272	VAL	N-CA-C	-6.66	106.30	112.96
1	A	430	GLY	CA-C-N	6.50	126.43	119.28
1	A	430	GLY	C-N-CA	6.50	126.43	119.28
1	A	335	ILE	CA-C-N	6.47	133.91	121.54
1	A	335	ILE	C-N-CA	6.47	133.91	121.54
1	A	319	ILE	N-CA-C	-6.47	104.45	110.53
1	A	416	LYS	N-CA-C	-5.96	105.78	113.16
1	A	311	ARG	N-CA-C	-5.90	104.83	112.68
1	A	340	TYR	CA-C-N	5.77	124.97	118.97
1	A	340	TYR	C-N-CA	5.77	124.97	118.97
1	A	306	SER	N-CA-C	-5.68	103.03	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	405	MET	N-CA-C	-5.64	98.79	110.80
1	A	35	ALA	CA-C-N	5.62	125.38	119.76
1	A	35	ALA	C-N-CA	5.62	125.38	119.76
1	A	407	HIS	CA-C-N	5.56	132.16	121.54
1	A	407	HIS	C-N-CA	5.56	132.16	121.54
1	A	274	CYS	N-CA-C	5.52	122.55	110.80
1	A	358	PRO	N-CA-C	-5.40	106.50	113.57
1	A	263	GLN	CA-C-N	5.39	126.58	119.84
1	A	263	GLN	C-N-CA	5.39	126.58	119.84
1	A	109	GLY	N-CA-C	-5.23	108.03	115.30
1	A	443	THR	N-CA-C	-5.22	106.92	113.28
1	A	338	ASN	N-CA-C	-5.06	101.90	109.79

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	3254	0	3231	390	0
2	A	2	0	0	0	0
All	All	3256	0	3231	390	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 60.

All (390) 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:28:LEU:HD11	1:A:145:MET:HE1	1.28	1.11
1:A:406:ILE:C	1:A:408:LEU:H	1.61	1.01
1:A:104:ARG:O	1:A:105:LEU:HB2	1.66	0.93
1:A:374:ALA:HB1	1:A:453:LEU:HD23	1.51	0.91
1:A:273:TYR:O	1:A:274:CYS:HB2	1.69	0.89
1:A:315:PHE:HB3	1:A:318:HIS:HB2	1.54	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:ILE:O	1:A:328:ARG:HB2	1.76	0.85
1:A:315:PHE:HD2	1:A:318:HIS:ND1	1.75	0.84
1:A:328:ARG:HG3	1:A:329:ASP:H	1.42	0.83
1:A:160:LEU:HD13	1:A:161:ARG:N	1.93	0.82
1:A:113:VAL:HG12	1:A:114:GLY:N	1.94	0.82
1:A:285:ASN:O	1:A:286:THR:HG23	1.79	0.82
1:A:117:ARG:HH12	1:A:238:ALA:HB2	1.44	0.82
1:A:117:ARG:NH1	1:A:238:ALA:HB2	1.94	0.82
1:A:302:ARG:NH1	1:A:337:ALA:HA	1.94	0.81
1:A:302:ARG:CZ	1:A:337:ALA:HA	2.11	0.81
1:A:421:ASN:H	1:A:424:ASN:HB3	1.45	0.80
1:A:423:GLU:N	1:A:456:GLN:HG3	1.97	0.80
1:A:61:ILE:HG13	1:A:82:GLU:HB3	1.62	0.80
1:A:126:THR:HG21	1:A:236:LEU:HD12	1.64	0.79
1:A:326:PHE:O	1:A:331:GLU:HA	1.83	0.79
1:A:310:TYR:O	1:A:428:VAL:HG21	1.84	0.78
1:A:430:GLY:HA2	1:A:455:VAL:HG21	1.65	0.78
1:A:309:LEU:HD21	1:A:343:ILE:HD11	1.64	0.78
1:A:315:PHE:HD2	1:A:318:HIS:HD1	1.31	0.77
1:A:117:ARG:NH2	1:A:238:ALA:HB2	2.00	0.77
1:A:236:LEU:O	1:A:236:LEU:HD23	1.85	0.77
1:A:455:VAL:O	1:A:459:ILE:HG13	1.83	0.76
1:A:28:LEU:HD11	1:A:145:MET:CE	2.11	0.76
1:A:115:GLU:O	1:A:117:ARG:N	2.17	0.76
1:A:360:PRO:HG3	1:A:435:ARG:HE	1.48	0.76
