



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 30, 2026 – 02:28 PM UTC

PDB ID : 3S5M / pdb_00003s5m
Title : Crystal structures of falcilysin, a M16 metalloprotease from the malaria parasite *Plasmodium falciparum*
Authors : Morgunova, E.; Ponpuak, M.; Istvan, E.; Popov, A.; Goldberg, D.; Eneqvist, T.
Deposited on : 2011-05-23
Resolution : 1.55 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

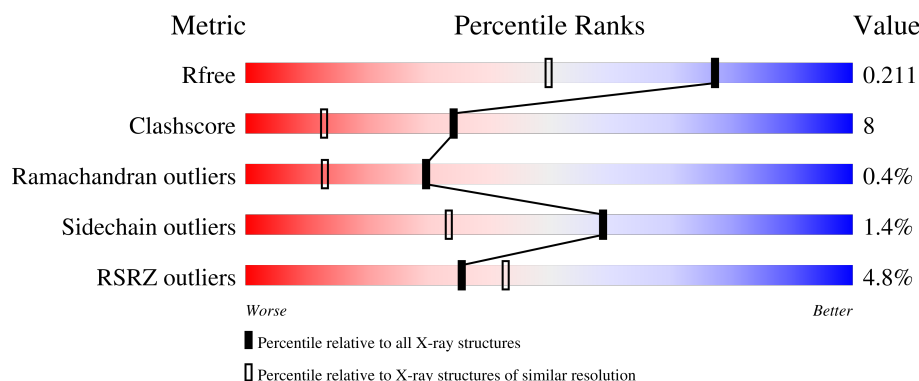
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.55 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}	180053	2145 (1.56-1.56)
Clashscore	190562	2189 (1.56-1.56)
Ramachandran outliers	187476	2153 (1.56-1.56)
Sidechain outliers	187428	2150 (1.56-1.56)
RSRZ outliers	180081	2146 (1.56-1.56)

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	1193	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 19225 atoms, of which 9022 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 Falcilysin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	1094	Total	C	H	N	O	S	0	24	0
			18119	5852	9022	1477	1734	34			

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

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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		

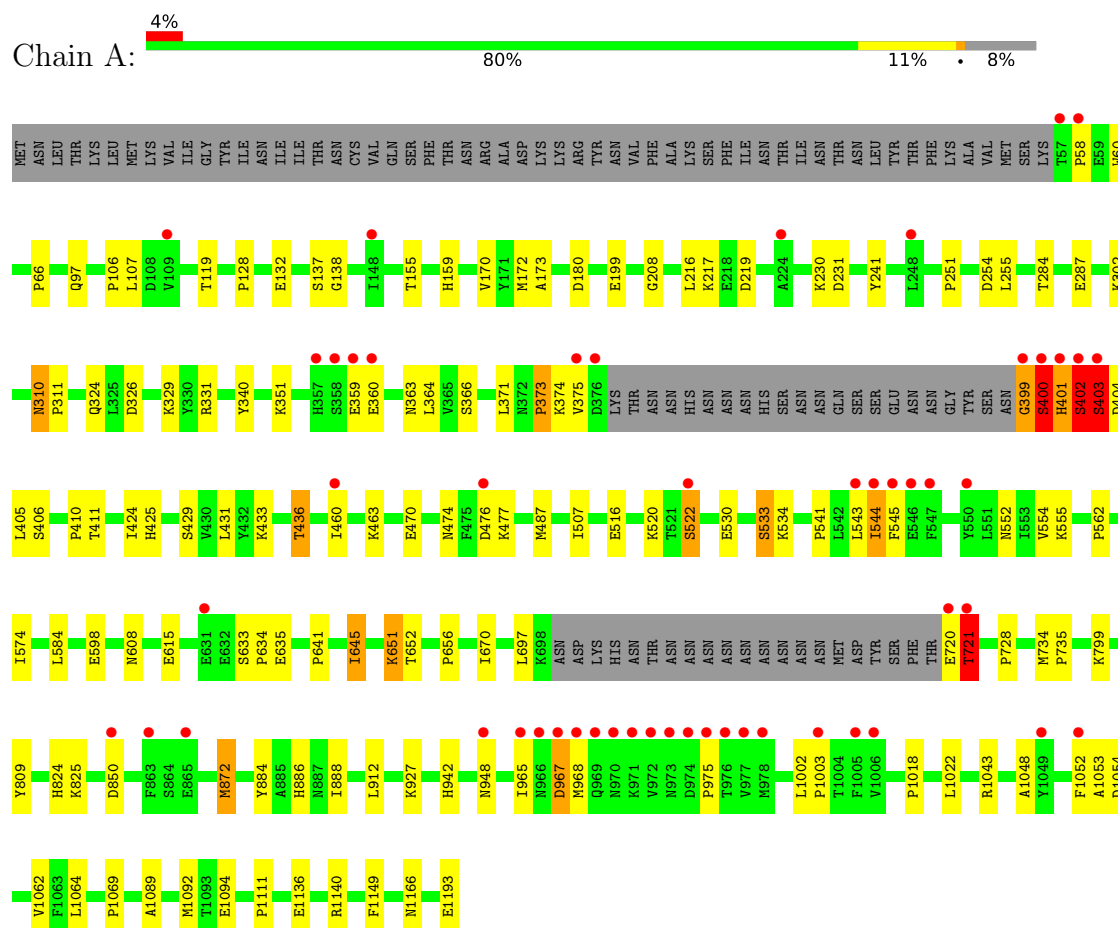
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1103	Total	O	0	0
			1103	1103		

