



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:03 AM UTC

PDB ID : 4GSK / pdb_00004gsk
Title : Crystal structure of an Atg7-Atg10 crosslinked complex
Authors : Kaiser, S.E.; Mao, K.; Taherbhoy, A.M.; Yu, S.; Olszewski, J.L.; Duda, D.M.;
Kurinov, I.; Deng, A.; Fenn, T.D.; Klionsky, D.J.; Schulman, B.A.
Deposited on : 2012-08-27
Resolution : 2.90 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

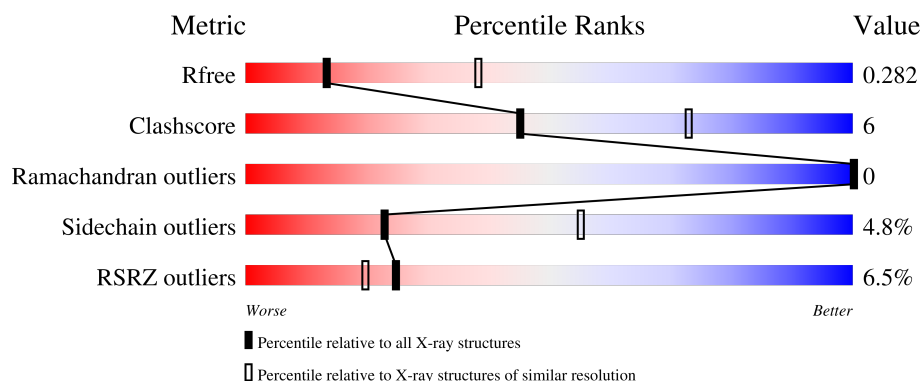
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	615	6% 75% 17% • 7%
1	B	615	4% 75% 17% • 7%
2	Y	173	10% 64% 14% • 21%
2	Z	173	8% 56% 18% • 24%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11408 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 Ubiquitin-like modifier-activating enzyme ATG7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	570	Total	C	N	O	S	0	0	0
			4548	2930	768	829	21			
1	B	572	Total	C	N	O	S	0	0	0
			4573	2946	774	832	21			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P38862
A	0	SER	-	expression tag	UNP P38862
A	39	SER	CYS	engineered mutation	UNP P38862
A	195	SER	CYS	engineered mutation	UNP P38862
A	375	ALA	CYS	engineered mutation	UNP P38862
B	-1	GLY	-	expression tag	UNP P38862
B	0	SER	-	expression tag	UNP P38862
B	39	SER	CYS	engineered mutation	UNP P38862
B	195	SER	CYS	engineered mutation	UNP P38862
B	375	ALA	CYS	engineered mutation	UNP P38862

- Molecule 2 is a protein called Ubiquitin-like-conjugating enzyme ATG10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Y	137	Total	C	N	O	S	0	0	0
			1161	758	190	210	3			
2	Z	131	Total	C	N	O	S	0	0	0
			1124	737	184	200	3			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	-5	GLY	-	expression tag	UNP Q07879
Y	-4	SER	-	expression tag	UNP Q07879

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Chain	Residue	Modelled	Actual	Comment	Reference
Y	-3	GLY	-	expression tag	UNP Q07879
Y	-2	GLY	-	expression tag	UNP Q07879
Y	-1	SER	-	expression tag	UNP Q07879
Y	0	GLY	-	expression tag	UNP Q07879
Y	26	SER	CYS	engineered mutation	UNP Q07879
Y	137	SER	CYS	engineered mutation	UNP Q07879
Z	-5	GLY	-	expression tag	UNP Q07879
Z	-4	SER	-	expression tag	UNP Q07879
Z	-3	GLY	-	expression tag	UNP Q07879
Z	-2	GLY	-	expression tag	UNP Q07879
Z	-1	SER	-	expression tag	UNP Q07879
Z	0	GLY	-	expression tag	UNP Q07879
Z	26	SER	CYS	engineered mutation	UNP Q07879
Z	137	SER	CYS	engineered mutation	UNP Q07879