1:A:376:ILE:HG21	1:A:381:GLU:HB2	1.68	0.76
1:A:75:GLU:HG3	1:A:97:GLY:H	1.51	0.75
1:A:28:LEU:HB2	1:A:232:PHE:HB3	1.66	0.75
1:A:75:GLU:HG3	1:A:97:GLY:N	2.02	0.75
1:A:328:ARG:C	1:A:330:GLY:H	1.93	0.75
1:A:117:ARG:HH22	1:A:238:ALA:HB2	1.51	0.74
1:A:389:VAL:HA	1:A:392:LEU:HG	1.70	0.73
1:A:406:ILE:C	1:A:408:LEU:N	2.41	0.73
1:A:217:VAL:HA	1:A:241:VAL:HG12	1.69	0.73
1:A:406:ILE:O	1:A:408:LEU:N	2.21	0.73
1:A:213:HIS:NE2	1:A:262:CYS:HB2	2.04	0.72
1:A:113:VAL:HG23	1:A:124:LEU:HD11	1.71	0.72
1:A:160:LEU:HD13	1:A:161:ARG:H	1.52	0.72
1:A:92:LEU:HD23	1:A:93:ALA:N	2.04	0.72
1:A:269:ILE:HG22	1:A:270:LYS:N	2.05	0.71
1:A:220:PHE:H	1:A:239:GLN:HG3	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:GLU:C	1:A:117:ARG:H	1.98	0.71
1:A:219:THR:HG21	1:A:237:ILE:HG13	1.71	0.71
1:A:117:ARG:CZ	1:A:238:ALA:HB2	2.22	0.70
1:A:405:MET:O	1:A:406:ILE:HG13	1.91	0.70
1:A:113:VAL:HG12	1:A:114:GLY:H	1.53	0.70
1:A:233:MET:HG2	1:A:251:HIS:CD2	2.27	0.69
1:A:296:ILE:CG2	1:A:407:HIS:HB3	2.23	0.69
1:A:362:ILE:HB	1:A:433:LEU:O	1.93	0.69
1:A:371:ILE:C	1:A:373:ALA:H	1.99	0.69
1:A:219:THR:HA	1:A:239:GLN:HG3	1.73	0.69
1:A:45:ARG:H	1:A:45:ARG:HD2	1.58	0.68
1:A:277:LEU:HD11	1:A:289:PRO:HG2	1.76	0.68
1:A:62:ILE:HD11	1:A:66:GLN:HG3	1.74	0.68
1:A:360:PRO:HG3	1:A:435:ARG:NE	2.08	0.68
1:A:28:LEU:CD1	1:A:145:MET:HE1	2.15	0.68
1:A:277:LEU:HD23	1:A:397:HIS:ND1	2.08	0.68
1:A:408:LEU:O	1:A:411:VAL:HB	1.93	0.68
1:A:113:VAL:CG1	1:A:114:GLY:H	2.06	0.68
1:A:119:GLU:OE1	1:A:124:LEU:HA	1.94	0.67
1:A:113:VAL:CG1	1:A:114:GLY:N	2.57	0.67
1:A:75:GLU:OE1	1:A:97:GLY:HA3	1.95	0.66
1:A:106:PHE:N	1:A:106:PHE:HD1	1.93	0.66
1:A:236:LEU:HD23	1:A:236:LEU:C	2.19	0.66
1:A:226:CYS:SG	1:A:228:TYR:HB3	2.35	0.66
1:A:103:TYR:O	1:A:104:ARG:HB2	1.96	0.66
1:A:106:PHE:N	1:A:106:PHE:CD1	2.61	0.65
1:A:277:LEU:HD11	1:A:289:PRO:CG	2.27	0.65
1:A:52:LYS:HE3	1:A:55:GLY:O	1.97	0.64
1:A:61:ILE:N	1:A:61:ILE:HD12	2.13	0.64
1:A:269:ILE:O	1:A:270:LYS:HB2	1.97	0.64
1:A:59:HIS:CD2	1:A:79:ILE:HD11	2.32	0.64
1:A:213:HIS:HE1	1:A:246:CYS:SG	2.20	0.64
1:A:138:ALA:O	1:A:142:ILE:HG13	1.98	0.63
1:A:225:TRP:N	1:A:225:TRP:CD1	2.66	0.63
1:A:213:HIS:CE1	1:A:262:CYS:HB2	2.34	0.63
1:A:328:ARG:C	1:A:330:GLY:N	2.57	0.63
1:A:226:CYS:C	1:A:228:TYR:H	2.07	0.63
1:A:111:HIS:HD2	1:A:121:ILE:HD13	1.63	0.62
1:A:425:LEU:HA	1:A:428:VAL:HG12	1.82	0.62
1:A:135:GLU:O	1:A:139:ALA:HB2	2.00	0.62
1:A:286:THR:O	1:A:288:ARG:N	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:HIS:ND1	1:A:70:LEU:HD13	2.14	0.62
1:A:404:LEU:O	1:A:404:LEU:HG	2.00	0.62
