



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:44 PM UTC

PDB ID : 5BW8 / pdb_00005bw8
Title : 2.8 Å crystal structure of a Get3-Get4-Get5 intermediate complex from *S.cerevisiae*
Authors : Gristick, H.B.; Chartron, J.W.; Clemons, W.M.
Deposited on : 2015-06-06
Resolution : 2.80 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

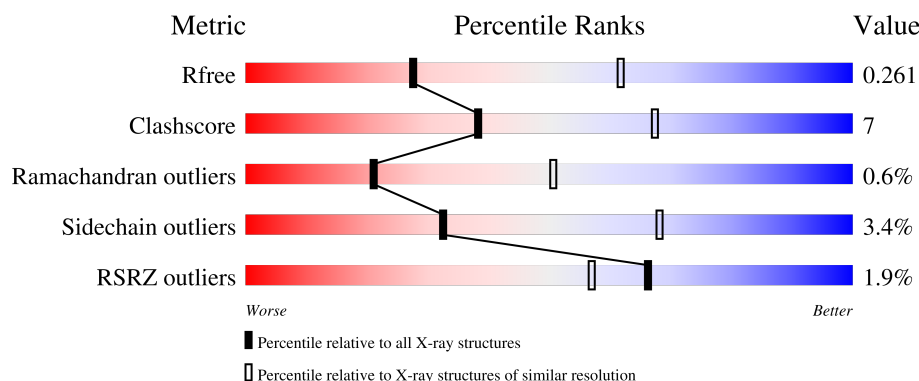
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	373	
1	B	373	
2	C	305	
3	D	54	
4	Z	13	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7742 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 ATPase GET3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	S	0	0	0
			2515	1589	417	491	18			
1	B	304	Total	C	N	O	S	0	0	0
			2412	1524	400	471	17			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	initiating methionine	UNP B3LGZ3
A	-17	GLY	-	expression tag	UNP B3LGZ3
A	-16	GLY	-	expression tag	UNP B3LGZ3
A	-15	SER	-	expression tag	UNP B3LGZ3
A	-14	HIS	-	expression tag	UNP B3LGZ3
A	-13	HIS	-	expression tag	UNP B3LGZ3
A	-12	HIS	-	expression tag	UNP B3LGZ3
A	-11	HIS	-	expression tag	UNP B3LGZ3
A	-10	HIS	-	expression tag	UNP B3LGZ3
A	-9	HIS	-	expression tag	UNP B3LGZ3
A	-8	GLY	-	expression tag	UNP B3LGZ3
A	-7	GLU	-	expression tag	UNP B3LGZ3
A	-6	ASN	-	expression tag	UNP B3LGZ3
A	-5	LEU	-	expression tag	UNP B3LGZ3
A	-4	TYR	-	expression tag	UNP B3LGZ3
A	-3	PHE	-	expression tag	UNP B3LGZ3
A	-2	GLN	-	expression tag	UNP B3LGZ3
A	-1	SER	-	expression tag	UNP B3LGZ3
A	0	VAL	-	expression tag	UNP B3LGZ3
A	1	ASP	-	expression tag	UNP B3LGZ3
B	-18	MET	-	initiating methionine	UNP B3LGZ3
B	-17	GLY	-	expression tag	UNP B3LGZ3
B	-16	GLY	-	expression tag	UNP B3LGZ3
B	-15	SER	-	expression tag	UNP B3LGZ3
B	-14	HIS	-	expression tag	UNP B3LGZ3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-13	HIS	-	expression tag	UNP B3LGZ3
B	-12	HIS	-	expression tag	UNP B3LGZ3
B	-11	HIS	-	expression tag	UNP B3LGZ3
B	-10	HIS	-	expression tag	UNP B3LGZ3
B	-9	HIS	-	expression tag	UNP B3LGZ3
B	-8	GLY	-	expression tag	UNP B3LGZ3
B	-7	GLU	-	expression tag	UNP B3LGZ3
B	-6	ASN	-	expression tag	UNP B3LGZ3
B	-5	LEU	-	expression tag	UNP B3LGZ3
B	-4	TYR	-	expression tag	UNP B3LGZ3
B	-3	PHE	-	expression tag	UNP B3LGZ3
B	-2	GLN	-	expression tag	UNP B3LGZ3
B	-1	SER	-	expression tag	UNP B3LGZ3
B	0	VAL	-	expression tag	UNP B3LGZ3
B	1	ASP	-	expression tag	UNP B3LGZ3