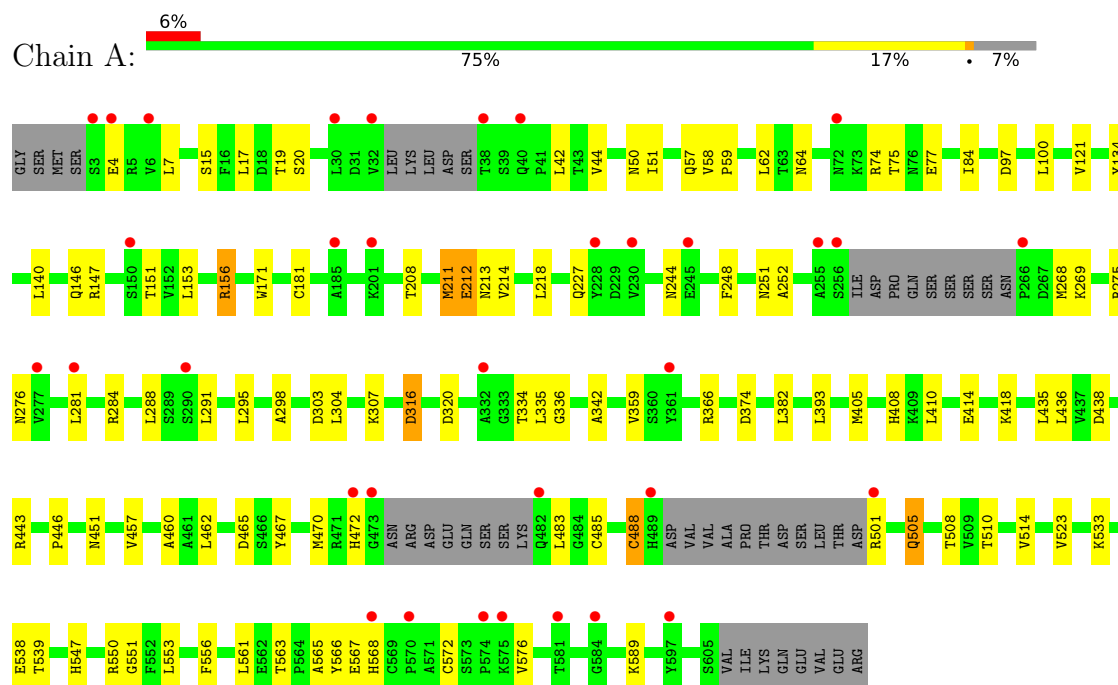
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

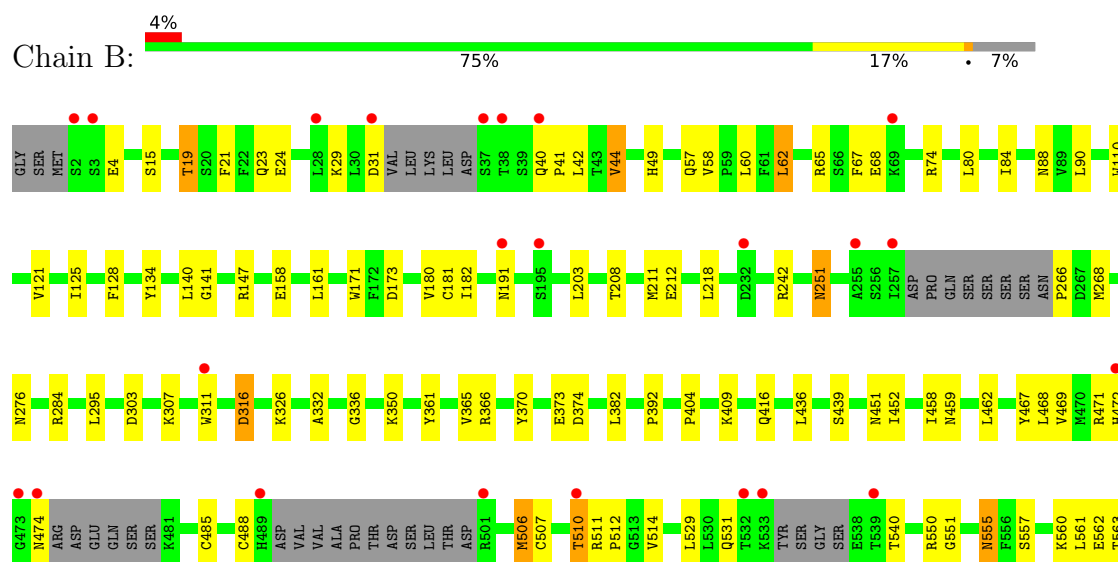
3 Residue-property plots [i](#)

