



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 09:50 AM UTC

PDB ID : 6W9D / pdb_00006w9d
Title : RNF12 RING domain in complex with a Ube2d2 Ub conjugate
Authors : Middleton, A.J.; Day, C.L.
Deposited on : 2020-03-22
Resolution : 3.19 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

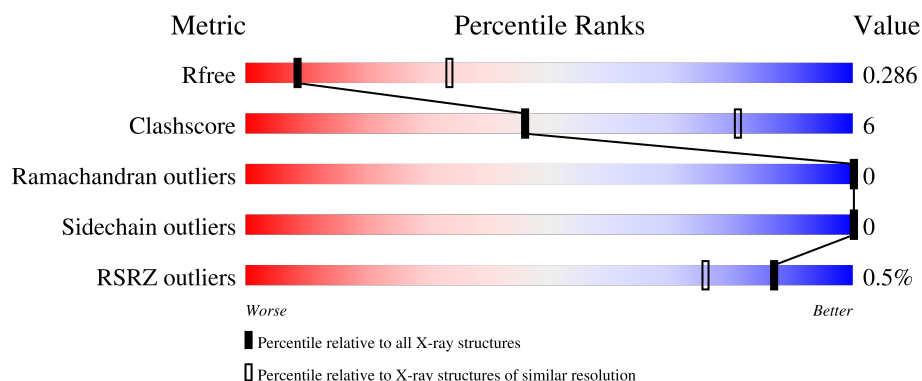
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.19 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	1466 (3.20-3.20)
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	155	
1	D	155	
1	G	155	
2	B	98	
2	E	98	

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Mol	Chain	Length	Quality of chain
2	H	98	% 56% 12% 32%
3	C	76	82% 13% 5%
3	F	76	3% 79% 13% 8%
3	I	76	86% 9% 5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6872 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-conjugating enzyme E2 D2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	148	Total	C	N	O	S	0	0	0
			1194	767	207	217	3			
1	D	148	Total	C	N	O	S	0	0	0
			1194	767	207	217	3			
1	G	148	Total	C	N	O	S	0	0	0
			1193	767	207	215	4			

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	21	SER	CYS	engineered mutation	UNP P62837
A	22	ARG	SER	engineered mutation	UNP P62837
A	85	LYS	CYS	engineered mutation	UNP P62837
A	107	SER	CYS	engineered mutation	UNP P62837
A	111	SER	CYS	engineered mutation	UNP P62837
A	148	LEU	-	expression tag	UNP P62837
A	149	GLU	-	expression tag	UNP P62837
A	150	HIS	-	expression tag	UNP P62837
A	151	HIS	-	expression tag	UNP P62837
A	152	HIS	-	expression tag	UNP P62837
A	153	HIS	-	expression tag	UNP P62837
A	154	HIS	-	expression tag	UNP P62837
A	155	HIS	-	expression tag	UNP P62837
D	21	SER	CYS	engineered mutation	UNP P62837
D	22	ARG	SER	engineered mutation	UNP P62837
D	85	LYS	CYS	engineered mutation	UNP P62837
D	107	SER	CYS	engineered mutation	UNP P62837
D	111	SER	CYS	engineered mutation	UNP P62837
D	148	LEU	-	expression tag	UNP P62837
D	149	GLU	-	expression tag	UNP P62837
D	150	HIS	-	expression tag	UNP P62837
D	151	HIS	-	expression tag	UNP P62837
D	152	HIS	-	expression tag	UNP P62837

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Chain	Residue	Modelled	Actual	Comment	Reference
D	153	HIS	-	expression tag	UNP P62837
D	154	HIS	-	expression tag	UNP P62837
D	155	HIS	-	expression tag	UNP P62837
G	21	SER	CYS	engineered mutation	UNP P62837
G	22	ARG	SER	engineered mutation	UNP P62837
G	85	LYS	CYS	engineered mutation	UNP P62837
G	107	SER	CYS	engineered mutation	UNP P62837
G	111	SER	CYS	engineered mutation	UNP P62837
G	148	LEU	-	expression tag	UNP P62837
G	149	GLU	-	expression tag	UNP P62837
G	150	HIS	-	expression tag	UNP P62837
G	151	HIS	-	expression tag	UNP P62837
G	152	HIS	-	expression tag	UNP P62837
G	153	HIS	-	expression tag	UNP P62837
G	154	HIS	-	expression tag	UNP P62837
G	155	HIS	-	expression tag	UNP P62837