- Molecule 2 is a protein called Golgi to ER traffic protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	283	Total	C	N	O	S	0	0	0
			2348	1528	370	445	5			

There are 17 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	258	ALA	LYS	engineered mutation	UNP Q12125
C	260	ALA	LYS	engineered mutation	UNP Q12125
C	291	GLU	-	expression tag	UNP Q12125
C	292	ASN	-	expression tag	UNP Q12125
C	293	LEU	-	expression tag	UNP Q12125
C	294	TYR	-	expression tag	UNP Q12125
C	295	PHE	-	expression tag	UNP Q12125
C	296	GLN	-	expression tag	UNP Q12125
C	297	SER	-	expression tag	UNP Q12125
C	298	LEU	-	expression tag	UNP Q12125
C	299	GLU	-	expression tag	UNP Q12125
C	300	HIS	-	expression tag	UNP Q12125
C	301	HIS	-	expression tag	UNP Q12125
C	302	HIS	-	expression tag	UNP Q12125
C	303	HIS	-	expression tag	UNP Q12125
C	304	HIS	-	expression tag	UNP Q12125
C	305	HIS	-	expression tag	UNP Q12125

- Molecule 3 is a protein called Ubiquitin-like protein MDY2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	51	Total	C	N	O	0	0	0
			401	265	62	74			

- Molecule 4 is a protein called Unknown Protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	Z	13	Total	C	N	O	0	0	0
			65	39	13	13			

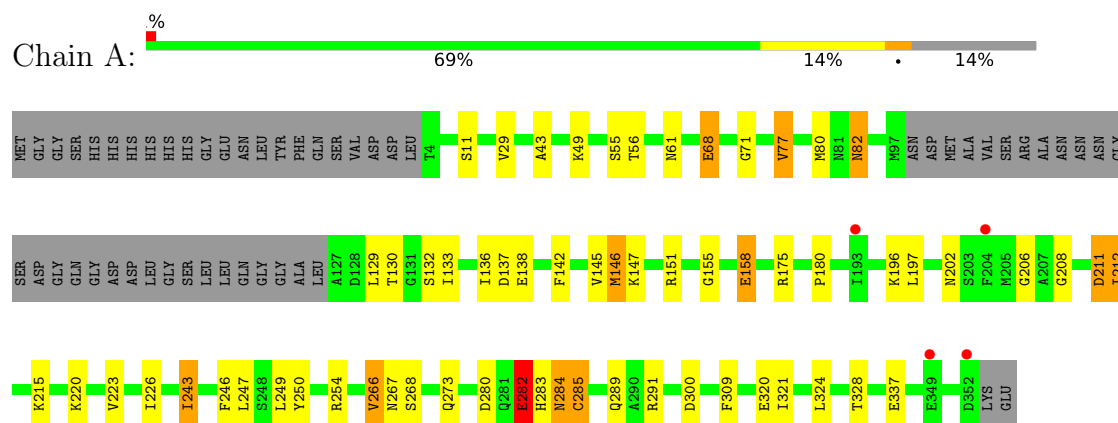
- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