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

- Molecule 1: Ubiquitin-like modifier-activating enzyme ATG7

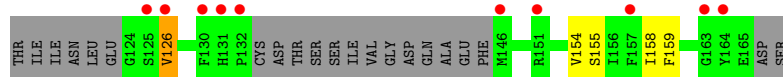


- Molecule 1: Ubiquitin-like modifier-activating enzyme ATG7

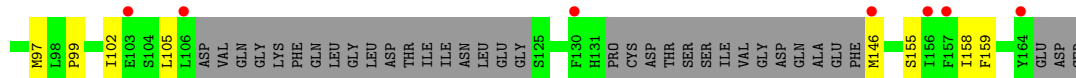
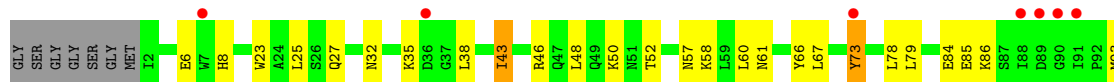




- Molecule 2: Ubiquitin-like-conjugating enzyme ATG10



- Molecule 2: Ubiquitin-like-conjugating enzyme ATG10



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	120.56Å 146.19Å 108.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.56 – 2.90 49.56 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.9 (49.56-2.90) 92.4 (49.56-2.90)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 2.91Å)	Xtriage
Refinement program	PHENIX dev_1000	Depositor
R, R_{free}	0.236 , 0.285 0.232 , 0.282	Depositor DCC
R_{free} test set	2154 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	51.5	Xtriage
Anisotropy	0.398	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 48.3	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	0.91	EDS
Total number of atoms	11408	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.86% 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	0.33	0/4646	0.76	1/6291 (0.0%)
1	B	0.33	0/4669	0.76	0/6318
2	Y	0.31	0/1193	0.74	2/1621 (0.1%)
2	Z	0.32	0/1155	0.71	0/1568
All	All	0.33	0/11663	0.75	3/15798 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	291	LEU	N-CA-C	-5.72	106.30	113.28
2	Y	98	LEU	CA-C-N	5.58	125.59	119.90
2	Y	98	LEU	C-N-CA	5.58	125.59	119.90

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	4548	0	4604	53	0
1	B	4573	0	4648	50	0
2	Y	1161	0	1139	15	0
2	Z	1124	0	1114	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
3	B	1	0	0	0	0
All	All	11408	0	11505	136	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 6.