1:A:296:ILE:HG21	1:A:407:HIS:CB	2.30	0.61
1:A:160:LEU:O	1:A:161:ARG:HB2	2.01	0.61
1:A:62:ILE:HG13	1:A:63:SER:N	2.15	0.61
1:A:104:ARG:O	1:A:105:LEU:CB	2.43	0.61
1:A:443:THR:HA	1:A:446:HIS:HD2	1.65	0.61
1:A:328:ARG:O	1:A:330:GLY:N	2.33	0.61
1:A:37:ARG:O	1:A:39:LYS:N	2.35	0.60
1:A:316:THR:CG2	1:A:317:GLU:N	2.64	0.60
1:A:371:ILE:O	1:A:373:ALA:N	2.33	0.60
1:A:219:THR:CG2	1:A:237:ILE:HG13	2.31	0.60
1:A:44:PRO:C	1:A:46:GLU:H	2.09	0.60
1:A:222:GLY:O	1:A:224:HIS:ND1	2.34	0.60
1:A:62:ILE:HG13	1:A:66:GLN:HB2	1.84	0.60
1:A:363:THR:HG22	1:A:397:HIS:CD2	2.37	0.59
1:A:296:ILE:HG21	1:A:407:HIS:HB3	1.84	0.59
1:A:297:ARG:HB2	1:A:297:ARG:NH1	2.16	0.59
1:A:421:ASN:H	1:A:424:ASN:CB	2.12	0.59
1:A:92:LEU:HD23	1:A:92:LEU:C	2.26	0.59
1:A:226:CYS:SG	1:A:250:VAL:HB	2.42	0.59
1:A:111:HIS:CD2	1:A:121:ILE:HB	2.38	0.59
1:A:155:GLY:C	1:A:157:ALA:H	2.11	0.59
1:A:105:LEU:C	1:A:106:PHE:HD1	2.10	0.59
1:A:363:THR:HG22	1:A:397:HIS:HD2	1.68	0.59
1:A:45:ARG:HH11	1:A:47:VAL:HG11	1.68	0.58
1:A:141:TYR:OH	1:A:231:ASN:ND2	2.34	0.58
1:A:404:LEU:O	1:A:405:MET:HE3	2.03	0.58
1:A:430:GLY:HA2	1:A:455:VAL:CG2	2.32	0.58
1:A:117:ARG:HH12	1:A:238:ALA:CB	2.14	0.58
1:A:246:CYS:HB3	1:A:262:CYS:SG	2.44	0.58
1:A:50:ARG:CB	1:A:51:PRO:HD3	2.34	0.58
1:A:111:HIS:O	1:A:112:PHE:HB3	2.03	0.58
1:A:229:CYS:SG	1:A:231:ASN:HB2	2.44	0.58
1:A:420:MET:SD	1:A:424:ASN:ND2	2.71	0.58
1:A:114:GLY:O	1:A:115:GLU:O	2.22	0.58
1:A:156:TYR:CE2	1:A:324:MET:HG3	2.39	0.58
1:A:322:VAL:O	1:A:325:ALA:HB3	2.03	0.57
1:A:430:GLY:CA	1:A:455:VAL:HG21	2.33	0.57
1:A:349:ALA:O	1:A:352:LEU:HB3	2.04	0.57
1:A:354:PHE:CZ	1:A:404:LEU:HD22	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:420:MET:CE	1:A:424:ASN:HD21	2.17	0.57
1:A:409:LYS:HD2	1:A:409:LYS:O	2.03	0.57
1:A:107:HIS:HD2	1:A:109:GLY:H	1.51	0.57
1:A:296:ILE:O	1:A:297:ARG:C	2.43	0.57
1:A:351:LYS:NZ	1:A:428:VAL:HG23	2.19	0.57
1:A:253:GLN:H	1:A:253:GLN:CD	2.13	0.56
1:A:93:ALA:HA	1:A:101:LEU:O	2.06	0.56
1:A:362:ILE:HG23	1:A:362:ILE:O	2.04	0.56
1:A:426:GLY:O	1:A:452:LYS:HA	2.06	0.56
1:A:438:GLU:HG2	1:A:439:ASP:H	1.69	0.56
1:A:62:ILE:HG13	1:A:63:SER:H	1.70	0.56
1:A:285:ASN:O	1:A:286:THR:CG2	2.52	0.56
1:A:328:ARG:CG	1:A:329:ASP:H	2.14	0.56
1:A:39:LYS:O	1:A:40:ARG:HB2	2.06	0.56
1:A:267:LYS:C	1:A:269:ILE:H	2.13	0.56
1:A:290:MET:O	1:A:294:ILE:HG12	2.05	0.56
1:A:362:ILE:HG21	1:A:434:MET:HG2	1.88	0.56
1:A:233:MET:HG2	1:A:251:HIS:HD2	1.71	0.56
1:A:138:ALA:HA	1:A:140:GLU:OE1	2.06	0.55
1:A:309:LEU:HD22	1:A:347:THR:HG21	1.89	0.55
1:A:27:TYR:HD2	1:A:141:TYR:CD2	2.25	0.55
1:A:344:ASN:HA	1:A:347:THR:OG1	2.05	0.55
