



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:12 PM UTC

PDB ID : 5CVN / pdb_00005cvn
Title : WDR48 (2-580):USP46 ubiquitin ternary complex
Authors : Harris, S.F.; Yin, J.
Deposited on : 2015-07-27
Resolution : 3.36 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

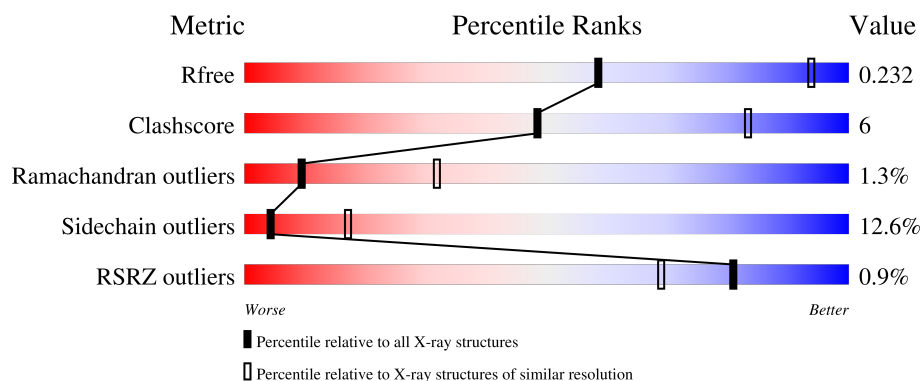
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.36 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	1099 (3.40-3.32)
Clashscore	190562	1116 (3.40-3.32)
Ramachandran outliers	187476	1101 (3.40-3.32)
Sidechain outliers	187428	1101 (3.40-3.32)
RSRZ outliers	180081	1099 (3.40-3.32)

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	598	% 64% 19% • 14%
2	B	358	% 69% 16% • • 10%
3	D	96	 56% 17% 6% 21%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7323 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 WD repeat-containing protein 48.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	514	Total	C	N	O	S	0	0	0
			4048	2559	710	757	22			

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	MET	-	expression tag	UNP Q8TAF3
A	-13	HIS	-	expression tag	UNP Q8TAF3
A	-12	HIS	-	expression tag	UNP Q8TAF3
A	-11	HIS	-	expression tag	UNP Q8TAF3
A	-10	HIS	-	expression tag	UNP Q8TAF3
A	-9	HIS	-	expression tag	UNP Q8TAF3
A	-8	HIS	-	expression tag	UNP Q8TAF3
A	-7	GLY	-	expression tag	UNP Q8TAF3
A	-6	GLU	-	expression tag	UNP Q8TAF3
A	-5	ASN	-	expression tag	UNP Q8TAF3
A	-4	LEU	-	expression tag	UNP Q8TAF3
A	-3	TYR	-	expression tag	UNP Q8TAF3
A	-2	PHE	-	expression tag	UNP Q8TAF3
A	-1	GLN	-	expression tag	UNP Q8TAF3
A	0	GLY	-	expression tag	UNP Q8TAF3
A	1	SER	-	expression tag	UNP Q8TAF3
A	581	GLY	-	expression tag	UNP Q8TAF3
A	582	ASN	-	expression tag	UNP Q8TAF3
A	583	SER	-	expression tag	UNP Q8TAF3

- Molecule 2 is a protein called Ubiquitin carboxyl-terminal hydrolase 46.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	321	Total	C	N	O	S	0	0	0
			2640	1677	449	497	17			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	9	MET	-	expression tag	UNP P62068
B	10	HIS	-	expression tag	UNP P62068
B	11	HIS	-	expression tag	UNP P62068
B	12	HIS	-	expression tag	UNP P62068
B	13	HIS	-	expression tag	UNP P62068
B	14	HIS	-	expression tag	UNP P62068
B	15	HIS	-	expression tag	UNP P62068
B	16	GLY	-	expression tag	UNP P62068
B	17	GLU	-	expression tag	UNP P62068
B	18	ASN	-	expression tag	UNP P62068
B	19	LEU	-	expression tag	UNP P62068
B	20	TYR	-	expression tag	UNP P62068
B	21	PHE	-	expression tag	UNP P62068
B	22	GLN	-	expression tag	UNP P62068
B	23	GLY	-	expression tag	UNP P62068
B	24	SER	-	expression tag	UNP P62068