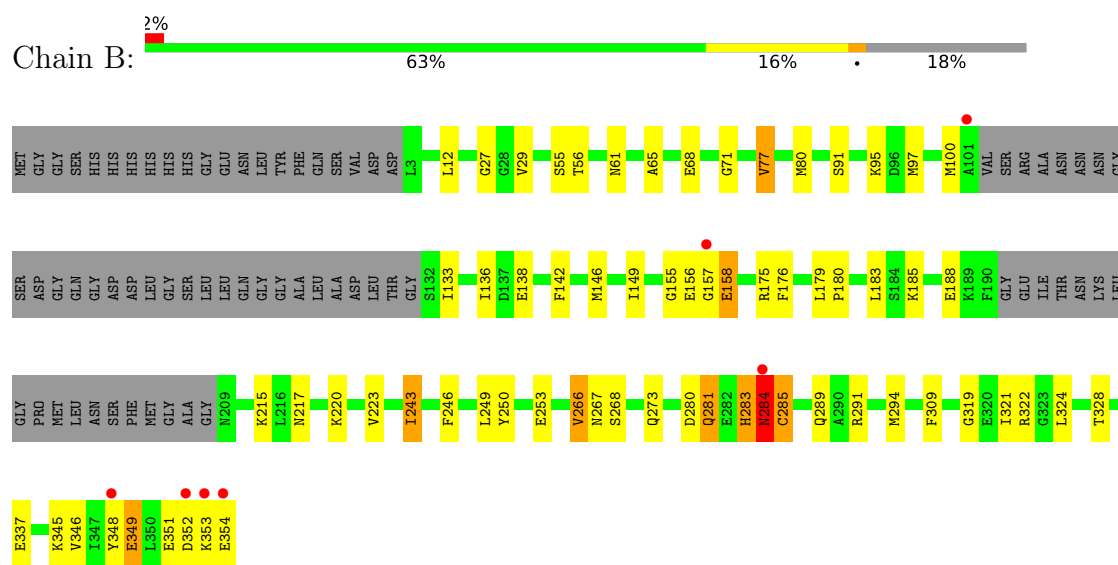
3 Residue-property plots [i](#)

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.

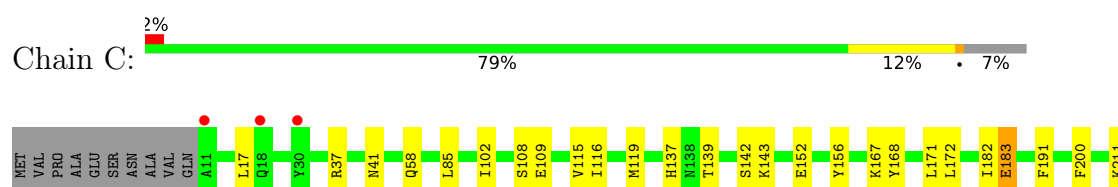
• Molecule 1: ATPase GET3



• Molecule 1: ATPase GET3

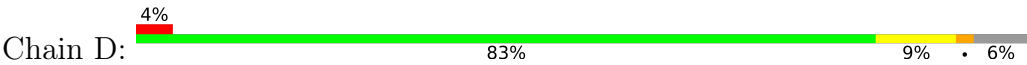


• Molecule 2: Golgi to ER traffic protein 4

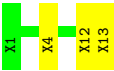




● Molecule 3: Ubiquitin-like protein MDY2



● Molecule 4: Unknown Protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	111.96Å 238.05Å 52.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.80 – 2.80 29.80 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.2 (29.80-2.80) 96.2 (29.80-2.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.60 (at 2.80Å)	Xtriage
Refinement program	REFMAC 5.8.0043	Depositor
R, R_{free}	0.224 , 0.262 0.226 , 0.261	Depositor DCC
R_{free} test set	1710 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	73.2	Xtriage
Anisotropy	0.806	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 86.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7742	wwPDB-VP
Average B, all atoms (Å ²)	112.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.23% 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	1.17	7/2558 (0.3%)	1.27	12/3451 (0.3%)
1	B	1.21	8/2452 (0.3%)	1.28	10/3306 (0.3%)
2	C	0.74	0/2405	1.02	4/3249 (0.1%)
3	D	0.74	0/412	1.03	2/560 (0.4%)
All	All	1.05	15/7827 (0.2%)	1.19	28/10566 (0.3%)