1:A:50:ARG:HB2	1:A:51:PRO:HD3	1.89	0.55
1:A:219:THR:OG1	1:A:237:ILE:HG12	2.07	0.55
1:A:246:CYS:SG	1:A:248:LEU:HB2	2.47	0.55
1:A:373:ALA:C	1:A:375:LYS:H	2.15	0.55
1:A:416:LYS:NZ	1:A:416:LYS:HB2	2.22	0.55
1:A:226:CYS:O	1:A:230:ALA:HA	2.07	0.55
1:A:273:TYR:HB3	1:A:323:LYS:HE3	1.89	0.55
1:A:450:TYR:H	1:A:450:TYR:HD1	1.53	0.55
1:A:121:ILE:O	1:A:122:HIS:HB3	2.07	0.54
1:A:31:LEU:O	1:A:34:GLU:N	2.36	0.54
1:A:220:PHE:HD1	1:A:239:GLN:HB3	1.72	0.54
1:A:50:ARG:CG	1:A:51:PRO:HD3	2.38	0.54
1:A:338:ASN:C	1:A:340:TYR:H	2.15	0.54
1:A:374:ALA:HA	1:A:382:ARG:NH1	2.22	0.54
1:A:408:LEU:HD11	1:A:459:ILE:HD13	1.89	0.54
1:A:262:CYS:SG	1:A:264:PRO:HD3	2.47	0.54
1:A:96:PHE:CZ	1:A:132:LEU:HB3	2.43	0.54
1:A:115:GLU:HB2	1:A:117:ARG:HG2	1.89	0.54
1:A:360:PRO:HD3	1:A:364:TYR:CE1	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:307:GLU:HA	1:A:418:ASN:HA	1.90	0.53
1:A:105:LEU:C	1:A:106:PHE:CD1	2.85	0.53
1:A:409:LYS:HD3	1:A:459:ILE:O	2.09	0.53
1:A:300:GLU:CD	1:A:407:HIS:HD1	2.17	0.53
1:A:302:ARG:HD2	1:A:337:ALA:HB2	1.90	0.53
1:A:290:MET:HE3	1:A:332:LYS:HA	1.91	0.52
1:A:220:PHE:CD1	1:A:239:GLN:HB3	2.44	0.52
1:A:211:LYS:HD3	1:A:212:THR:N	2.25	0.52
1:A:316:THR:HG23	1:A:317:GLU:N	2.25	0.52
1:A:317:GLU:O	1:A:317:GLU:HG2	2.10	0.52
1:A:272:VAL:HG22	1:A:327:ASP:OD1	2.10	0.52
1:A:318:HIS:HA	1:A:321:ASP:OD2	2.10	0.52
1:A:42:ILE:HG23	1:A:42:ILE:O	2.09	0.51
1:A:269:ILE:CG2	1:A:270:LYS:N	2.73	0.51
1:A:366:THR:HG22	1:A:370:PHE:CD2	2.46	0.51
1:A:156:TYR:HE2	1:A:324:MET:HG3	1.76	0.51
1:A:40:ARG:CG	1:A:42:ILE:HB	2.41	0.51
1:A:131:THR:O	1:A:135:GLU:HG3	2.10	0.51
1:A:291:VAL:HG22	1:A:326:PHE:CD2	2.46	0.51
1:A:294:ILE:O	1:A:297:ARG:HB3	2.10	0.51
1:A:296:ILE:HD13	1:A:407:HIS:HB2	1.92	0.51
1:A:94:LEU:HD23	1:A:94:LEU:O	2.11	0.50
1:A:242:ARG:O	1:A:243:CYS:C	2.54	0.50
1:A:378:ASN:O	1:A:380:ASP:N	2.44	0.50
1:A:366:THR:HG23	1:A:389:VAL:CG2	2.41	0.50
1:A:450:TYR:O	1:A:454:ILE:HG12	2.11	0.50
1:A:114:GLY:O	1:A:115:GLU:C	2.53	0.50
1:A:299:ILE:HD11	1:A:347:THR:HA	1.93	0.50
1:A:326:PHE:HA	1:A:334:ASP:OD2	2.12	0.50
1:A:351:LYS:HZ2	1:A:428:VAL:HG23	1.77	0.50
1:A:251:HIS:HB2	1:A:254:CYS:SG	2.51	0.50
1:A:309:LEU:HD21	1:A:343:ILE:CD1	2.39	0.50
1:A:338:ASN:C	1:A:340:TYR:N	2.69	0.50
1:A:280:LEU:C	1:A:280:LEU:HD13	2.36	0.50
1:A:421:ASN:ND2	1:A:424:ASN:HB2	2.27	0.50
1:A:425:LEU:HA	1:A:428:VAL:CG1	2.41	0.50
1:A:212:THR:HA	1:A:260:ASN:OD1	2.12	0.50
1:A:96:PHE:O	1:A:98:ASN:N	2.45	0.50
1:A:420:MET:HA	1:A:424:ASN:ND2	2.26	0.50
1:A:120:SER:O	1:A:121:ILE:HG22	2.11	0.49