- Molecule 3 is a protein called Polyubiquitin-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	76	Total	C	N	O	S	0	0	0
			600	378	105	116	1			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-19	MET	-	expression tag	UNP P0CG47
D	-18	GLY	-	expression tag	UNP P0CG47
D	-17	SER	-	expression tag	UNP P0CG47
D	-16	SER	-	expression tag	UNP P0CG47
D	-15	HIS	-	expression tag	UNP P0CG47
D	-14	HIS	-	expression tag	UNP P0CG47
D	-13	HIS	-	expression tag	UNP P0CG47
D	-12	HIS	-	expression tag	UNP P0CG47
D	-11	HIS	-	expression tag	UNP P0CG47
D	-10	HIS	-	expression tag	UNP P0CG47
D	-9	SER	-	expression tag	UNP P0CG47
D	-8	SER	-	expression tag	UNP P0CG47
D	-7	GLY	-	expression tag	UNP P0CG47
D	-6	LEU	-	expression tag	UNP P0CG47
D	-5	VAL	-	expression tag	UNP P0CG47

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-4	PRO	-	expression tag	UNP P0CG47
D	-3	ARG	-	expression tag	UNP P0CG47
D	-2	GLY	-	expression tag	UNP P0CG47
D	-1	SER	-	expression tag	UNP P0CG47
D	0	HIS	-	expression tag	UNP P0CG47

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Zn	0	0
			1	1		

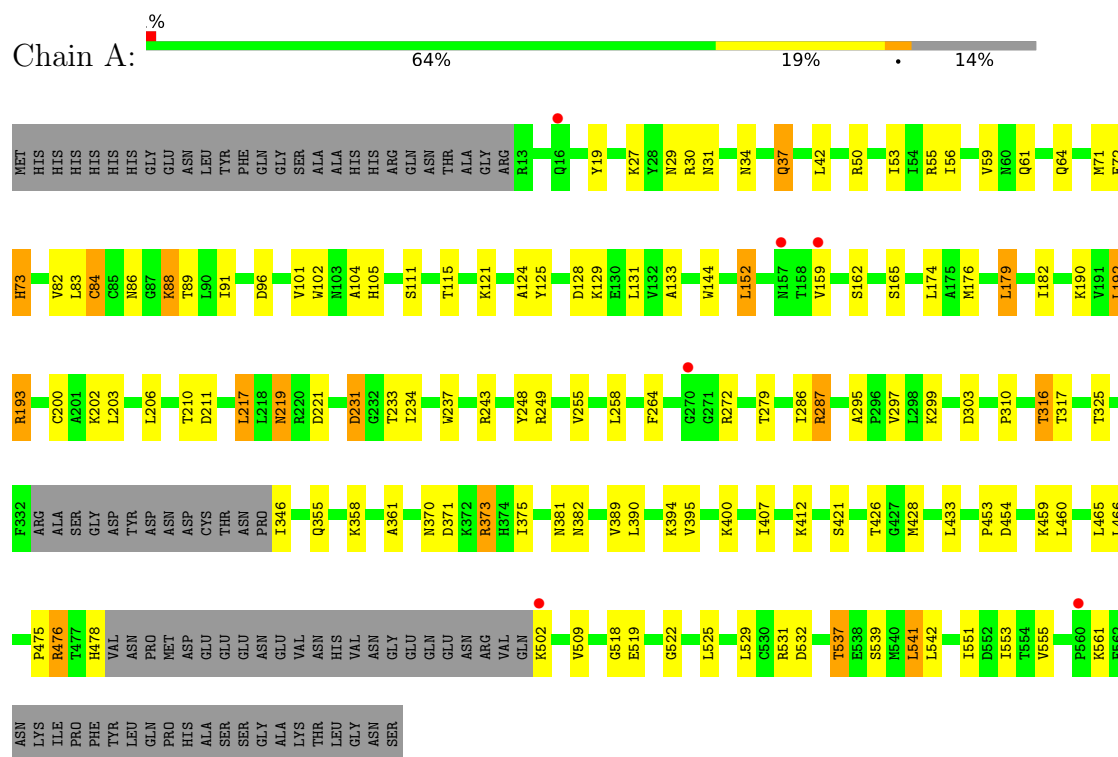
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	15	Total	O	0	0
			15	15		
5	B	13	Total	O	0	0
			13	13		
5	D	6	Total	O	0	0
			6	6		