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	3
1	B	0	2
All	All	0	5

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	68	GLU	C-O	-8.61	1.13	1.23
1	B	71	GLY	C-O	-7.29	1.18	1.23
1	A	68	GLU	C-O	-7.15	1.15	1.23
1	A	71	GLY	C-O	-6.28	1.19	1.23
1	A	55	SER	C-O	-5.89	1.16	1.24
1	A	212	ILE	C-O	5.83	1.30	1.24
1	B	55	SER	C-O	-5.70	1.17	1.24
1	B	217	ASN	C-O	-5.61	1.17	1.24
1	B	149	ILE	C-O	-5.60	1.17	1.24
1	A	133	ILE	N-CA	-5.55	1.41	1.46
1	A	300	ASP	CA-C	5.52	1.59	1.52
1	B	253	GLU	C-O	-5.27	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	319	GLY	C-O	-5.25	1.19	1.24
1	B	155	GLY	C-O	-5.06	1.18	1.24
1	A	282	GLU	C-O	-5.03	1.18	1.24

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	266	VAL	CB-CA-C	-8.58	100.63	110.41
1	A	82	ASN	N-CA-CB	-7.84	100.63	110.98
1	A	136	ILE	CB-CA-C	-6.88	103.00	112.02
2	C	290	ASN	N-CA-C	-6.74	96.44	110.80
2	C	289	PHE	CB-CA-C	6.68	123.72	110.42
1	B	337	GLU	CB-CA-C	-6.53	100.63	109.71
1	A	266	VAL	CB-CA-C	-6.47	101.32	110.12
2	C	290	ASN	N-CA-CB	6.38	121.26	110.49
1	A	284	ASN	N-CA-C	6.32	119.73	107.71
1	A	133	ILE	N-CA-C	6.30	114.82	107.77
1	B	285	CYS	CA-CB-SG	-6.23	100.08	114.40
1	B	136	ILE	CB-CA-C	-6.22	103.87	112.02
1	A	337	GLU	CB-CA-C	-6.06	101.28	109.71
1	B	185	LYS	O-C-N	5.97	128.96	122.15
1	B	27	GLY	N-CA-C	5.90	127.16	113.18
1	B	158	GLU	N-CA-C	5.84	118.27	107.99
1	A	133	ILE	CA-C-O	5.80	123.43	119.20
1	B	185	LYS	CA-C-O	-5.67	114.41	120.42
1	B	133	ILE	N-CA-C	5.26	113.72	107.73
1	A	211	ASP	O-C-N	5.24	127.48	122.03
1	A	146	MET	CA-C-N	5.21	127.22	120.44
1	A	146	MET	C-N-CA	5.21	127.22	120.44
1	B	294	MET	N-CA-CB	5.17	117.82	110.16
3	D	7	GLY	CA-C-N	5.17	124.62	119.24
3	D	7	GLY	C-N-CA	5.17	124.62	119.24
1	A	155	GLY	CA-C-N	5.07	129.53	122.08
1	A	155	GLY	C-N-CA	5.07	129.53	122.08
2	C	283	PHE	N-CA-CB	5.03	117.31	110.01

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	196	LYS	Peptide
1	A	206	GLY	Peptide

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Mol	Chain	Res	Type	Group
1	A	68	GLU	Mainchain
1	B	100	MET	Peptide
1	B	283	HIS	Peptide

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	2515	0	2494	39	0
1	B	2412	0	2390	35	0
2	C	2348	0	2275	31	0
3	D	401	0	425	3	0
4	Z	65	0	16	2	0
5	A	1	0	0	0	0
All	All	7742	0	7600	106	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 7.

