



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 12:08 AM UTC

PDB ID : 5WQ4 / pdb_00005wq4
Title : Crystal structure of OPTN and linear diubiquitin complex
Authors : Li, F.; Pan, L.
Deposited on : 2016-11-23
Resolution : 3.00 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

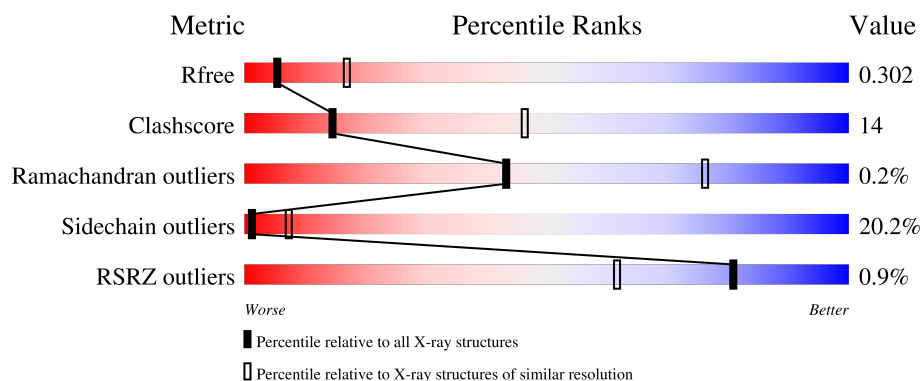
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	152	0% 60% 26% 7% 7%
1	B	152	2% 66% 26% 7%
2	C	97	51% 20% 26%
2	D	97	52% 18% 5% 26%
2	E	97	46% 22% 29%

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Mol	Chain	Length	Quality of chain
2	F	97	51% 23% 5% 22%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4030 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	151	Total	C	N	O	S	0	0	0
			1047	658	187	201	1			
1	A	141	Total	C	N	O	S	0	0	0
			982	613	176	192	1			

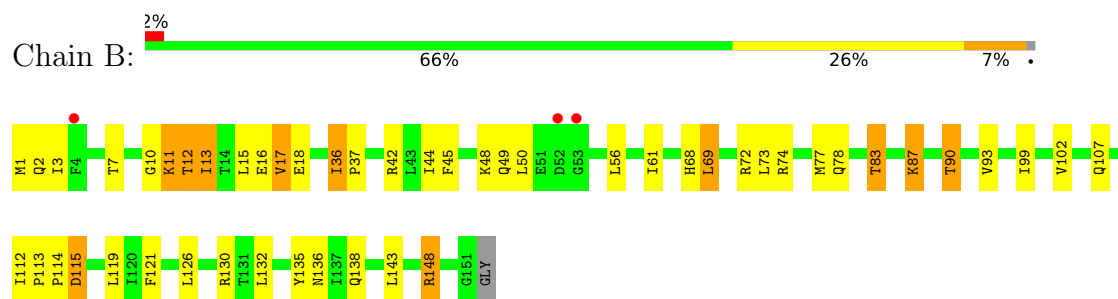
- Molecule 2 is a protein called Optineurin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	72	Total	C	N	O	S	0	0	0
			495	304	88	99	4			
2	D	72	Total	C	N	O	S	0	0	0
			497	307	86	101	3			
2	E	69	Total	C	N	O	S	0	0	0
			480	294	89	94	3			
2	F	76	Total	C	N	O	S	0	0	0
			529	326	93	107	3			

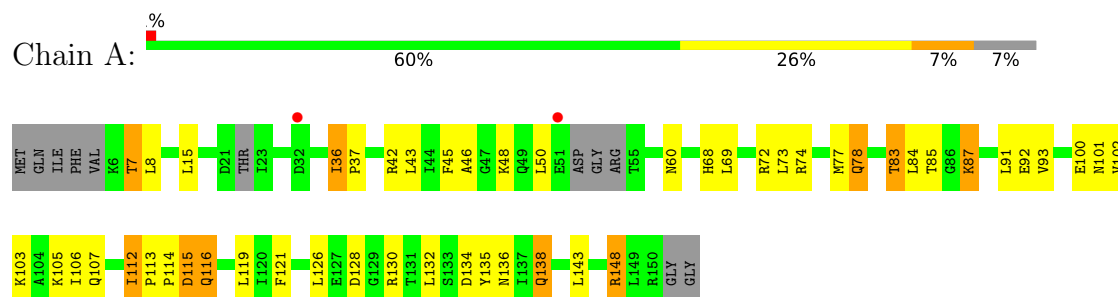
3 Residue-property plots [i](#)

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.