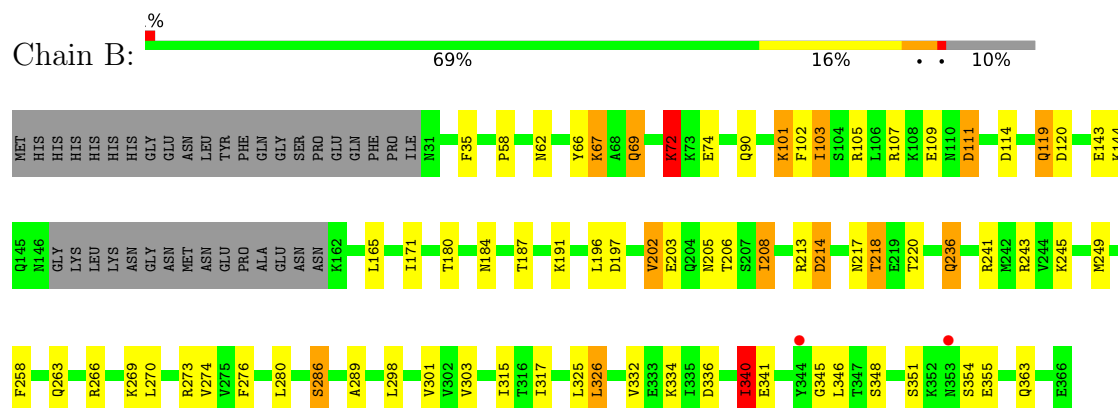
3 Residue-property plots [i](#)

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.

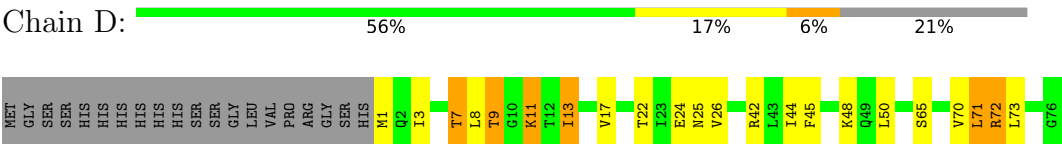
- Molecule 1: WD repeat-containing protein 48



- Molecule 2: Ubiquitin carboxyl-terminal hydrolase 46



- Molecule 3: Polyubiquitin-B



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	103.44Å 154.19Å 182.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.36 – 3.36 47.36 – 3.36	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.36-3.36) 99.5 (47.36-3.36)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.33 (at 3.40Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.175 , 0.222 0.182 , 0.232	Depositor DCC
R_{free} test set	1060 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	88.8	Xtriage
Anisotropy	0.471	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 77.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7323	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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	0.77	1/4132 (0.0%)	1.30	17/5608 (0.3%)
2	B	0.80	0/2693	1.32	13/3631 (0.4%)
3	D	0.72	0/606	1.29	1/815 (0.1%)
All	All	0.78	1/7431 (0.0%)	1.31	31/10054 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	73	HIS	CA-C	6.17	1.61	1.52

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	88	LYS	CA-C-N	8.50	137.77	121.54
1	A	88	LYS	C-N-CA	8.50	137.77	121.54
3	D	25	ASN	CA-CB-CG	8.04	120.64	112.60
1	A	316	THR	CA-C-N	7.19	130.23	120.38
1	A	316	THR	C-N-CA	7.19	130.23	120.38
2	B	286	SER	CA-C-N	7.18	130.62	120.28
2	B	286	SER	C-N-CA	7.18	130.62	120.28
2	B	214	ASP	CA-CB-CG	7.13	119.73	112.60
1	A	96	ASP	CA-CB-CG	6.60	119.20	112.60
1	A	371	ASP	N-CA-C	-6.51	99.41	109.76
2	B	289	ALA	N-CA-C	-6.16	105.89	113.41
1	A	152	LEU	CA-C-N	6.13	128.50	120.28
1	A	152	LEU	C-N-CA	6.13	128.50	120.28
2	B	72	LYS	CA-C-N	6.04	130.88	121.76
2	B	72	LYS	C-N-CA	6.04	130.88	121.76
1	A	72	GLU	N-CA-C	5.94	120.81	113.50
2	B	345	GLY	CA-C-N	5.76	132.55	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	345	GLY	C-N-CA	5.76	132.55	121.54
1	A	231	ASP	CA-CB-CG	5.57	118.17	112.60
2	B	144	LYS	CA-C-N	5.56	127.67	120.44
2	B	144	LYS	C-N-CA	5.56	127.67	120.44
1	A	190	LYS	CA-C-N	5.55	127.94	120.50
1	A	190	LYS	C-N-CA	5.55	127.94	120.50
2	B	197	ASP	CA-CB-CG	5.41	118.01	112.60
1	A	407	ILE	CA-C-N	5.40	127.96	120.29
1	A	407	ILE	C-N-CA	5.40	127.96	120.29
2	B	67	LYS	CA-C-N	5.36	127.78	120.54
2	B	67	LYS	C-N-CA	5.36	127.78	120.54
1	A	219	ASN	CA-CB-CG	5.15	117.75	112.60
1	A	519	GLU	CA-C-N	5.07	127.08	120.28
1	A	519	GLU	C-N-CA	5.07	127.08	120.28