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: Falcilysin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	94.32Å 106.70Å 128.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.20 – 1.55 29.20 – 1.55	Depositor EDS
% Data completeness (in resolution range)	98.9 (29.20-1.55) 99.4 (29.20-1.55)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.00 (at 1.55Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.179 , 0.214 0.177 , 0.211	Depositor DCC
R_{free} test set	3716 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	18.1	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 36.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	19225	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.96% 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: MG, 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	0.85	9/9351 (0.1%)	0.95	34/12594 (0.3%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	119	THR	CA-CB	10.37	1.63	1.53
1	A	401	HIS	CA-CB	-10.27	1.36	1.53
1	A	651	LYS	C-O	-7.66	1.14	1.23
1	A	402	SER	C-O	-7.64	1.14	1.24
1	A	400	SER	CA-CB	-7.63	1.40	1.53
1	A	404	ASP	C-O	-7.53	1.15	1.24
1	A	401	HIS	CA-C	-6.48	1.44	1.52
1	A	400	SER	CA-C	-6.46	1.44	1.52
1	A	405	LEU	C-O	-5.07	1.17	1.24

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	975	PRO	N-CA-C	7.12	127.14	112.47
1	A	522	SER	N-CA-C	7.00	121.41	112.86
1	A	1069	PRO	N-CA-C	6.89	122.80	113.84
1	A	1002	LEU	CA-C-N	-6.74	112.17	119.98
1	A	1002	LEU	C-N-CA	-6.74	112.17	119.98
1	A	721	THR	N-CA-C	6.68	125.02	110.80
1	A	1003	PRO	CB-CA-C	6.66	120.37	111.71
1	A	311	PRO	N-CA-C	6.60	122.12	114.20
1	A	1003	PRO	N-CA-C	6.57	121.60	110.95
1	A	373	PRO	CA-C-O	-6.49	114.17	121.43
1	A	106	PRO	N-CA-C	6.24	122.86	113.81
1	A	1111	PRO	N-CA-C	6.16	121.30	111.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1111	PRO	CA-C-O	-6.02	114.76	121.32
1	A	634	PRO	N-CA-C	6.02	122.71	113.75
1	A	541	PRO	N-CA-C	5.99	122.49	113.81
1	A	533	SER	N-CA-C	-5.84	104.60	110.97
1	A	728	PRO	CA-C-O	-5.75	114.19	120.92
1	A	208	GLY	O-C-N	5.62	124.99	121.85
1	A	399	GLY	CA-C-N	-5.61	110.83	121.54
1	A	399	GLY	C-N-CA	-5.61	110.83	121.54
1	A	251	PRO	N-CA-C	5.60	121.22	113.65
1	A	641	PRO	N-CA-C	5.54	119.78	111.14
1	A	641	PRO	CB-CA-C	5.48	118.53	111.46
1	A	1018	PRO	N-CA-C	5.38	123.55	112.47
1	A	975	PRO	CB-CA-C	5.35	120.38	111.56
1	A	436[A]	THR	N-CA-C	5.32	117.49	111.11
1	A	436[B]	THR	N-CA-C	5.32	117.49	111.11
1	A	656	PRO	CB-CA-C	5.21	118.18	111.46
1	A	562	PRO	N-CA-C	5.19	123.16	112.47
1	A	403	SER	N-CA-C	-5.17	99.78	110.80
1	A	656	PRO	CA-C-O	-5.17	115.45	121.34
1	A	436[A]	THR	OG1-CB-CG2	5.10	119.51	109.30
1	A	436[B]	THR	OG1-CB-CG2	5.10	119.51	109.30
1	A	128	PRO	N-CA-C	5.09	120.52	113.65