All (136) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:49:GLN:HE22	2:Y:60:LEU:H	1.19	0.89
1:A:15:SER:HB3	1:A:140:LEU:HD22	1.59	0.84
2:Y:81:ARG:HH21	2:Y:126:VAL:HB	1.56	0.70
1:B:15:SER:HB3	1:B:140:LEU:HD22	1.77	0.66
2:Z:61:ASN:HD22	2:Z:85:GLU:HG2	1.62	0.64
1:B:307:LYS:HE2	1:B:311:TRP:HE1	1.62	0.64
1:B:462:LEU:HD22	1:B:514:VAL:HG12	1.80	0.62
1:A:462:LEU:HD22	1:A:514:VAL:HG12	1.82	0.61
1:B:295:LEU:HD21	1:B:392:PRO:HB2	1.82	0.61
1:A:533:LYS:NZ	1:A:538:GLU:OE1	2.33	0.61
1:B:374:ASP:HB3	1:B:382:LEU:HD21	1.82	0.61
1:B:409:LYS:HA	1:B:593:GLU:HG2	1.82	0.61
1:A:212:GLU:HG2	1:A:213:ASN:HD22	1.64	0.61
2:Z:27:GLN:HE21	2:Z:43:ILE:HG13	1.66	0.60
2:Z:155:SER:HA	2:Z:159:PHE:HB2	1.84	0.59
1:B:58:VAL:HG12	1:B:208:THR:HB	1.85	0.59
1:A:457:VAL:HB	1:A:472:HIS:HB2	1.84	0.59
1:B:276:ASN:HA	1:B:284:ARG:HE	1.68	0.59
2:Y:97:MET:HE3	2:Y:99:PRO:HG3	1.83	0.59
2:Z:67:LEU:HD21	2:Z:158:ILE:HD11	1.83	0.58
1:A:467:TYR:CZ	1:A:551:GLY:HA3	2.39	0.58
1:A:20:SER:HB2	1:A:64:ASN:HD22	1.68	0.57
1:A:147:ARG:HD2	1:A:268:MET:HE2	1.86	0.57
1:A:472:HIS:CE1	1:A:485:CYS:HB2	2.38	0.57
2:Y:8:HIS:CE1	2:Y:35:LYS:HB2	2.39	0.57
1:B:147:ARG:HH21	1:B:268:MET:HE3	1.70	0.57
1:A:435:LEU:HD21	1:A:446:PRO:HB2	1.86	0.57
1:A:211:MET:HB3	1:A:214:VAL:HB	1.89	0.55
2:Z:58:LYS:HD3	2:Z:84:GLU:CD	2.31	0.55
1:B:439:SER:HB3	1:B:506:MET:HB2	1.88	0.55
1:B:121:VAL:HG22	1:B:218:LEU:HD22	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:6:GLU:HG2	2:Z:146:MET:HE1	1.88	0.54
1:A:298:ALA:HB2	1:B:361:TYR:HB3	1.89	0.53
1:A:58:VAL:HG12	1:A:208:THR:HB	1.88	0.53
2:Y:3:PRO:HG2	2:Y:6:GLU:HB2	1.89	0.53
2:Y:52:THR:HG21	2:Y:60:LEU:HD13	1.90	0.53
2:Y:155:SER:HA	2:Y:159:PHE:HB2	1.90	0.53
2:Y:65:LEU:HD22	2:Y:78:LEU:HD11	1.90	0.53
1:B:467:TYR:CZ	1:B:551:GLY:HA3	2.44	0.52
2:Y:49:GLN:NE2	2:Y:60:LEU:H	1.98	0.52
1:B:326:LYS:HG2	1:B:350:LYS:HD3	1.91	0.52
1:A:335:LEU:HD21	1:A:462:LEU:HD21	1.91	0.52
2:Z:48:LEU:O	2:Z:52:THR:HG23	2.09	0.51
1:B:555:ASN:ND2	1:B:557:SER:OG	2.44	0.51
1:B:583:LEU:HB2	1:B:587:PHE:HB2	1.94	0.50
1:A:97:ASP:OD1	1:A:100:LEU:N	2.39	0.50
2:Y:67:LEU:HD21	2:Y:158:ILE:HD11	1.92	0.50
1:A:295:LEU:HD11	1:A:393:LEU:HG	1.93	0.50
1:A:374:ASP:HB3	1:A:382:LEU:HD21	1.94	0.49
1:A:405:MET:HE2	1:A:408:HIS:CE1	2.47	0.49
1:B:171:TRP:CZ3	1:B:181:CYS:HB3	2.47	0.49
2:Y:52:THR:HG21	2:Y:60:LEU:HD22	1.94	0.49
1:B:507:CYS:HB3	2:Z:73:TYR:CE1	2.48	0.49
1:A:443:ARG:NH2	1:A:460:ALA:O	2.39	0.49
1:B:21:PHE:CE1	1:B:62:LEU:HD12	2.47	0.49
1:A:121:VAL:HG22	1:A:218:LEU:HD22	1.94	0.48
1:A:336:GLY:HA2	1:A:436:LEU:HD13	1.95	0.48
1:A:505:GLN:O	1:A:508:THR:HG22	2.14	0.48
1:A:483:LEU:HB3	1:A:547:HIS:CD2	2.49	0.48
1:B:468:LEU:HD13	1:B:550:ARG:HG2	1.96	0.47
1:B:29:LYS:HE3	1:B:88:ASN:HD22	1.78	0.47
1:B:65:ARG:NH1	1:B:68:GLU:OE1	2.34	0.47
1:A:156:ARG:HG2	1:A:251:ASN:HB3	1.97	0.47
1:A:334:THR:HG23	1:A:366:ARG:O	2.16	0.46
1:A:414:GLU:O	1:A:418:LYS:HG2	2.15	0.46
1:B:212:GLU:OE1	1:B:212:GLU:N	2.45	0.46
2:Y:67:LEU:HD23	2:Y:78:LEU:HD13	1.97	0.46
1:B:471:ARG:HD2	1:B:529:LEU:HD21	1.98	0.46
1:A:276:ASN:HA	1:A:284:ARG:HE	1.81	0.45
1:A:465:ASP:HB2	1:A:553:LEU:HB2	1.97	0.45
1:A:288:LEU:HD23	1:A:288:LEU:HA	1.80	0.45
1:A:316:ASP:OD1	1:A:316:ASP:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:49:HIS:HE1	1:B:173:ASP:OD1	2.00	0.45