- Molecule 2 is a protein called E3 ubiquitin-protein ligase RLIM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	62	Total	C	N	O	S	0	0	0
			500	308	92	93	7			
2	E	67	Total	C	N	O	S	0	0	0
			537	331	100	99	7			
2	H	67	Total	C	N	O	S	0	0	0
			537	331	100	99	7			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	526	GLY	-	expression tag	UNP Q9NVW2
B	527	PRO	-	expression tag	UNP Q9NVW2
B	528	LEU	-	expression tag	UNP Q9NVW2
B	529	GLY	-	expression tag	UNP Q9NVW2
E	526	GLY	-	expression tag	UNP Q9NVW2
E	527	PRO	-	expression tag	UNP Q9NVW2
E	528	LEU	-	expression tag	UNP Q9NVW2
E	529	GLY	-	expression tag	UNP Q9NVW2
H	526	GLY	-	expression tag	UNP Q9NVW2
H	527	PRO	-	expression tag	UNP Q9NVW2
H	528	LEU	-	expression tag	UNP Q9NVW2
H	529	GLY	-	expression tag	UNP Q9NVW2

- Molecule 3 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	72	Total	C	N	O	S	0	0	0
			574	362	98	113	1			
3	F	70	Total	C	N	O	S	0	0	0
			555	350	93	111	1			
3	I	72	Total	C	N	O	S	0	0	0
			574	362	98	113	1			

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Zn	0	0
			2	2		
4	E	2	Total	Zn	0	0
			2	2		
4	H	2	Total	Zn	0	0
			2	2		

- Molecule 5 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	I	0	0
			1	1		
5	C	1	Total	I	0	0
			1	1		
5	D	1	Total	I	0	0
			1	1		
5	E	1	Total	I	0	0
			1	1		
5	F	1	Total	I	0	0
			1	1		
5	G	1	Total	I	0	0
			1	1		
5	H	1	Total	I	0	0
			1	1		
5	I	1	Total	I	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: Ubiquitin-conjugating enzyme E2 D2

Chain A: 



- Molecule 1: Ubiquitin-conjugating enzyme E2 D2

Chain D: 



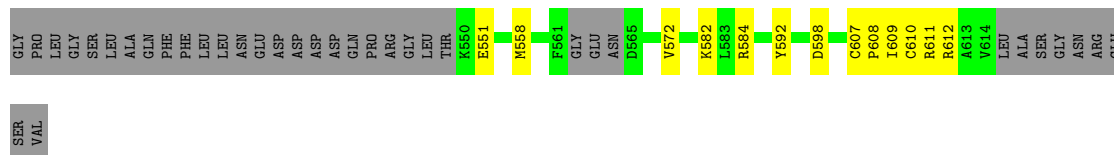
- Molecule 1: Ubiquitin-conjugating enzyme E2 D2

Chain G: 



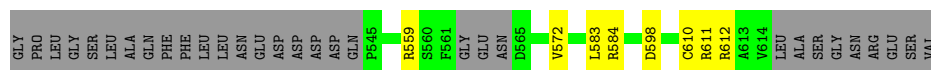
- Molecule 2: E3 ubiquitin-protein ligase RLIM

Chain B: 

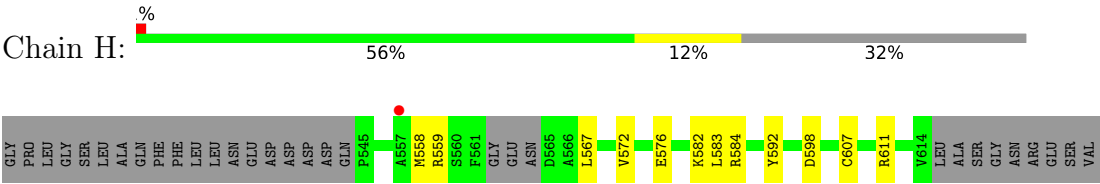


- Molecule 2: E3 ubiquitin-protein ligase RLIM

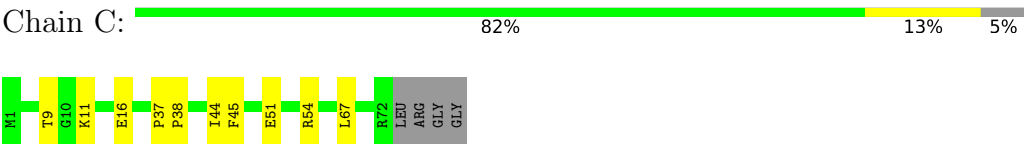
Chain E: 