1:A:49:ASN:OD1	1:A:51:PRO:HD2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:367:TYR:OH	1:A:451:GLN:NE2	2.42	0.49
1:A:374:ALA:HB2	1:A:454:ILE:CD1	2.42	0.49
1:A:50:ARG:HG3	1:A:51:PRO:HD3	1.94	0.49
1:A:429:PHE:O	1:A:430:GLY:C	2.55	0.49
1:A:121:ILE:O	1:A:123:ASP:N	2.40	0.49
1:A:421:ASN:O	1:A:424:ASN:HB3	2.12	0.49
1:A:83:SER:HB3	1:A:86:GLN:O	2.13	0.49
1:A:276:ASP:OD2	1:A:277:LEU:N	2.46	0.49
1:A:299:ILE:CD1	1:A:347:THR:HG22	2.43	0.49
1:A:65:GLU:CD	1:A:65:GLU:H	2.21	0.49
1:A:335:ILE:HG13	1:A:336:SER:N	2.27	0.49
1:A:438:GLU:CG	1:A:439:ASP:H	2.26	0.49
1:A:125:VAL:HG12	1:A:129:LEU:CD1	2.43	0.49
1:A:335:ILE:HG21	1:A:340:TYR:CE1	2.48	0.49
1:A:122:HIS:O	1:A:123:ASP:C	2.56	0.48
1:A:450:TYR:CD1	1:A:450:TYR:N	2.80	0.48
1:A:117:ARG:NH1	1:A:238:ALA:CB	2.73	0.48
1:A:100:THR:C	1:A:101:LEU:HD12	2.38	0.48
1:A:219:THR:HA	1:A:239:GLN:CG	2.42	0.48
1:A:449:ARG:HE	1:A:449:ARG:HA	1.78	0.48
1:A:126:THR:HG22	1:A:127:ASP:N	2.28	0.48
1:A:62:ILE:CG1	1:A:63:SER:H	2.26	0.48
1:A:125:VAL:HG12	1:A:129:LEU:HD11	1.95	0.48
1:A:296:ILE:HG23	1:A:407:HIS:HB3	1.95	0.48
1:A:95:ARG:NH2	1:A:99:GLN:HA	2.29	0.48
1:A:405:MET:HE2	1:A:459:ILE:HG12	1.96	0.48
1:A:50:ARG:HG3	1:A:50:ARG:HH11	1.79	0.48
1:A:62:ILE:CG1	1:A:63:SER:N	2.76	0.48
1:A:443:THR:HA	1:A:446:HIS:CD2	2.46	0.48
1:A:405:MET:O	1:A:406:ILE:CG1	2.61	0.47
1:A:345:ILE:O	1:A:348:GLY:N	2.46	0.47
1:A:422:ALA:O	1:A:423:GLU:C	2.56	0.47
1:A:56:ARG:HG3	1:A:56:ARG:HH11	1.79	0.47
1:A:423:GLU:HA	1:A:456:GLN:OE1	2.14	0.47
1:A:52:LYS:HB2	1:A:58:PHE:CE2	2.48	0.47
1:A:57:GLU:O	1:A:79:ILE:HD12	2.14	0.47
1:A:115:GLU:HB2	1:A:117:ARG:CD	2.44	0.47
1:A:156:TYR:OH	1:A:324:MET:HA	2.14	0.47
1:A:335:ILE:HG21	1:A:340:TYR:HE1	1.79	0.47
1:A:115:GLU:C	1:A:117:ARG:N	2.62	0.47
1:A:405:MET:C	1:A:406:ILE:HG13	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:PRO:HB3	1:A:59:HIS:CD2	2.50	0.47
1:A:376:ILE:O	1:A:377:SER:HB2	2.15	0.47
1:A:52:LYS:O	1:A:52:LYS:HD3	2.14	0.47
1:A:422:ALA:C	1:A:456:GLN:HG3	2.40	0.47
1:A:425:LEU:C	1:A:427:ILE:N	2.68	0.47
1:A:103:TYR:O	1:A:104:ARG:CB	2.62	0.46
1:A:147:THR:O	1:A:148:ASN:C	2.56	0.46
1:A:322:VAL:O	1:A:325:ALA:N	2.44	0.46
1:A:376:ILE:C	1:A:378:ASN:H	2.23	0.46
1:A:107:HIS:HD2	1:A:109:GLY:N	2.14	0.46
1:A:281:VAL:HG13	1:A:287:GLN:N	2.30	0.46
1:A:58:PHE:CE2	1:A:60:GLY:HA2	2.50	0.46
1:A:124:LEU:C	1:A:124:LEU:HD23	2.40	0.46
1:A:347:THR:O	1:A:351:LYS:HG3	2.15	0.46
1:A:260:ASN:O	1:A:261:ASP:C	2.56	0.46
1:A:338:ASN:O	1:A:339:VAL:HB	2.15	0.46
1:A:126:THR:CG2	1:A:236:LEU:HD12	2.39	0.46
1:A:236:LEU:C	1:A:236:LEU:CD2	2.88	0.46
