



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 18, 2023 – 10:23 PM EDT

PDB ID : 5CVN
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 : 4.02b-467
Xtrriage (Phenix) : 1.13
EDS : 2.35.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

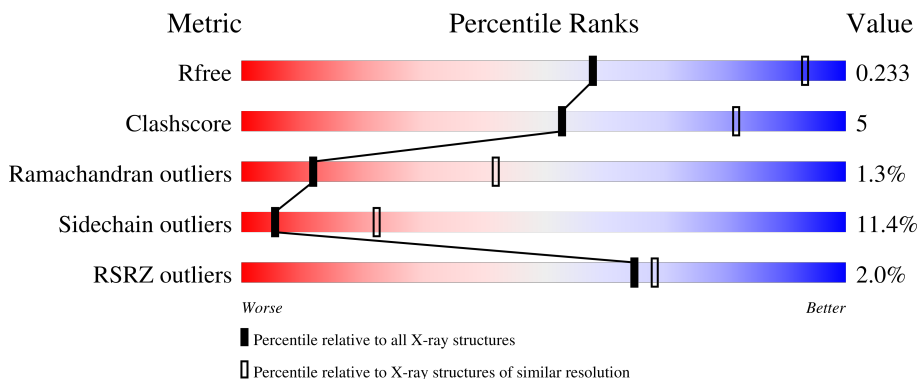
1 Overall quality at a glance

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}	130704	1558 (3.42-3.30)
Clashscore	141614	1627 (3.42-3.30)
Ramachandran outliers	138981	1599 (3.42-3.30)
Sidechain outliers	138945	1598 (3.42-3.30)
RSRZ outliers	127900	1507 (3.42-3.30)

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	 2% 66% 18% 14%
2	B	358	 % 70% 16% 10%
3	D	96	 59% 16% 21%

2 Entry composition [i](#)

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
			Total	C	N	O	S			
1	A	514	4048	2559	710	757	22	0	0	0

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
			Total	C	N	O	S			
2	B	321	2640	1677	449	497	17	0	0	0

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
			Total	C	N	O	S			
3	D	76	600	378	105	116	1	0	0	0

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 (three-letter code: ZN) (formula: Zn).

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

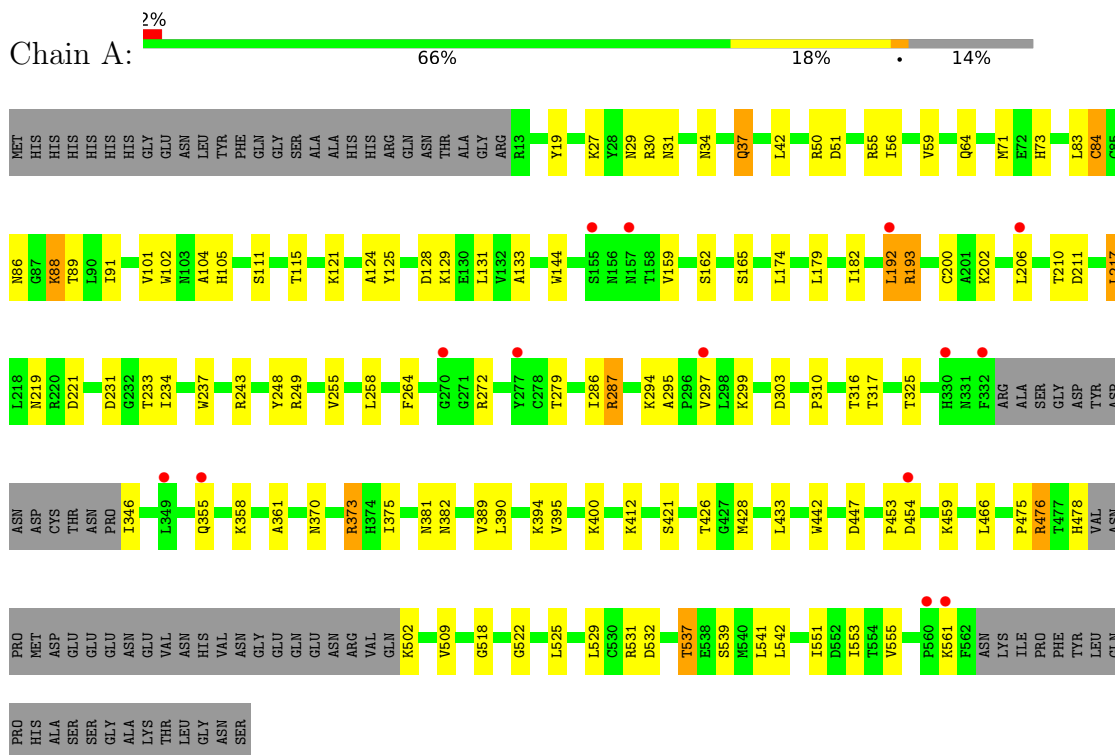
- Molecule 5 is water.