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	9097	9022	9110	138	1
2	A	1	0	0	0	0
3	A	2	0	0	0	0
4	A	1103	0	0	42	1
All	All	10203	9022	9110	138	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 8.

All (138) 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:374:LYS:HA	1:A:402:SER:CA	1.84	1.06
1:A:374:LYS:CA	1:A:402:SER:HA	1.87	1.05
1:A:533:SER:C	4:A:2179:HOH:O	2.00	1.02
1:A:324[A]:GLN:HG3	4:A:2194:HOH:O	1.64	0.97
1:A:425:HIS:O	1:A:429[B]:SER:OG	1.88	0.92
1:A:137:SER:C	4:A:2176:HOH:O	2.13	0.90
1:A:329:LYS:HG2	4:A:2211:HOH:O	1.72	0.89
1:A:608:ASN:CG	4:A:2275:HOH:O	2.15	0.89
1:A:402:SER:CB	4:A:1993:HOH:O	2.22	0.87
1:A:374:LYS:HA	1:A:402:SER:HA	0.92	0.87
1:A:436[B]:THR:HG21	4:A:1309:HOH:O	1.74	0.86
1:A:254:ASP:HB2	4:A:2087:HOH:O	1.80	0.82
1:A:180:ASP:OD1	4:A:2208:HOH:O	1.98	0.81
1:A:399:GLY:O	1:A:400:SER:CB	2.22	0.80
1:A:364[B]:LEU:HD22	1:A:463:LYS:CB	2.12	0.79
1:A:544:ILE:HB	4:A:1638:HOH:O	1.83	0.79
1:A:410:PRO:HB3	1:A:543:LEU:HD11	1.64	0.79
1:A:401:HIS:O	1:A:406:SER:HB3	1.82	0.79
1:A:375:VAL:CG1	1:A:403:SER:CB	2.61	0.78
1:A:172[B]:MET:HG3	1:A:173:ALA:N	1.97	0.77
1:A:410:PRO:HB3	1:A:543:LEU:CD1	2.16	0.76
1:A:850:ASP:OD2	4:A:2191:HOH:O	2.03	0.76
1:A:326:ASP:O	4:A:2211:HOH:O	2.04	0.75
1:A:530:GLU:HG2	1:A:544:ILE:HG12	1.69	0.74
1:A:522:SER:HA	4:A:1392:HOH:O	1.86	0.74
1:A:138:GLY:N	4:A:2176:HOH:O	2.21	0.74
1:A:375:VAL:HG11	1:A:403:SER:CB	2.18	0.74
1:A:1094:GLU:OE1	4:A:1580:HOH:O	2.05	0.73
1:A:364[B]:LEU:HD22	1:A:463:LYS:HB2	1.71	0.72
1:A:544:ILE:C	1:A:544:ILE:HD12	2.17	0.70
1:A:375:VAL:HG13	1:A:403:SER:CB	2.22	0.69
1:A:324[A]:GLN:CG	4:A:2194:HOH:O	2.33	0.68
1:A:359:GLU:O	4:A:2205:HOH:O	2.13	0.67
1:A:255:LEU:HD21	1:A:366[A]:SER:HB2	1.77	0.66
1:A:255:LEU:HD21	1:A:366[B]:SER:HB3	1.78	0.66
1:A:824[A]:HIS:ND1	4:A:2180:HOH:O	2.29	0.66
1:A:216:LEU:HD12	1:A:231:ASP:HA	1.78	0.65
1:A:470:GLU:OE1	4:A:2268:HOH:O	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:552:ASN:OD1	4:A:2207:HOH:O	2.15	0.65
1:A:402:SER:C	4:A:2089:HOH:O	2.40	0.64
1:A:363:ASN:C	1:A:364[B]:LEU:HD23	2.22	0.64
1:A:399:GLY:O	4:A:1315:HOH:O	2.15	0.64