1:A:278:THR:HG23	1:A:396:ALA:CB	2.46	0.46
1:A:290:MET:HE1	1:A:331:GLU:O	2.16	0.46
1:A:261:ASP:O	1:A:262:CYS:HB3	2.16	0.46
1:A:385:ALA:O	1:A:388:GLU:HB3	2.15	0.46
1:A:267:LYS:C	1:A:269:ILE:N	2.71	0.45
1:A:64:ARG:HG3	1:A:64:ARG:HH11	1.80	0.45
1:A:389:VAL:C	1:A:391:MET:N	2.72	0.45
1:A:42:ILE:HG22	1:A:78:TYR:O	2.16	0.45
1:A:61:ILE:N	1:A:61:ILE:CD1	2.79	0.45
1:A:291:VAL:O	1:A:293:ASP:N	2.50	0.45
1:A:340:TYR:N	1:A:341:PRO:HD3	2.31	0.45
1:A:447:ASP:O	1:A:448:MET:C	2.59	0.45
1:A:113:VAL:O	1:A:114:GLY:C	2.59	0.45
1:A:453:LEU:O	1:A:454:ILE:C	2.58	0.45
1:A:455:VAL:HG12	1:A:459:ILE:HD11	1.98	0.45
1:A:221:ARG:HG2	1:A:221:ARG:HH11	1.81	0.45
1:A:44:PRO:C	1:A:46:GLU:N	2.75	0.45
1:A:117:ARG:O	1:A:118:PHE:HB2	2.16	0.45
1:A:229:CYS:SG	1:A:231:ASN:CB	3.05	0.45
1:A:269:ILE:O	1:A:270:LYS:CB	2.64	0.45
1:A:278:THR:HG23	1:A:396:ALA:HB3	1.98	0.45
1:A:215:PHE:HA	1:A:243:CYS:HA	1.98	0.45
1:A:275:CYS:O	1:A:276:ASP:C	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:THR:HG22	1:A:148:ASN:N	2.32	0.44
1:A:151:TYR:HB2	1:A:228:TYR:HA	1.98	0.44
1:A:27:TYR:O	1:A:30:GLN:HB2	2.17	0.44
1:A:28:LEU:HD13	1:A:234:TRP:CE3	2.52	0.44
1:A:245:ASP:HB3	1:A:264:PRO:HB3	2.00	0.44
1:A:326:PHE:CA	1:A:334:ASP:OD2	2.65	0.44
1:A:425:LEU:C	1:A:427:ILE:H	2.25	0.44
1:A:280:LEU:HD22	1:A:284:HIS:CD2	2.52	0.44
1:A:425:LEU:O	1:A:427:ILE:N	2.50	0.44
1:A:41:ILE:O	1:A:42:ILE:C	2.61	0.44
1:A:154:ILE:HG13	1:A:155:GLY:N	2.32	0.44
1:A:217:VAL:CA	1:A:241:VAL:HG12	2.43	0.44
1:A:315:PHE:O	1:A:316:THR:C	2.58	0.44
1:A:273:TYR:CG	1:A:323:LYS:HG3	2.53	0.44
1:A:62:ILE:CG1	1:A:66:GLN:HB2	2.47	0.44
1:A:374:ALA:HB2	1:A:454:ILE:HD11	1.99	0.44
1:A:376:ILE:HG22	1:A:378:ASN:H	1.83	0.44
1:A:401:LEU:O	1:A:402:ARG:C	2.60	0.44
1:A:406:ILE:O	1:A:410:LYS:N	2.41	0.44
1:A:115:GLU:HB2	1:A:117:ARG:CG	2.48	0.44
1:A:302:ARG:HD2	1:A:337:ALA:CB	2.48	0.44
1:A:406:ILE:O	1:A:409:LYS:N	2.51	0.44
1:A:31:LEU:O	1:A:32:GLN:C	2.61	0.44
1:A:364:TYR:C	1:A:366:THR:N	2.76	0.44
1:A:73:GLY:O	1:A:74:VAL:C	2.60	0.43
1:A:338:ASN:O	1:A:340:TYR:N	2.39	0.43
1:A:150:ILE:O	1:A:150:ILE:HG22	2.18	0.43
1:A:346:ILE:N	1:A:346:ILE:CD1	2.82	0.43
1:A:427:ILE:HA	1:A:452:LYS:HG2	1.99	0.43
1:A:364:TYR:C	1:A:366:THR:H	2.25	0.43
1:A:263:GLN:HA	1:A:264:PRO:HD2	1.79	0.43
1:A:298:GLU:O	1:A:299:ILE:C	2.60	0.43
1:A:381:GLU:O	1:A:382:ARG:C	2.61	0.43
1:A:398:TYR:OH	1:A:466:PHE:HB3	2.18	0.43
1:A:92:LEU:C	1:A:92:LEU:CD2	2.90	0.43
1:A:39:LYS:O	1:A:40:ARG:CB	2.67	0.43
1:A:339:VAL:C	1:A:341:PRO:HD3	2.43	0.43
1:A:357:LEU:HA	1:A:358:PRO:HD3	1.87	0.43
1:A:397:HIS:O	1:A:398:TYR:C	2.62	0.43