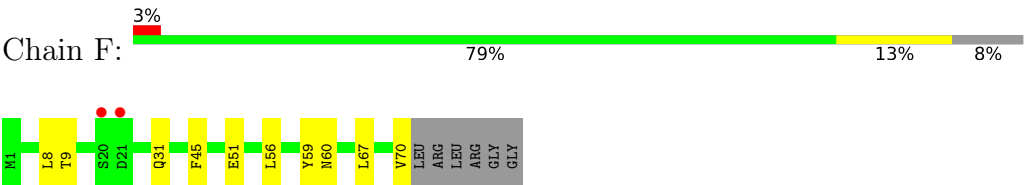
• Molecule 2: E3 ubiquitin-protein ligase RLIM



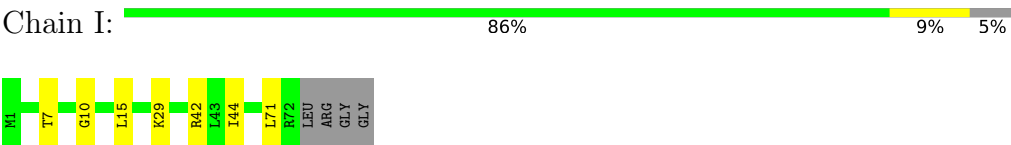
• Molecule 3: Ubiquitin



• Molecule 3: Ubiquitin



• Molecule 3: Ubiquitin



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	135.47Å 135.47Å 51.37Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.06 – 3.19 47.06 – 3.19	Depositor EDS
% Data completeness (in resolution range)	98.2 (47.06-3.19) 98.3 (47.06-3.19)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.222 , 0.281 0.223 , 0.286	Depositor DCC
R_{free} test set	829 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å ²)	88.8	Xtriage
Anisotropy	0.096	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 53.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.045 for -h,-k,l 0.045 for h,-h-k,-l 0.048 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6872	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.70% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, IOD

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	0.09	0/1230	0.28	0/1676
1	D	0.10	0/1230	0.30	0/1676
1	G	0.11	0/1229	0.30	0/1674
2	B	0.12	0/508	0.33	0/683
2	E	0.09	0/546	0.32	0/734
2	H	0.10	0/546	0.34	0/734
3	C	0.10	0/580	0.30	0/781
3	F	0.09	0/561	0.28	0/756
3	I	0.09	0/580	0.29	0/781
All	All	0.10	0/7010	0.30	0/9495

There are no bond length outliers.

There are no bond angle outliers.