1:A:254:ASP:OD2	4:A:2289:HOH:O	2.15	0.63
1:A:159:HIS:HE2	1:A:172[B]:MET:CG	2.12	0.61
1:A:431:LEU:HB3	1:A:460:ILE:CD1	2.31	0.61
1:A:373:PRO:O	1:A:402:SER:CB	2.49	0.60
1:A:230:LYS:HE3	1:A:615:GLU:HG3	1.85	0.58
1:A:402:SER:CB	4:A:2089:HOH:O	2.51	0.58
1:A:137:SER:CA	4:A:2176:HOH:O	2.50	0.58
1:A:137:SER:HA	4:A:2176:HOH:O	2.04	0.58
1:A:927:LYS:HD2	1:A:965:ILE:HD12	1.86	0.57
1:A:734:MET:HE2	4:A:2225:HOH:O	2.05	0.57
1:A:824[B]:HIS:CE1	1:A:942:HIS:CE1	2.92	0.57
1:A:363:ASN:O	1:A:364[B]:LEU:HD23	2.04	0.57
1:A:340:TYR:H	1:A:399:GLY:N	2.04	0.56
1:A:401:HIS:O	1:A:402:SER:C	2.48	0.56
1:A:824[A]:HIS:CD2	1:A:825:LYS:HG2	2.40	0.56
1:A:436[B]:THR:CG2	4:A:2270:HOH:O	2.55	0.54
1:A:364[B]:LEU:HD22	1:A:463:LYS:HB3	1.90	0.54
1:A:967:ASP:O	1:A:968:MET:HB2	2.08	0.52
1:A:403:SER:N	4:A:2089:HOH:O	2.42	0.52
1:A:436[B]:THR:HG23	4:A:2270:HOH:O	2.09	0.52
1:A:1022:LEU:C	1:A:1022:LEU:HD23	2.34	0.52
1:A:255:LEU:HD22	1:A:364[A]:LEU:HD13	1.91	0.52
1:A:1089:ALA:HA	1:A:1092:MET:HE3	1.91	0.52
1:A:872:MET:HE1	1:A:1052[A]:PHE:CD1	2.44	0.52
1:A:431:LEU:HB3	1:A:460:ILE:HD13	1.90	0.52
1:A:170:VAL:HG12	1:A:172[A]:MET:CG	2.41	0.51
1:A:324[A]:GLN:CD	4:A:2194:HOH:O	2.51	0.51
1:A:375:VAL:HG22	1:A:402:SER:O	2.11	0.51
1:A:670:ILE:HD12	1:A:948:ASN:ND2	2.26	0.50
1:A:872:MET:HE3	1:A:1064:LEU:HD22	1.93	0.50
1:A:487:MET:HE1	1:A:574:ILE:HA	1.93	0.50
1:A:516:GLU:O	1:A:520:LYS:HD3	2.12	0.50
1:A:401:HIS:O	1:A:406:SER:CB	2.57	0.49
1:A:66:PRO:HG3	1:A:310[A]:ASN:ND2	2.28	0.49
1:A:720:GLU:HG3	1:A:721:THR:N	2.27	0.49
1:A:507:ILE:HG21	1:A:555:LYS:HE2	1.94	0.49
1:A:159:HIS:NE2	1:A:172[B]:MET:CG	2.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:720:GLU:HG3	1:A:721:THR:H	1.78	0.49
1:A:331:ARG:HD2	4:A:1974:HOH:O	2.12	0.48
1:A:411:THR:HG23	1:A:554:VAL:CG2	2.43	0.48
1:A:364[B]:LEU:CD2	1:A:463:LYS:HB2	2.40	0.48
1:A:402:SER:CA	4:A:2089:HOH:O	2.62	0.48
1:A:402:SER:CB	1:A:406:SER:HB3	2.43	0.48
1:A:433:LYS:HA	1:A:436[B]:THR:HG22	1.96	0.48
1:A:1043:ARG:HD3	1:A:1043:ARG:C	2.39	0.48
1:A:720:GLU:O	1:A:721:THR:CB	2.62	0.47
1:A:255:LEU:HD22	1:A:364[A]:LEU:CD1	2.45	0.47