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	4048	0	4050	48	0
2	B	2640	0	2590	25	0
3	D	600	0	629	11	0
4	B	1	0	0	0	0
5	A	15	0	0	1	0
5	B	13	0	0	1	0
5	D	6	0	0	0	0
All	All	7323	0	7269	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:A:29:ASN:HA	1:A:55:ARG:HH11	1.44	0.82
3:D:8:LEU:HD11	3:D:71:LEU:HD22	1.65	0.79
2:B:340:ILE:HG13	2:B:341:GLU:H	1.47	0.78
1:A:370:ASN:HB2	1:A:412:LYS:HB2	1.70	0.72
1:A:192:LEU:HG	1:A:206:LEU:HB2	1.74	0.69
1:A:219:ASN:HB3	5:A:603:HOH:O	1.93	0.69
2:B:184:ASN:HB2	2:B:236:GLN:HG2	1.75	0.69
1:A:88:LYS:HB3	1:A:104:ALA:HB3	1.77	0.67
2:B:120:ASP:HB2	3:D:72:ARG:HG3	1.79	0.64
2:B:107:ARG:HG2	2:B:114:ASP:HA	1.79	0.64
2:B:202:VAL:HG22	2:B:274:VAL:HG21	1.80	0.63
2:B:315:ILE:HD12	2:B:326:LEU:HD11	1.80	0.63
1:A:475:PRO:HA	1:A:478:HIS:ND1	2.16	0.61
1:A:88:LYS:HB2	1:A:105:HIS:CE1	2.35	0.61
1:A:233:THR:HG22	1:A:249:ARG:HG2	1.83	0.60
3:D:45:PHE:HB3	3:D:50:LEU:HD21	1.85	0.58
2:B:340:ILE:HG13	2:B:341:GLU:N	2.17	0.57
1:A:124:ALA:HB3	1:A:133:ALA:HB3	1.88	0.56
2:B:66:TYR:O	2:B:69:GLN:HG3	2.08	0.54
1:A:30:ARG:HH11	1:A:428:MET:HG2	1.73	0.54
1:A:518:GLY:HA2	1:A:525:LEU:HG	1.90	0.53
2:B:218:THR:HG23	2:B:241:ARG:HB2	1.89	0.53
1:A:115:THR:HG21	1:A:144:TRP:HZ2	1.73	0.53
1:A:382:ASN:HB2	1:A:400:LYS:HE3	1.90	0.53
2:B:203:GLU:O	2:B:206:THR:HG22	2.09	0.53
1:A:476:ARG:HD2	1:A:555:VAL:HG21	1.90	0.53
2:B:101:LYS:HZ3	2:B:102:PHE:H	1.57	0.53
3:D:8:LEU:CD1	3:D:71:LEU:HD22	2.36	0.52
1:A:115:THR:HG21	1:A:144:TRP:CZ2	2.45	0.52
1:A:373:ARG:HH11	1:A:390:LEU:HB3	1.74	0.52
1:A:88:LYS:HD3	1:A:105:HIS:CD2	2.45	0.52
2:B:191:LYS:HE2	3:D:65:SER:HA	1.91	0.52
1:A:84:CYS:HB3	1:A:125:TYR:CZ	2.45	0.52
1:A:71:MET:HB3	1:A:102:TRP:CZ3	2.46	0.51
1:A:234:ILE:HB	1:A:248:TYR:HB2	1.93	0.51
1:A:297:VAL:HA	1:A:316:THR:HG22	1.93	0.50
2:B:35:PHE:CZ	2:B:90:GLN:HG2	2.47	0.50
1:A:217:LEU:HD22	1:A:258:LEU:HB3	1.93	0.50
1:A:128:ASP:HB2	1:A:179:LEU:HA	1.95	0.49
1:A:59:VAL:HA	1:A:355:GLN:HE22	1.78	0.48