2:Z:97:MET:HE2	2:Z:99:PRO:HG3	1.97	0.45
1:B:44:VAL:HG13	1:B:80:LEU:HB3	1.99	0.45
2:Z:35:LYS:HA	2:Z:35:LYS:HD3	1.71	0.45
1:B:472:HIS:CE1	1:B:485:CYS:HB2	2.52	0.44
2:Z:46:ARG:O	2:Z:50:LYS:HG2	2.16	0.44
1:A:342:ALA:HB3	1:A:523:VAL:HG21	1.98	0.44
2:Z:8:HIS:HE1	2:Z:35:LYS:HB2	1.81	0.44
1:B:140:LEU:HG	1:B:141:GLY:N	2.32	0.44
2:Z:38:LEU:HD23	2:Z:67:LEU:HD12	2.00	0.44
1:A:7:LEU:HD22	1:A:153:LEU:HD23	1.99	0.44
1:A:550:ARG:HE	1:A:550:ARG:HB2	1.64	0.44
2:Z:60:LEU:HD12	2:Z:60:LEU:HA	1.87	0.44
1:A:153:LEU:HD11	1:A:252:ALA:HB1	1.99	0.44
1:B:24:GLU:HG2	1:B:67:PHE:CD1	2.52	0.44
1:B:211:MET:O	1:B:242:ARG:NH2	2.34	0.44
2:Y:23:TRP:CZ2	2:Y:25:LEU:HD12	2.52	0.43
2:Z:23:TRP:CZ2	2:Z:25:LEU:HD12	2.53	0.43
1:A:556:PHE:HB2	1:B:560:LYS:HD3	1.99	0.43
1:B:110:TRP:CH2	1:B:147:ARG:HD2	2.54	0.43
1:B:182:ILE:HG22	1:B:203:LEU:HD12	2.01	0.43
1:A:359:VAL:HG21	1:A:382:LEU:HD23	2.01	0.42
1:B:42:LEU:HD11	1:B:84:ILE:HB	1.99	0.42
1:B:40:GLN:HA	1:B:41:PRO:HD3	1.87	0.42
1:B:158:GLU:OE1	1:B:251:ASN:ND2	2.51	0.42
1:A:303:ASP:O	1:A:307:LYS:HG2	2.18	0.42
1:B:90:LEU:HB2	1:B:128:PHE:CE2	2.55	0.42
2:Z:86:LYS:HD3	2:Z:93:MET:HE3	2.00	0.42
1:A:42:LEU:HD11	1:A:84:ILE:HB	2.01	0.42
1:A:213:ASN:HA	1:A:248:PHE:CZ	2.54	0.42
1:A:74:ARG:HB2	1:A:77:GLU:HG3	2.01	0.42
1:A:410:LEU:HD11	1:A:589:LYS:HG3	2.02	0.42
1:A:171:TRP:CZ3	1:A:181:CYS:HB3	2.55	0.41
1:A:366:ARG:NH2	1:A:510:THR:O	2.51	0.41
1:B:303:ASP:O	1:B:307:LYS:HG2	2.20	0.41
2:Y:80:LEU:HD12	2:Y:81:ARG:H	1.85	0.41
1:B:316:ASP:OD1	1:B:316:ASP:N	2.52	0.41
1:B:531:GLN:HB2	1:B:540:THR:HB	2.02	0.41
1:A:275:ARG:HG2	1:A:281:LEU:HD23	2.01	0.41
1:B:511:ARG:HA	1:B:512:PRO:HD3	1.90	0.41
2:Z:66:TYR:HB3	2:Z:79:LEU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:566:TYR:CE2	1:A:568:HIS:HB2	2.56	0.41
2:Z:32:ASN:OD1	2:Z:32:ASN:N	2.54	0.41
1:B:332:ALA:HB1	1:B:370:TYR:OH	2.19	0.41
1:B:562:GLU:HG2	1:B:563:THR:H	1.86	0.41
1:A:17:LEU:HD22	1:A:62:LEU:HB2	2.02	0.41
1:A:51:ILE:HG23	1:A:59:PRO:HD3	2.03	0.41
1:A:488:CYS:SG	1:A:565:ALA:HA	2.61	0.41
1:B:336:GLY:HA2	1:B:436:LEU:HD13	2.03	0.41
1:B:404:PRO:HB3	1:B:416:GLN:NE2	2.35	0.41
1:B:459:ASN:O	1:B:469:VAL:HA	2.20	0.41
1:B:366:ARG:NH1	1:B:510:THR:O	2.36	0.41
1:A:550:ARG:HH21	1:A:561:LEU:HD21	1.86	0.40
2:Y:154:VAL:HG13	2:Y:158:ILE:HD12	2.03	0.40
2:Z:52:THR:HA	2:Z:105:LEU:HD11	2.03	0.40
1:A:146:GLN:OE1	1:A:269:LYS:HE2	2.22	0.40
1:A:151:THR:HG21	1:A:227:GLN:HE22	1.87	0.40
1:B:19:THR:O	1:B:23:GLN:HG2	2.22	0.40
2:Z:52:THR:HG21	2:Z:60:LEU:HD22	2.03	0.40
2:Z:67:LEU:HD23	2:Z:78:LEU:HD13	2.03	0.40
1:A:17:LEU:HD22	1:A:62:LEU:HD12	2.02	0.40
1:A:470:MET:HE3	1:A:470:MET:HB2	1.91	0.40
1:B:147:ARG:HH11	1:B:266:PRO:HD2	1.87	0.40
1:B:573:SER:HA	1:B:574:PRO:HD3	1.92	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	560/615 (91%)	549 (98%)	11 (2%)	0	100	100
1	B	560/615 (91%)	550 (98%)	10 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Y	131/173 (76%)	125 (95%)	6 (5%)	0	100	100
2	Z	125/173 (72%)	121 (97%)	4 (3%)	0	100	100
All	All	1376/1576 (87%)	1345 (98%)	31 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	510/555 (92%)	486 (95%)	24 (5%)	23	56
1	B	515/555 (93%)	487 (95%)	28 (5%)	20	51
2	Y	130/160 (81%)	125 (96%)	5 (4%)	29	64
2	Z	127/160 (79%)	123 (97%)	4 (3%)	35	69
All	All	1282/1430 (90%)	1221 (95%)	61 (5%)	23	55