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	1194	0	1186	16	0
1	D	1194	0	1186	14	0
1	G	1193	0	1192	20	0
2	B	500	0	485	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	537	0	527	6	0
2	H	537	0	527	8	0
3	C	574	0	599	8	0
3	F	555	0	575	7	0
3	I	574	0	599	6	0
4	B	2	0	0	0	0
4	E	2	0	0	0	0
4	H	2	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	1	0
5	G	1	0	0	0	0
5	H	1	0	0	0	0
5	I	1	0	0	1	0
All	All	6872	0	6876	80	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 (80) 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:D:143:GLN:HA	1:D:147:MET:HG3	1.68	0.75
2:H:558:MET:HE3	2:H:582:LYS:HG2	1.68	0.74
3:I:15:LEU:HD22	3:I:29:LYS:HG2	1.74	0.68
1:G:108:SER:HB2	3:I:44:ILE:HD11	1.77	0.67
2:B:558:MET:HE3	2:B:582:LYS:HD3	1.76	0.66
2:B:584:ARG:NH1	2:B:598:ASP:OD1	2.30	0.65
1:A:108:SER:HB2	3:C:44:ILE:HD11	1.79	0.63
1:A:5:ARG:NH1	2:B:572:VAL:O	2.32	0.63
2:H:584:ARG:NH1	2:H:598:ASP:OD1	2.34	0.61
1:A:5:ARG:NH2	1:A:97:LEU:O	2.34	0.60
1:A:20:GLN:HB3	1:A:38:MET:HB2	1.85	0.59
1:D:19:ALA:O	1:D:22:ARG:NH2	2.35	0.59
1:G:5:ARG:NH1	2:H:572:VAL:O	2.36	0.59
1:A:92:GLN:O	2:B:611:ARG:NH2	2.36	0.58
1:G:1:MET:SD	1:G:1:MET:N	2.76	0.57
1:G:5:ARG:HH21	1:G:98:THR:HG22	1.67	0.57
1:G:135:ASN:HB3	1:G:139:ARG:HH21	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:5:ARG:NH1	2:E:572:VAL:O	2.40	0.55
2:B:610:CYS:SG	2:B:612:ARG:NH1	2.80	0.55
3:F:51:GLU:OE1	3:F:59:TYR:OH	2.25	0.54
1:A:147:MET:SD	1:A:148:LEU:N	2.76	0.54
1:D:26:VAL:HG23	1:D:27:GLY:H	1.74	0.53
1:A:26:VAL:HG23	1:A:27:GLY:H	1.74	0.53
3:C:51:GLU:HB2	3:C:54:ARG:HG3	1.90	0.53
2:B:592:TYR:OH	2:B:607:CYS:SG	2.67	0.51
3:C:16:GLU:H	3:C:16:GLU:CD	2.17	0.51
3:F:56:LEU:O	3:F:60:ASN:N	2.44	0.51
1:G:128:LYS:HG3	1:G:129:THR:HG23	1.93	0.50
2:E:584:ARG:NH1	2:E:598:ASP:OD1	2.44	0.50
2:H:567:LEU:HB3	2:H:576:GLU:OE2	2.12	0.49
1:G:92:GLN:O	2:H:611:ARG:NH2	2.45	0.49
1:A:59:ASP:OD1	1:A:59:ASP:N	2.40	0.48
1:G:108:SER:HA	3:I:42:ARG:HH21	1.78	0.48
2:H:567:LEU:HD13	2:H:576:GLU:OE2	2.14	0.48
1:G:26:VAL:HG23	1:G:27:GLY:H	1.79	0.48
1:A:147:MET:O	1:A:149:GLU:N	2.40	0.47
1:A:135:ASN:HB3	1:A:139:ARG:HH21	1.79	0.47
1:A:95:PRO:HB2	2:B:572:VAL:HG13	1.97	0.47
2:H:592:TYR:OH	2:H:607:CYS:SG	2.64	0.47
1:G:111:SER:HB2	3:I:42:ARG:NH2	2.30	0.47
1:G:100:SER:O	1:G:104:LEU:HG	2.15	0.47
1:D:85:LYS:HD2	1:D:90:ARG:NH2	2.31	0.46
1:G:59:ASP:OD1	1:G:59:ASP:N	2.46	0.46
1:D:92:GLN:O	2:E:611:ARG:NH2	2.48	0.46
2:B:610:CYS:HA	3:C:11:LYS:HE2	1.98	0.45
2:E:610:CYS:SG	2:E:612:ARG:NH1	2.90	0.45
1:G:1:MET:HE2	1:G:62:PHE:HE2	1.82	0.45
2:B:609:ILE:HA	3:C:9:THR:HB	2.00	0.44
1:D:5:ARG:NH1	1:D:61:PRO:HG3	2.32	0.44
1:D:85:LYS:HD2	1:D:90:ARG:HH22	1.82	0.44
1:D:95:PRO:HB2	2:E:572:VAL:HG13	2.00	0.44
1:D:101:LYS:HB3	3:F:8:LEU:HB3	1.99	0.44
1:D:76:PRO:HG3	1:D:123:ILE:HG22	2.00	0.44
1:G:17:PRO:HA	1:G:18:PRO:HD3	1.82	0.44
3:C:16:GLU:OE1	3:C:16:GLU:N	2.47	0.43
1:G:45:TYR:HB3	1:G:50:PHE:CZ	2.53	0.43
1:A:125:ARG:NH1	3:F:31:GLN:O	2.51	0.43
1:G:18:PRO:O	1:G:20:GLN:N	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:VAL:H	1:A:146:ALA:HB1	1.83	0.43
3:C:45:PHE:HB2	3:C:67:LEU:HD22	2.00	0.43
1:G:86:LEU:HG	1:G:88:ILE:HG12	2.00	0.43
3:F:45:PHE:HB2	3:F:67:LEU:HD22	2.00	0.43
2:B:592:TYR:CZ	2:B:608:PRO:HD2	2.54	0.43
3:I:7:THR:N	3:I:10:GLY:O	2.50	0.42