2:B:72:LYS:HD3	2:B:72:LYS:HA	1.79	0.48
1:A:37:GLN:HE21	1:A:37:GLN:HA	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:7:THR:HG23	3:D:9:THR:H	1.77	0.48
1:A:19:TYR:CE1	1:A:466:LEU:HD21	2.49	0.47
1:A:279:THR:HG23	1:A:287:ARG:HB2	1.96	0.47
1:A:91:ILE:HD12	1:A:101:VAL:HG22	1.96	0.47
1:A:539:SER:HA	1:A:542:LEU:HD12	1.96	0.47
3:D:42:ARG:HD2	3:D:72:ARG:HD3	1.97	0.47
1:A:303:ASP:O	1:A:310:PRO:HD2	2.14	0.46
1:A:211:ASP:HB2	1:A:231:ASP:HB3	1.95	0.46
1:A:193:ARG:HH21	1:A:202:LYS:HZ3	1.64	0.46
2:B:111:ASP:HA	2:B:114:ASP:HB3	1.96	0.46
1:A:537:THR:O	1:A:541:LEU:HD12	2.16	0.46
1:A:295:ALA:HB1	1:A:317:THR:HB	1.97	0.46
1:A:375:ILE:HD12	1:A:389:VAL:CG2	2.47	0.45
2:B:58:PRO:HB2	2:B:171:ILE:HG12	1.99	0.44
3:D:1:MET:HE3	3:D:17:VAL:HG23	1.99	0.44
3:D:22:THR:O	3:D:26:VAL:HG23	2.17	0.44
2:B:74:GLU:HB3	2:B:105:ARG:HH21	1.83	0.43
1:A:453:PRO:HA	1:A:454:ASP:HA	1.61	0.43
2:B:269:LYS:HG3	3:D:73:LEU:HD11	2.00	0.43
1:A:29:ASN:HA	1:A:55:ARG:NH1	2.23	0.43
1:A:433:LEU:HD21	1:A:466:LEU:HD23	2.00	0.42
1:A:34:ASN:ND2	1:A:50:ARG:HG2	2.35	0.42
1:A:42:LEU:HD12	1:A:88:LYS:HD2	2.02	0.42
2:B:119:GLN:HG3	5:B:1004:HOH:O	2.19	0.42
1:A:37:GLN:HG2	1:A:83:LEU:CB	2.50	0.42
1:A:124:ALA:HB2	1:A:174:LEU:HB3	2.01	0.41
2:B:102:PHE:HD1	2:B:103:ILE:HD12	1.84	0.41
2:B:208:ILE:HD13	2:B:276:PHE:HB3	2.01	0.41
3:D:11:LYS:HD3	3:D:13:ILE:HG23	2.01	0.41
1:A:165:SER:O	1:A:202:LYS:HE2	2.20	0.41
2:B:340:ILE:CG1	2:B:341:GLU:N	2.83	0.41
1:A:529:LEU:HB2	1:A:532:ASP:OD2	2.21	0.41
1:A:206:LEU:HB3	1:A:237:TRP:CZ3	2.57	0.40
2:B:171:ILE:HA	2:B:249:MET:HE3	2.03	0.40
2:B:202:VAL:CG2	2:B:274:VAL:HG21	2.49	0.40
1:A:272:ARG:HH22	2:B:187:THR:HG22	1.87	0.40
1:A:361:ALA:HB2	1:A:381:ASN:ND2	2.36	0.40
1:A:37:GLN:HG2	1:A:83:LEU:HB2	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	508/598 (85%)	472 (93%)	29 (6%)	7 (1%)	9	30
2	B	317/358 (88%)	288 (91%)	24 (8%)	5 (2%)	7	28
3	D	74/96 (77%)	71 (96%)	3 (4%)	0	100	100
All	All	899/1052 (86%)	831 (92%)	56 (6%)	12 (1%)	9	32