All (106) 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:345:LYS:O	1:B:349:GLU:HG2	1.59	1.01
1:B:215:LYS:HE2	4:Z:4:UNK:O	1.64	0.96
1:B:324:LEU:O	1:B:328:THR:HG23	1.69	0.93
1:A:324:LEU:O	1:A:328:THR:HG23	1.69	0.93
1:A:142:PHE:HE2	1:A:146:MET:HE3	1.37	0.90
1:A:142:PHE:CE2	1:A:146:MET:HE3	2.08	0.88
2:C:212:ASP:O	2:C:216:GLU:HG2	1.72	0.88
1:B:345:LYS:O	1:B:349:GLU:CG	2.23	0.86
1:B:351:GLU:O	1:B:354:GLU:HG3	1.77	0.85
1:A:142:PHE:HE2	1:A:146:MET:CE	1.91	0.83
1:A:280:ASP:OD1	1:A:283:HIS:CD2	2.31	0.83
1:A:280:ASP:OD1	1:A:283:HIS:HD2	1.62	0.81
1:B:285:CYS:O	1:B:289:GLN:HG2	1.81	0.81
2:C:171:LEU:HD12	2:C:172:LEU:N	2.02	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:283:HIS:O	1:B:284:ASN:C	2.30	0.74
1:B:283:HIS:C	1:B:284:ASN:O	2.30	0.73
1:B:283:HIS:O	1:B:284:ASN:O	2.08	0.72
1:A:49:LYS:O	1:A:82:ASN:OD1	2.09	0.71
2:C:259:ASP:C	2:C:289:PHE:HE1	1.99	0.71
2:C:37:ARG:NH2	2:C:41:ASN:HD21	1.90	0.70
2:C:102:ILE:HG12	2:C:119:MET:HE1	1.75	0.69
1:B:348:TYR:CD2	1:B:352:ASP:OD2	2.47	0.68
3:D:7:GLY:O	3:D:11:GLU:HG2	1.95	0.66
1:B:348:TYR:CE2	1:B:352:ASP:OD1	2.48	0.66
2:C:17:LEU:HD13	2:C:58:GLN:HG2	1.77	0.66
2:C:142:SER:OG	2:C:167:LYS:HE3	1.96	0.65
1:A:291:ARG:NH1	1:B:291:ARG:HD2	2.11	0.65
1:A:43:ALA:O	1:A:82:ASN:ND2	2.31	0.64
1:B:346:VAL:HA	1:B:349:GLU:HG3	1.80	0.64
1:A:285:CYS:O	1:A:289:GLN:HG2	1.99	0.61
2:C:102:ILE:CG1	2:C:119:MET:HE1	2.33	0.59
1:B:91:SER:O	1:B:95:LYS:HG3	2.04	0.58
4:Z:12:UNK:O	4:Z:13:UNK:CB	2.52	0.57
2:C:236:ILE:HD11	2:C:253:ILE:HD12	1.85	0.57
1:A:129:LEU:HD12	1:A:130:THR:N	2.20	0.57
1:A:77:VAL:HG22	1:A:80:MET:CG	2.37	0.55
2:C:263:PHE:HB2	2:C:289:PHE:CZ	2.42	0.55
2:C:171:LEU:HD12	2:C:171:LEU:C	2.32	0.54
2:C:212:ASP:O	2:C:216:GLU:CG	2.53	0.53
2:C:259:ASP:C	2:C:289:PHE:CE1	2.84	0.53
1:B:346:VAL:CA	1:B:349:GLU:HG3	2.39	0.52
1:B:243:ILE:HD11	1:B:273:GLN:CD	2.34	0.52
2:C:102:ILE:HG21	2:C:139:THR:HG22	1.92	0.52
2:C:289:PHE:O	2:C:290:ASN:HB2	2.10	0.52
2:C:200:PHE:HB3	3:D:41:LEU:O	2.09	0.52
1:B:77:VAL:HG22	1:B:80:MET:CG	2.39	0.51
1:B:29:VAL:HA	1:B:243:ILE:HD13	1.91	0.51
1:B:138:GLU:OE2	1:B:175:ARG:NH1	2.42	0.51
1:A:246:PHE:C	1:A:246:PHE:CD1	2.89	0.51
1:A:138:GLU:OE2	1:A:175:ARG:NH1	2.41	0.51
1:A:146:MET:HE1	1:A:226:ILE:HG12	1.93	0.51
1:A:129:LEU:HD12	1:A:129:LEU:C	2.37	0.50
1:B:142:PHE:O	1:B:146:MET:HG3	2.12	0.49
1:B:176:PHE:O	1:B:179:LEU:HB2	2.12	0.49
1:A:280:ASP:OD2	1:A:282:GLU:OE2	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:PRO:HD3	1:B:223:VAL:HG11	1.94	0.49