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

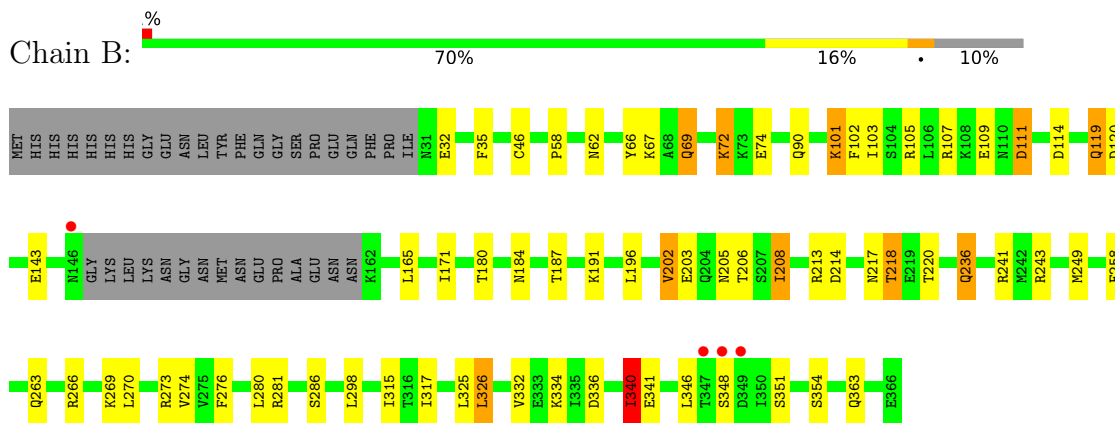
3 Residue-property plots [i](#)

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: WD repeat-containing protein 48



- Molecule 2: Ubiquitin carboxyl-terminal hydrolase 46



- Molecule 3: Polyubiquitin-B

Chain D:  59% 16% • 21%



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) 99.6 (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)	Xtrriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.175 , 0.222 0.182 , 0.233	Depositor DCC
R_{free} test set	1060 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	88.8	Xtrriage
Anisotropy	0.471	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 65.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7323	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtrriage'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 [i](#)

5.1 Standard geometry [i](#)

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	0.43	0/4132	0.71	1/5608 (0.0%)
2	B	0.47	0/2693	0.72	0/3631
3	D	0.42	0/606	0.72	0/815
All	All	0.45	0/7431	0.71	1/10054 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	88	LYS	C-N-CA	6.43	137.77	121.70

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	10	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7323	0	7269	79	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 5.

All (79) 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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:101:LYS:HZ3	2:B:102:PHE:H	1.61	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
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
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: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:193:ARG:HH21	1:A:202:LYS:HZ3	1.68	0.42
2:B:171:ILE:HA	2:B:249:MET:HE3	2.01	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:LEU:HB3	1:A:237:TRP:CZ3	2.57	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 [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	508/598 (85%)	472 (93%)	29 (6%)	7 (1%)	11	40
2	B	317/358 (88%)	288 (91%)	24 (8%)	5 (2%)	9	38
3	D	74/96 (77%)	71 (96%)	3 (4%)	0	100	100
All	All	899/1052 (86%)	831 (92%)	56 (6%)	12 (1%)	12	42

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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	450/521 (86%)	407 (90%)	43 (10%)	8	30
2	B	297/330 (90%)	256 (86%)	41 (14%)	3	15
3	D	68/85 (80%)	59 (87%)	9 (13%)	4	17
All	All	815/936 (87%)	722 (89%)	93 (11%)	5	22

All (93) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	A	51	ASP
1	A	56	ILE
1	A	64	GLN
1	A	73	HIS
1	A	84	CYS
1	A	111	SER
1	A	121	LYS
1	A	129	LYS
1	A	131	LEU
1	A	162	SER
1	A	182	ILE
1	A	192	LEU
1	A	193	ARG
1	A	200	CYS
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	294	LYS
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	442	TRP
1	A	447	ASP
1	A	459	LYS
1	A	476	ARG
1	A	502	LYS
1	A	509	VAL
1	A	531	ARG
1	A	537	THR
1	A	551	ILE
1	A	553	ILE
1	A	561	LYS
2	B	32	GLU
2	B	46	CYS
2	B	62	ASN
2	B	67	LYS
2	B	69	GLN
2	B	72	LYS
2	B	101	LYS
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	258	PHE

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Mol	Chain	Res	Type
2	B	263	GLN
2	B	266	ARG
2	B	270	LEU
2	B	273	ARG
2	B	280	LEU
2	B	281	ARG
2	B	298	LEU
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	363	GLN
3	D	7	THR
3	D	9	THR
3	D	11	LYS
3	D	13	ILE
3	D	24	GLU
3	D	39	ASP
3	D	44	ILE
3	D	48	LYS
3	D	70	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	105	HIS
1	A	251	HIS
1	A	381	ASN
2	B	119	GLN
2	B	146	ASN
2	B	239	GLN
3	D	68	HIS

5.3.3 RNA

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 monosaccharides 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 [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	514/598 (85%)	-0.05	14 (2%) 54 57	65, 107, 162, 208	0
2	B	321/358 (89%)	-0.16	4 (1%) 79 82	56, 85, 160, 205	0
3	D	76/96 (79%)	-0.33	0 100 100	58, 71, 89, 96	0
All	All	911/1052 (86%)	-0.11	18 (1%) 65 68	56, 97, 161, 208	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	155	SER	3.6
1	A	332	PHE	3.5
2	B	348	SER	3.4
1	A	157	ASN	3.2
1	A	560	PRO	3.1
1	A	270	GLY	3.0
2	B	146	ASN	2.9
2	B	349	ASP	2.6
1	A	277	TYR	2.6
2	B	347	THR	2.5
1	A	561	LYS	2.3
1	A	454	ASP	2.2
1	A	206	LEU	2.2
1	A	355	GLN	2.2
1	A	349	LEU	2.2
1	A	297	VAL	2.1
1	A	192	LEU	2.0
1	A	330	HIS	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 monosaccharides 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(\AA^2)	Q<0.9
4	ZN	B	900	1/1	1.00	0.15	88,88,88,88	0

6.5 Other polymers [i](#)

There are no such residues in this entry.