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	GLU
1	A	19	THR
1	A	44	VAL
1	A	50	ASN
1	A	57	GLN
1	A	75	THR
1	A	134	TYR
1	A	156	ARG
1	A	211	MET
1	A	212	GLU
1	A	244	ASN
1	A	304	LEU
1	A	316	ASP
1	A	320	ASP

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Mol	Chain	Res	Type
1	A	438	ASP
1	A	451	ASN
1	A	488	CYS
1	A	501	ARG
1	A	505	GLN
1	A	539	THR
1	A	563	THR
1	A	567	GLU
1	A	572	CYS
1	A	576	VAL
1	B	4	GLU
1	B	19	THR
1	B	31	ASP
1	B	44	VAL
1	B	57	GLN
1	B	60	LEU
1	B	62	LEU
1	B	74	ARG
1	B	125	ILE
1	B	134	TYR
1	B	161	LEU
1	B	180	VAL
1	B	191	ASN
1	B	251	ASN
1	B	316	ASP
1	B	365	VAL
1	B	373	GLU
1	B	451	ASN
1	B	452	ILE
1	B	458	ILE
1	B	474	ASN
1	B	488	CYS
1	B	506	MET
1	B	510	THR
1	B	555	ASN
1	B	561	LEU
1	B	596	LEU
1	B	600	GLU
2	Y	34	GLU
2	Y	57	ASN
2	Y	82	ILE
2	Y	106	LEU

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Mol	Chain	Res	Type
2	Y	126	VAL
2	Z	43	ILE
2	Z	57	ASN
2	Z	73	TYR
2	Z	102	ILE

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	23	GLN
1	A	50	ASN
1	A	57	GLN
1	A	64	ASN
1	A	191	ASN
1	A	213	ASN
1	A	417	HIS
1	A	568	HIS
1	B	49	HIS
1	B	57	GLN
1	B	81	GLN
1	B	86	ASN
1	B	88	ASN
1	B	104	GLN
1	B	408	HIS
1	B	416	GLN
1	B	417	HIS
1	B	474	ASN
1	B	505	GLN
1	B	548	GLN
1	B	555	ASN
2	Y	5	GLN
2	Y	49	GLN
2	Y	61	ASN
2	Z	5	GLN
2	Z	8	HIS
2	Z	12	GLN
2	Z	21	HIS
2	Z	27	GLN
2	Z	61	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no 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