1:A:886:HIS:HE1	4:A:2039:HOH:O	1.98	0.47
1:A:645:ILE:HG22	4:A:1414:HOH:O	2.13	0.47
1:A:402:SER:CB	1:A:406:SER:CA	2.92	0.47
1:A:824[B]:HIS:ND1	1:A:942:HIS:CE1	2.83	0.47
1:A:872:MET:HE1	1:A:1052[A]:PHE:HD1	1.79	0.47
1:A:912:LEU:HD23	1:A:912:LEU:C	2.40	0.47
1:A:155:THR:HA	4:A:2208:HOH:O	2.14	0.47
1:A:608:ASN:OD1	4:A:2275:HOH:O	2.17	0.47
1:A:1052[A]:PHE:CZ	1:A:1054:ASP:HB2	2.50	0.47
1:A:107:LEU:HD11	1:A:735:PRO:HG2	1.97	0.46
1:A:411:THR:HG23	1:A:554:VAL:HG22	1.98	0.46
1:A:241:TYR:OH	1:A:598:GLU:OE2	2.25	0.45
1:A:401:HIS:O	1:A:403:SER:N	2.49	0.45
1:A:97:GLN:HB2	1:A:302:LYS:HD3	1.99	0.45
1:A:474:ASN:ND2	1:A:477:LYS:HG2	2.32	0.45
1:A:608:ASN:CB	4:A:2275:HOH:O	2.59	0.45
1:A:824[A]:HIS:HD2	1:A:825:LYS:HG2	1.81	0.45
1:A:199:GLU:HA	1:A:199:GLU:OE1	2.17	0.45
1:A:720:GLU:O	1:A:721:THR:HB	2.15	0.45
1:A:651:LYS:HG2	1:A:652:THR:O	2.17	0.44
1:A:351:LYS:NZ	1:A:476:ASP:OD1	2.50	0.44
1:A:544:ILE:HD12	1:A:545:PHE:N	2.32	0.44
1:A:1140:ARG:HA	1:A:1140:ARG:HD2	1.85	0.44
1:A:58:PRO:HB2	1:A:60:TRP:CD1	2.54	0.43
1:A:431:LEU:CB	1:A:460:ILE:CD1	2.94	0.43
1:A:284:THR:OG1	1:A:287:GLU:HG3	2.18	0.43
1:A:544:ILE:C	1:A:544:ILE:CD1	2.87	0.43
1:A:1053:ALA:HA	1:A:1062:VAL:O	2.19	0.43
1:A:170:VAL:HG12	1:A:172[A]:MET:HG2	1.99	0.43
1:A:402:SER:CB	1:A:406:SER:HA	2.48	0.43
1:A:402:SER:O	1:A:403:SER:CB	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1136[B]:GLU:HG2	4:A:2223:HOH:O	2.19	0.42
1:A:534:LYS:N	4:A:2179:HOH:O	2.38	0.42
1:A:1092:MET:HE1	1:A:1149:PHE:CE2	2.53	0.42
1:A:375:VAL:HG13	1:A:402:SER:O	2.19	0.42
1:A:635[B]:GLU:H	1:A:635[B]:GLU:CD	2.28	0.42
1:A:371:LEU:C	1:A:373:PRO:HD3	2.44	0.42
1:A:329:LYS:CB	4:A:2211:HOH:O	2.67	0.42
1:A:697:LEU:HD23	1:A:799:LYS:HE2	2.00	0.42
1:A:1043:ARG:HG2	1:A:1048:ALA:O	2.19	0.42
1:A:530:GLU:HG2	1:A:544:ILE:CG1	2.44	0.41
1:A:720:GLU:O	1:A:721:THR:HG22	2.20	0.41
1:A:734:MET:CE	4:A:2225:HOH:O	2.64	0.41
1:A:424:ILE:HD13	1:A:460:ILE:CD1	2.51	0.41
1:A:425:HIS:C	1:A:429[B]:SER:HG	2.26	0.40
1:A:884:TYR:CE2	1:A:888:ILE:HD11	2.56	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)
1:A:809:TYR:HH	4:A:2275:HOH:O[2_355]	1.52	0.08