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	159	VAL
2	B	346	LEU
1	A	27	LYS
1	A	89	THR
2	B	354	SER
1	A	86	ASN
1	A	264	PHE
2	B	286	SER
1	A	31	ASN
2	B	340	ILE
1	A	522	GLY
2	B	348	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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	450/521 (86%)	401 (89%)	49 (11%)	6	22
2	B	297/330 (90%)	254 (86%)	43 (14%)	3	13
3	D	68/85 (80%)	57 (84%)	11 (16%)	2	10
All	All	815/936 (87%)	712 (87%)	103 (13%)	4	17

All (103) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	A	53	ILE
1	A	56	ILE
1	A	61	GLN
1	A	64	GLN
1	A	73	HIS
1	A	82	VAL
1	A	84	CYS
1	A	111	SER
1	A	121	LYS
1	A	129	LYS
1	A	131	LEU
1	A	152	LEU
1	A	162	SER
1	A	176	MET
1	A	179	LEU
1	A	182	ILE
1	A	192	LEU
1	A	193	ARG
1	A	200	CYS
1	A	203	LEU
1	A	210	THR
1	A	217	LEU
1	A	221	ASP
1	A	243	ARG
1	A	255	VAL
1	A	286	ILE
1	A	287	ARG
1	A	299	LYS
1	A	325	THR
1	A	346	ILE

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Mol	Chain	Res	Type
1	A	358	LYS
1	A	373	ARG
1	A	394	LYS
1	A	395	VAL
1	A	421	SER
1	A	426	THR
1	A	459	LYS
1	A	460	LEU
1	A	465	LEU
1	A	476	ARG
1	A	502	LYS
1	A	509	VAL
1	A	531	ARG
1	A	537	THR
1	A	541	LEU
1	A	551	ILE
1	A	553	ILE
1	A	561	LYS
2	B	62	ASN
2	B	67	LYS
2	B	69	GLN
2	B	72	LYS
2	B	101	LYS
2	B	103	ILE
2	B	109	GLU
2	B	111	ASP
2	B	119	GLN
2	B	143	GLU
2	B	165	LEU
2	B	180	THR
2	B	196	LEU
2	B	202	VAL
2	B	205	ASN
2	B	208	ILE
2	B	213	ARG
2	B	214	ASP
2	B	217	ASN
2	B	218	THR
2	B	220	THR
2	B	236	GLN
2	B	243	ARG
2	B	245	LYS

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Mol	Chain	Res	Type
2	B	258	PHE
2	B	263	GLN
2	B	266	ARG
2	B	270	LEU
2	B	273	ARG
2	B	280	LEU
2	B	298	LEU
2	B	301	VAL
2	B	303	VAL
2	B	317	ILE
2	B	325	LEU
2	B	326	LEU
2	B	332	VAL
2	B	334	LYS
2	B	336	ASP
2	B	340	ILE
2	B	351	SER
2	B	355	GLU
2	B	363	GLN
3	D	3	ILE
3	D	7	THR
3	D	9	THR
3	D	11	LYS
3	D	13	ILE
3	D	24	GLU
3	D	44	ILE
3	D	48	LYS
3	D	70	VAL
3	D	71	LEU
3	D	72	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	ASN
1	A	61	GLN
1	A	79	ASN
1	A	105	HIS
1	A	157	ASN
1	A	224	GLN
1	A	251	HIS
1	A	283	ASN

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Mol	Chain	Res	Type
1	A	381	ASN
1	A	558	ASN
2	B	119	GLN
2	B	146	ASN
2	B	184	ASN
2	B	204	GLN
2	B	205	ASN
2	B	239	GLN
2	B	313	HIS
2	B	321	HIS

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 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 [i](#)

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 [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	514/598 (85%)	-0.25	6 (1%) 76 63	65, 107, 162, 208	0
2	B	321/358 (89%)	-0.36	2 (0%) 85 75	56, 85, 160, 205	0
3	D	76/96 (79%)	-0.74	0 100 100	58, 71, 89, 96	0
All	All	911/1052 (86%)	-0.33	8 (0%) 81 69	56, 97, 161, 208	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	344	TYR	4.0
1	A	270	GLY	3.2
2	B	353	ASN	3.1
1	A	159	VAL	3.0
1	A	502	LYS	2.8
1	A	560	PRO	2.3
1	A	16	GLN	2.3
1	A	157	ASN	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
4	ZN	B	900	1/1	1.00	0.02	88,88,88,88	0

6.5 Other polymers [i](#)

There are no such residues in this entry.