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	570/615 (92%)	0.77	34 (5%) 27 21	61, 80, 97, 105	0
1	B	572/615 (93%)	0.63	27 (4%) 36 28	60, 76, 94, 104	0
2	Y	137/173 (79%)	1.06	17 (12%) 8 7	66, 83, 96, 103	0
2	Z	131/173 (75%)	0.93	14 (10%) 11 9	68, 79, 93, 100	0
All	All	1410/1576 (89%)	0.76	92 (6%) 25 20	60, 78, 96, 105	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	32	VAL	5.9
1	A	473	GLY	4.6
2	Z	73	TYR	4.0
2	Y	125	SER	3.8
1	B	606	VAL	3.8
2	Y	163	GLY	3.8
2	Y	108	VAL	3.7
1	B	38	THR	3.6
1	B	607	ILE	3.6
1	B	489	HIS	3.5
2	Y	126	VAL	3.5
1	A	256	SER	3.4
1	A	290	SER	3.4
2	Y	131	HIS	3.4
1	A	575	LYS	3.4
2	Y	2	ILE	3.2
2	Y	132	PRO	3.1
2	Y	157	PHE	3.1
1	A	40	GLN	3.0
1	A	266	PRO	3.0
2	Y	89	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
2	Y	73	TYR	2.9
2	Y	1	MET	2.9
2	Z	90	GLY	2.9
1	A	185	ALA	2.9
2	Z	36	ASP	2.9
2	Z	89	ASP	2.8
2	Y	130	PHE	2.8
1	B	31	ASP	2.8
1	A	482	GLN	2.8
1	A	230	VAL	2.8
1	A	30	LEU	2.8
1	B	472	HIS	2.8
2	Z	88	ILE	2.8
1	A	332	ALA	2.7
2	Z	106	LEU	2.7
2	Z	130	PHE	2.7
1	B	257	ILE	2.7
1	A	597	TYR	2.7
1	B	474	ASN	2.7
1	A	255	ALA	2.6
1	A	6	VAL	2.6
1	A	3	SER	2.6
1	A	472	HIS	2.6
1	B	2	SER	2.5
1	A	489	HIS	2.5
2	Y	7	TRP	2.5
1	A	361	TYR	2.4
2	Y	151	ARG	2.4
1	B	37	SER	2.4
2	Z	103	GLU	2.4
2	Y	88	ILE	2.4
1	A	150	SER	2.3
1	A	570	PRO	2.3
1	B	232	ASP	2.3
1	A	38	THR	2.3
2	Y	164	TYR	2.3
2	Z	7	TRP	2.3
2	Z	156	ILE	2.3
1	A	4	GLU	2.3
2	Z	146	MET	2.2
1	B	28	LEU	2.2
1	A	574	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	581	THR	2.2
1	B	510	THR	2.2
2	Z	157	PHE	2.2
1	A	245	GLU	2.2
1	B	3	SER	2.2
2	Z	164	TYR	2.2
1	A	277	VAL	2.2
1	B	501	ARG	2.2
1	B	532	THR	2.2
1	A	584	GLY	2.2
1	A	501	ARG	2.1
1	B	195	SER	2.1
1	B	565	ALA	2.1
1	B	191	ASN	2.1
1	A	281	LEU	2.1
1	B	69	LYS	2.1
1	B	533	LYS	2.1
1	B	311	TRP	2.1
1	A	201	LYS	2.0
1	A	72	ASN	2.0
1	B	473	GLY	2.0
2	Z	91	ILE	2.0
1	B	255	ALA	2.0
1	B	597	TYR	2.0
1	A	568	HIS	2.0
1	B	40	GLN	2.0
1	B	539	THR	2.0
2	Y	146	MET	2.0
1	A	228	TYR	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 ⓘ

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(Å ²)	Q<0.9
3	ZN	B	701	1/1	0.97	0.10	92,92,92,92	0
3	ZN	A	701	1/1	0.99	0.13	88,88,88,88	0

6.5 Other polymers [i](#)

There are no such residues in this entry.