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	1112/1193 (93%)	1077 (97%)	31 (3%)	4 (0%)	30 13

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	400	SER

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Mol	Chain	Res	Type
1	A	403	SER
1	A	721	THR
1	A	402	SER

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	1029/1104 (93%)	1014 (98%)	15 (2%)	57	31

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	132	GLU
1	A	217	LYS
1	A	219	ASP
1	A	310[A]	ASN
1	A	310[B]	ASN
1	A	360	GLU
1	A	544	ILE
1	A	584	LEU
1	A	633	SER
1	A	645	ILE
1	A	721	THR
1	A	872	MET
1	A	967	ASP
1	A	1166	ASN
1	A	1193	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	111	GLN
1	A	242	ASN
1	A	357	HIS

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Mol	Chain	Res	Type
1	A	443	ASN
1	A	538	ASN
1	A	886	HIS
1	A	901	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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

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	1094/1193 (91%)	0.28	52 (4%) 35 43	8, 23, 51, 85	24 (2%)

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	402	SER	14.0
1	A	401	HIS	7.6
1	A	972	VAL	7.2
1	A	399	GLY	7.1
1	A	403	SER	7.1
1	A	400	SER	4.9
1	A	971	LYS	4.6
1	A	975	PRO	4.5
1	A	376	ASP	4.4
1	A	970	ASN	4.3
1	A	966	ASN	4.0
1	A	1005	PHE	3.9
1	A	375	VAL	3.7
1	A	543	LEU	3.7
1	A	969	GLN	3.6
1	A	57	THR	3.5
1	A	721	THR	3.5
1	A	977	VAL	3.5
1	A	967	ASP	3.2
1	A	550	TYR	3.2
1	A	968	MET	3.1
1	A	976	THR	3.1
1	A	1052[A]	PHE	3.1
1	A	965	ILE	3.1
1	A	224	ALA	3.0
1	A	546	GLU	2.9
1	A	863	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	974	ASP	2.8
1	A	544	ILE	2.8
1	A	476	ASP	2.7
1	A	358	SER	2.7
1	A	1049	TYR	2.7
1	A	973	ASN	2.6
1	A	460	ILE	2.6
1	A	545	PHE	2.5
1	A	148	ILE	2.5
1	A	978	MET	2.4
1	A	1006	VAL	2.4
1	A	1003	PRO	2.4
1	A	522	SER	2.4
1	A	631	GLU	2.4
1	A	720	GLU	2.4
1	A	865	GLU	2.4
1	A	850	ASP	2.2
1	A	357	HIS	2.2
1	A	248	LEU	2.2
1	A	360	GLU	2.2
1	A	547	PHE	2.1
1	A	109	VAL	2.1
1	A	359	GLU	2.1
1	A	948	ASN	2.1
1	A	58	PRO	2.1

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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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
3	MG	A	2000	1/1	0.96	0.07	21,21,21,21	0
3	MG	A	2001	1/1	0.96	0.08	31,31,31,31	0
2	ZN	A	1194	1/1	0.98	0.10	27,27,27,27	1

6.5 Other polymers [i](#)

There are no such residues in this entry.