1:A:409:LYS:HE3	1:A:413:MET:HE3	2.01	0.43
1:A:273:TYR:O	1:A:274:CYS:CB	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:GLN:OE1	1:A:87:PRO:HD2	2.19	0.43
1:A:101:LEU:HD12	1:A:101:LEU:N	2.34	0.42
1:A:73:GLY:O	1:A:75:GLU:N	2.52	0.42
1:A:253:GLN:O	1:A:255:SER:N	2.52	0.42
1:A:265:ASP:C	1:A:267:LYS:H	2.28	0.42
1:A:40:ARG:C	1:A:42:ILE:N	2.75	0.42
1:A:118:PHE:C	1:A:119:GLU:HG3	2.42	0.42
1:A:288:ARG:NH2	1:A:293:ASP:OD1	2.41	0.42
1:A:367:TYR:OH	1:A:436:PRO:HG3	2.19	0.42
1:A:405:MET:O	1:A:462:GLU:HG3	2.19	0.42
1:A:71:LEU:HD21	1:A:79:ILE:HG22	2.00	0.42
1:A:462:GLU:CD	1:A:463:ASP:N	2.77	0.42
1:A:124:LEU:O	1:A:125:VAL:C	2.63	0.42
1:A:50:ARG:HG3	1:A:50:ARG:NH1	2.34	0.42
1:A:108:ASP:CB	1:A:118:PHE:HE1	2.33	0.42
1:A:362:ILE:HG13	1:A:370:PHE:CE2	2.53	0.42
1:A:119:GLU:OE1	1:A:124:LEU:CA	2.64	0.42
1:A:121:ILE:C	1:A:123:ASP:N	2.77	0.42
1:A:54:TYR:CE2	1:A:107:HIS:CE1	3.08	0.42
1:A:290:MET:HB2	1:A:290:MET:HE2	1.77	0.42
1:A:316:THR:CG2	1:A:317:GLU:H	2.32	0.42
1:A:316:THR:HG22	1:A:317:GLU:H	1.84	0.42
1:A:53:TYR:CD2	1:A:53:TYR:C	2.98	0.42
1:A:117:ARG:HH22	1:A:238:ALA:CB	2.28	0.41
1:A:218:HIS:O	1:A:239:GLN:HB2	2.20	0.41
1:A:339:VAL:HG12	1:A:340:TYR:CE1	2.55	0.41
1:A:331:GLU:O	1:A:334:ASP:OD1	2.38	0.41
1:A:409:LYS:O	1:A:409:LYS:CD	2.68	0.41
1:A:420:MET:HA	1:A:420:MET:HE2	2.01	0.41
1:A:330:GLY:O	1:A:332:LYS:N	2.54	0.41
1:A:357:LEU:O	1:A:435:ARG:NH2	2.50	0.41
1:A:216:LYS:HD2	1:A:244:SER:OG	2.20	0.41
1:A:59:HIS:CG	1:A:79:ILE:HD11	2.56	0.41
1:A:85:ARG:O	1:A:87:PRO:HD3	2.20	0.41
1:A:291:VAL:O	1:A:292:VAL:C	2.63	0.41
1:A:462:GLU:CD	1:A:462:GLU:C	2.89	0.41
1:A:94:LEU:HD23	1:A:94:LEU:H	1.86	0.41
1:A:112:PHE:HB3	1:A:118:PHE:HA	2.02	0.41
1:A:158:THR:HB	1:A:159:LEU:HD22	2.03	0.41
1:A:211:LYS:O	1:A:260:ASN:HB3	2.21	0.41
1:A:120:SER:O	1:A:121:ILE:O	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:GLU:OE2	1:A:407:HIS:ND1	2.47	0.41
1:A:107:HIS:CD2	1:A:107:HIS:C	2.99	0.40
1:A:272:VAL:CG2	1:A:273:TYR:N	2.83	0.40
1:A:364:TYR:O	1:A:366:THR:N	2.54	0.40
1:A:404:LEU:O	1:A:404:LEU:CG	2.62	0.40
1:A:161:ARG:HG2	1:A:161:ARG:HH11	1.86	0.40
1:A:290:MET:CE	1:A:332:LYS:HA	2.51	0.40
1:A:414:ASN:C	1:A:416:LYS:H	2.27	0.40
1:A:220:PHE:N	1:A:239:GLN:HG3	2.29	0.40
1:A:328:ARG:CG	1:A:329:ASP:N	2.82	0.40
1:A:382:ARG:NH1	1:A:453:LEU:HD21	2.37	0.40
1:A:463:ASP:C	1:A:464:VAL:HG23	2.47	0.40
1:A:97:GLY:O	1:A:98:ASN:C	2.65	0.40
1:A:309:LEU:O	1:A:310:TYR:HB2	2.21	0.40
1:A:401:LEU:HD12	1:A:401:LEU:HA	1.89	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	395/466 (85%)	242 (61%)	104 (26%)	49 (12%)	0 1