3:F:9:THR:HG23	5:F:101:IOD:I	2.89	0.42
1:G:76:PRO:HG3	1:G:123:ILE:HG22	2.01	0.42
1:G:98:THR:H	1:G:101:LYS:HD2	1.85	0.42
2:H:559:ARG:NH2	2:H:583:LEU:HD22	2.35	0.42
1:A:128:LYS:HG3	1:A:129:THR:HG23	2.02	0.41
3:F:8:LEU:HD11	3:F:70:VAL:HG22	2.03	0.41
3:C:37:PRO:HA	3:C:38:PRO:HD3	1.93	0.41
1:D:98:THR:OG1	1:D:101:LYS:HD2	2.21	0.41
1:D:100:SER:O	1:D:104:LEU:HG	2.20	0.41
3:I:71:LEU:HD13	5:I:101:IOD:I	2.89	0.41
1:A:128:LYS:HB3	1:A:128:LYS:HE2	1.90	0.41
1:D:128:LYS:HB3	1:D:128:LYS:HE2	1.84	0.41
2:B:551:GLU:H	2:B:551:GLU:HG2	1.68	0.40
1:G:85:LYS:HD2	1:G:90:ARG:NH2	2.37	0.40
2:E:559:ARG:NH2	2:E:583:LEU:HD22	2.37	0.40
1:A:39:GLY:HA3	1:A:45:TYR:O	2.20	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	146/155 (94%)	139 (95%)	7 (5%)	0	100	100
1	D	146/155 (94%)	140 (96%)	6 (4%)	0	100	100
1	G	146/155 (94%)	140 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	58/98 (59%)	49 (84%)	9 (16%)	0	100	100
2	E	63/98 (64%)	53 (84%)	10 (16%)	0	100	100
2	H	63/98 (64%)	56 (89%)	7 (11%)	0	100	100
3	C	70/76 (92%)	68 (97%)	2 (3%)	0	100	100
3	F	68/76 (90%)	67 (98%)	1 (2%)	0	100	100
3	I	70/76 (92%)	67 (96%)	3 (4%)	0	100	100
All	All	830/987 (84%)	779 (94%)	51 (6%)	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	132/139 (95%)	132 (100%)	0	100	100
1	D	132/139 (95%)	132 (100%)	0	100	100
1	G	132/139 (95%)	132 (100%)	0	100	100
2	B	58/87 (67%)	58 (100%)	0	100	100
2	E	62/87 (71%)	62 (100%)	0	100	100
2	H	62/87 (71%)	62 (100%)	0	100	100
3	C	66/68 (97%)	66 (100%)	0	100	100
3	F	64/68 (94%)	64 (100%)	0	100	100
3	I	66/68 (97%)	66 (100%)	0	100	100
All	All	774/882 (88%)	774 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	GLN
3	C	25	ASN
1	G	92	GLN
3	I	60	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 14 ligands modelled in this entry, 14 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	148/155 (95%)	-0.14	0 100 100	51, 83, 117, 128	0
1	D	148/155 (95%)	-0.19	0 100 100	55, 84, 122, 131	0
1	G	148/155 (95%)	-0.22	1 (0%) 84 69	53, 78, 123, 148	0
2	B	62/98 (63%)	0.08	0 100 100	66, 104, 132, 136	0
2	E	67/98 (68%)	0.09	0 100 100	68, 99, 121, 129	0
2	H	67/98 (68%)	0.04	1 (1%) 72 52	61, 85, 130, 144	0
3	C	72/76 (94%)	-0.22	0 100 100	80, 101, 119, 125	0
3	F	70/76 (92%)	0.06	2 (2%) 53 35	83, 125, 168, 193	0
3	I	72/76 (94%)	-0.09	0 100 100	75, 109, 137, 160	0
All	All	854/987 (86%)	-0.10	4 (0%) 87 76	51, 94, 134, 193	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	1	MET	3.8
3	F	21	ASP	2.7
2	H	557	ALA	2.3
3	F	20	SER	2.1

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

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
5	IOD	F	101	1/1	0.93	0.10	151,151,151,151	0
5	IOD	G	201	1/1	0.95	0.07	137,137,137,137	1
5	IOD	C	101	1/1	0.98	0.04	138,138,138,138	0
5	IOD	D	201	1/1	0.98	0.05	120,120,120,120	1
4	ZN	B	702	1/1	0.98	0.04	102,102,102,102	0
5	IOD	B	703	1/1	0.98	0.05	76,76,76,76	0
5	IOD	I	101	1/1	0.98	0.03	70,70,70,70	1
4	ZN	E	701	1/1	0.99	0.03	75,75,75,75	0
4	ZN	E	702	1/1	0.99	0.03	69,69,69,69	0
4	ZN	H	701	1/1	0.99	0.06	66,66,66,66	0
4	ZN	H	702	1/1	0.99	0.02	64,64,64,64	0
4	ZN	B	701	1/1	0.99	0.03	68,68,68,68	0
5	IOD	H	703	1/1	1.00	0.04	64,64,64,64	0
5	IOD	E	703	1/1	1.00	0.02	83,83,83,83	0

6.5 Other polymers

There are no such residues in this entry.