2:C:259:ASP:O	2:C:289:PHE:HE1	1.96	0.49
1:A:180:PRO:HD3	1:A:223:VAL:HG11	1.95	0.48
2:C:263:PHE:CD1	2:C:289:PHE:CE2	3.00	0.48
1:A:142:PHE:CE2	1:A:146:MET:CE	2.78	0.48
1:B:345:LYS:O	1:B:349:GLU:HG3	2.12	0.48
1:A:129:LEU:HA	1:A:132:SER:HB3	1.96	0.48
1:B:349:GLU:O	1:B:353:LYS:HG3	2.14	0.47
1:B:246:PHE:CD1	1:B:246:PHE:C	2.92	0.47
2:C:152:GLU:OE1	2:C:152:GLU:N	2.44	0.47
1:B:348:TYR:HD2	1:B:352:ASP:OD2	1.96	0.47
1:B:179:LEU:HD22	1:B:183:LEU:HG	1.95	0.47
1:B:348:TYR:CD2	1:B:352:ASP:CG	2.93	0.47
1:B:65:ALA:HA	1:B:322:ARG:HD3	1.96	0.47
1:A:29:VAL:HA	1:A:243:ILE:HD13	1.97	0.46
2:C:168:TYR:O	2:C:171:LEU:HG	2.16	0.46
2:C:115:VAL:HG12	2:C:119:MET:HE2	1.97	0.46
2:C:285:GLY:O	2:C:289:PHE:HB2	2.16	0.46
2:C:102:ILE:HG23	2:C:143:LYS:HG3	1.97	0.46
1:A:267:ASN:HA	1:A:309:PHE:CD2	2.51	0.45
1:A:197:LEU:HB2	1:A:202:ASN:OD1	2.17	0.45
1:A:208:GLY:O	1:A:211:ASP:HB3	2.16	0.45
1:A:61:ASN:OD1	1:A:61:ASN:N	2.50	0.45
1:B:267:ASN:HA	1:B:309:PHE:CD2	2.52	0.45
1:A:243:ILE:HD11	1:A:273:GLN:CD	2.42	0.45
2:C:137:HIS:CD2	2:C:156:TYR:HD1	2.36	0.44
1:A:280:ASP:O	1:A:284:ASN:N	2.51	0.44
1:A:142:PHE:CD2	1:A:146:MET:HE3	2.49	0.44
1:A:211:ASP:O	1:A:215:LYS:HG3	2.17	0.44
1:A:147:LYS:HE2	1:A:151:ARG:HH21	1.82	0.44
2:C:229:ILE:CD1	2:C:238:PHE:HB2	2.47	0.44
1:A:130:THR:HB	1:A:137:ASP:OD1	2.17	0.43
1:B:156:GLU:C	1:B:158:GLU:H	2.26	0.43
1:A:280:ASP:O	1:A:284:ASN:HB2	2.18	0.43
1:B:61:ASN:OD1	1:B:61:ASN:N	2.50	0.43
1:A:197:LEU:O	1:A:202:ASN:ND2	2.51	0.43
1:B:280:ASP:O	1:B:281:GLN:CB	2.67	0.43
2:C:108:SER:O	2:C:109:GLU:C	2.61	0.43
1:A:77:VAL:HG22	1:A:80:MET:HG3	2.00	0.42
2:C:143:LYS:HA	2:C:143:LYS:HD2	1.83	0.42
2:C:182:ILE:HG22	2:C:183:GLU:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:PRO:HA	1:B:220:LYS:HG3	2.01	0.41
1:A:250:TYR:CZ	1:A:254:ARG:HD2	2.55	0.41
1:A:142:PHE:O	1:A:146:MET:HG3	2.21	0.41
1:A:247:LEU:HD23	1:A:247:LEU:HA	1.91	0.41
1:B:250:TYR:CD1	1:B:250:TYR:C	2.98	0.41
2:C:191:PHE:HE1	2:C:211:LYS:HA	1.85	0.41
2:C:219:ILE:HA	2:C:224:PRO:HD2	2.03	0.40
1:A:142:PHE:O	1:A:145:VAL:HG22	2.21	0.40
2:C:240:GLU:OE2	3:D:3:THR:HB	2.21	0.40
1:A:180:PRO:HA	1:A:220:LYS:HG3	2.03	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	316/373 (85%)	306 (97%)	8 (2%)	2 (1%)	21	51
1	B	298/373 (80%)	286 (96%)	9 (3%)	3 (1%)	12	38
2	C	281/305 (92%)	271 (96%)	9 (3%)	1 (0%)	30	60
3	D	49/54 (91%)	47 (96%)	2 (4%)	0	100	100
All	All	944/1105 (85%)	910 (96%)	28 (3%)	6 (1%)	21	51