All (49) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	74	VAL
1	A	97	GLY
1	A	104	ARG
1	A	105	LEU
1	A	114	GLY
1	A	115	GLU

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Mol	Chain	Res	Type
1	A	117	ARG
1	A	121	ILE
1	A	160	LEU
1	A	303	GLY
1	A	336	SER
1	A	372	ASP
1	A	379	ALA
1	A	405	MET
1	A	406	ILE
1	A	414	ASN
1	A	42	ILE
1	A	52	LYS
1	A	72	GLY
1	A	73	GLY
1	A	116	LYS
1	A	227	GLU
1	A	254	CYS
1	A	274	CYS
1	A	329	ASP
1	A	331	GLU
1	A	422	ALA
1	A	464	VAL
1	A	38	PRO
1	A	40	ARG
1	A	210	GLU
1	A	262	CYS
1	A	407	HIS
1	A	442	LEU
1	A	239	GLN
1	A	264	PRO
1	A	276	ASP
1	A	292	VAL
1	A	45	ARG
1	A	112	PHE
1	A	124	LEU
1	A	448	MET
1	A	149	PRO
1	A	382	ARG
1	A	395	PRO
1	A	150	ILE
1	A	237	ILE
1	A	454	ILE

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Mol	Chain	Res	Type
1	A	51	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	356/418 (85%)	315 (88%)	41 (12%)	5 24

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	ILE
1	A	39	LYS
1	A	45	ARG
1	A	50	ARG
1	A	54	TYR
1	A	56	ARG
1	A	61	ILE
1	A	69	GLU
1	A	86	GLN
1	A	92	LEU
1	A	94	LEU
1	A	99	GLN
1	A	106	PHE
1	A	111	HIS
1	A	116	LYS
1	A	125	VAL
1	A	159	LEU
1	A	160	LEU
1	A	161	ARG
1	A	227	GLU
1	A	246	CYS
1	A	249	ASN
1	A	253	GLN
1	A	269	ILE
1	A	272	VAL

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Mol	Chain	Res	Type
1	A	278	THR
1	A	293	ASP
1	A	304	LEU
1	A	309	LEU
1	A	316	THR
1	A	318	HIS
1	A	362	ILE
1	A	370	PHE
1	A	389	VAL
1	A	390	LEU
1	A	395	PRO
1	A	405	MET
1	A	416	LYS
1	A	428	VAL
1	A	439	ASP
1	A	466	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	ASN
1	A	99	GLN
1	A	102	ASN
1	A	107	HIS
1	A	213	HIS
1	A	214	ASN
1	A	263	GLN
1	A	284	HIS
1	A	285	ASN
1	A	378	ASN
1	A	414	ASN
1	A	446	HIS
1	A	451	GLN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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 [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	399/466 (85%)	0.38	22 (5%) 30 19	31, 85, 166, 196	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	41	ILE	5.8
1	A	157	ALA	5.4
1	A	334	ASP	5.2
1	A	47	VAL	4.4
1	A	407	HIS	3.9
1	A	49	ASN	3.7
1	A	160	LEU	3.5
1	A	44	PRO	3.4
1	A	115	GLU	3.1
1	A	380	ASP	2.9
1	A	51	PRO	2.7
1	A	154	ILE	2.7
1	A	444	THR	2.5
1	A	437	PRO	2.5
1	A	45	ARG	2.4
1	A	58	PHE	2.4
1	A	159	LEU	2.3
1	A	382	ARG	2.2
1	A	449	ARG	2.2
1	A	40	ARG	2.1
1	A	98	ASN	2.0
1	A	381	GLU	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	ZN	A	467	1/1	0.99	0.09	86,86,86,86	0
2	ZN	A	468	1/1	0.99	0.11	62,62,62,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.