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	284	ASN
2	C	290	ASN
1	A	158	GLU
1	B	157	GLY
1	B	281	GLN

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Mol	Chain	Res	Type
1	A	285	CYS

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	284/325 (87%)	272 (96%)	12 (4%)	26	61
1	B	274/325 (84%)	262 (96%)	12 (4%)	25	59
2	C	254/274 (93%)	251 (99%)	3 (1%)	63	87
3	D	47/50 (94%)	45 (96%)	2 (4%)	26	60
All	All	859/974 (88%)	830 (97%)	29 (3%)	32	68

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	SER
1	A	56	THR
1	A	77	VAL
1	A	158	GLU
1	A	212	ILE
1	A	243	ILE
1	A	249	LEU
1	A	266	VAL
1	A	268	SER
1	A	282	GLU
1	A	320	GLU
1	A	321	ILE
1	B	12	LEU
1	B	56	THR
1	B	77	VAL
1	B	97	MET
1	B	188	GLU
1	B	243	ILE
1	B	249	LEU
1	B	266	VAL

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Mol	Chain	Res	Type
1	B	268	SER
1	B	284	ASN
1	B	321	ILE
1	B	349	GLU
2	C	85	LEU
2	C	116	ILE
2	C	183	GLU
3	D	36	LYS
3	D	39	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	82	ASN
1	A	148	HIS
1	A	195	ASN
1	A	283	HIS
1	A	289	GLN
1	A	326	ASN
1	B	41	GLN
1	B	98	ASN
1	B	289	GLN
2	C	41	ASN
2	C	51	HIS
2	C	162	HIS
2	C	269	HIS
2	C	275	GLN
3	D	40	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is 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	320/373 (85%)	0.01	4 (1%) 75 66	56, 94, 210, 324	0
1	B	304/373 (81%)	-0.02	7 (2%) 61 51	55, 80, 159, 198	0
2	C	283/305 (92%)	0.06	5 (1%) 67 58	66, 122, 201, 222	0
3	D	51/54 (94%)	0.44	2 (3%) 43 34	122, 170, 225, 240	0
4	Z	0/13	-	-	-	-
All	All	958/1118 (85%)	0.04	18 (1%) 66 57	55, 97, 198, 324	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	354	GLU	4.6
1	B	352	ASP	3.5
2	C	293	LEU	3.3
2	C	11	ALA	3.2
1	A	204	PHE	3.2
1	B	353	LYS	2.8
1	B	101	ALA	2.6
1	B	348	TYR	2.5
1	A	349	GLU	2.5
2	C	292	ASN	2.5
1	B	284	ASN	2.5
2	C	18	GLN	2.3
1	A	193	ILE	2.3
3	D	5	ALA	2.2
1	B	157	GLY	2.1
2	C	30	TYR	2.1
1	A	352	ASP	2.1
3	D	13	VAL	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
5	ZN	A	401	1/1	0.99	0.03	111,111,111,111	0

6.5 Other polymers [i](#)

There are no such residues in this entry.