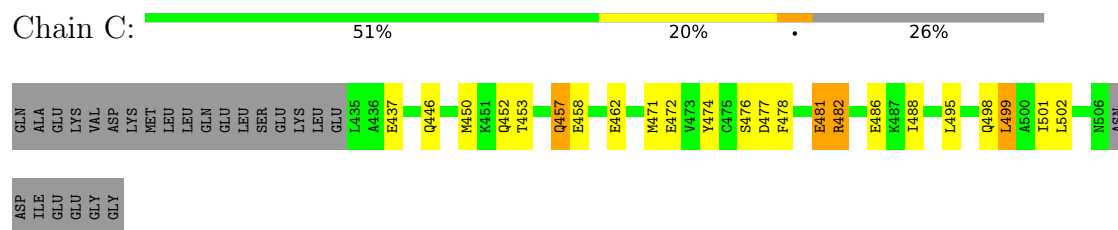
- Molecule 1: ubiquitin



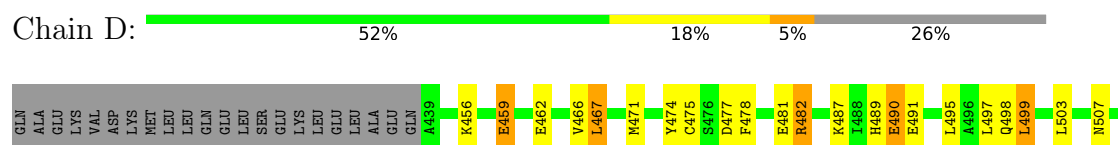
- Molecule 1: ubiquitin



- Molecule 2: Optineurin



- Molecule 2: Optineurin



E510

GLU
GLY
GLY

● Molecule 2: Optineurin



GLN
ALA
GLU
LYS
VAL
ASP
LYS
MET
LEU
LEU
GLN
GLU
LEU
SER
GLU
LYS
LEU
GLU
LEU
ALA
GLU
Q438
E449
T453
L454
D460
L461
E462
T463
R468
M471
Y474
C475
S476
D477
F478
E481
R482
R485
I488
H489
E493
Q494
L495
Q498
L499
A500
I501
L502

L503

K504
E505
N506

ASP
ILE
GLU
GLY
GLY

● Molecule 2: Optineurin



GLN
ALA
GLU
LYS
VAL
ASP
LYS
MET
LEU
LEU
GLN
GLU
LEU
SER
GLU
LYS
LEU
E434
E437
K456
E459
E462
T463
V466
L467
M471
E472
V473
Y474
C475
S476
D477
E481
R482
K487
I488
H489
E490
E491
K492
E493
Q494
L495
A496
L497
Q498
L499
L502
N506
N507

D508

I509

GLU
GLY
GLY

4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	77.66Å 77.66Å 166.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.05 – 3.00 32.05 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (32.05-3.00) 99.9 (32.05-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.90 (at 3.00Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.245 , 0.303 0.246 , 0.302	Depositor DCC
R_{free} test set	1009 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	73.7	Xtriage
Anisotropy	0.136	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 92.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.479 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4030	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.47% 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

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	0.65	0/992	1.02	4/1348 (0.3%)
1	B	0.67	0/1059	1.11	4/1442 (0.3%)
2	C	0.85	1/498 (0.2%)	1.07	0/672
2	D	0.69	0/500	1.03	0/679
2	E	0.89	1/483 (0.2%)	1.02	0/654
2	F	0.72	0/532	1.10	2/721 (0.3%)
All	All	0.73	2/4064 (0.0%)	1.06	10/5516 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	462	GLU	C-O	5.61	1.30	1.24
2	E	461	LEU	C-O	5.23	1.30	1.24

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	148	ARG	N-CA-C	-6.92	100.19	110.23
1	B	36	ILE	CA-C-N	6.12	126.69	120.38
1	B	36	ILE	C-N-CA	6.12	126.69	120.38
1	A	36	ILE	CA-C-N	5.87	126.43	120.38
1	A	36	ILE	C-N-CA	5.87	126.43	120.38
1	A	15	LEU	N-CA-C	5.80	117.92	108.76
2	F	473	VAL	N-CA-C	5.59	115.78	110.53
2	F	506	ASN	N-CA-C	-5.49	106.58	113.72
1	B	15	LEU	N-CA-C	5.23	117.03	108.76
1	A	60	ASN	N-CA-C	5.14	116.98	108.49

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	982	0	867	29	0
1	B	1047	0	949	28	0
2	C	495	0	405	19	0
2	D	497	0	412	17	0
2	E	480	0	406	22	0
2	F	529	0	449	25	0
All	All	4030	0	3488	105	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 14.

All (105) 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:C:482:ARG:HH11	2:C:482:ARG:HG3	1.30	0.95
2:E:482:ARG:NH1	2:F:481:GLU:OE2	2.15	0.79
1:A:115:ASP:O	1:A:148:ARG:NH1	2.18	0.77
2:E:478:PHE:CE1	2:F:481:GLU:HG3	2.20	0.76
1:B:115:ASP:O	1:B:148:ARG:NH1	2.21	0.73
1:A:121:PHE:HB2	1:A:143:LEU:HD22	1.70	0.72
1:A:74:ARG:HH11	2:F:481:GLU:HG2	1.55	0.71
2:E:499:LEU:HD23	2:F:499:LEU:HD23	1.75	0.68
2:C:482:ARG:HG3	2:C:482:ARG:NH1	2.04	0.67
1:B:74:ARG:HH11	2:D:481:GLU:HG2	1.57	0.67
1:A:83:THR:HG21	1:A:87:LYS:HD3	1.75	0.66
2:E:485:ARG:NH1	2:F:481:GLU:OE2	2.29	0.66
2:C:478:PHE:CE1	2:D:481:GLU:HG3	2.32	0.64
2:C:472:GLU:O	1:A:116:GLN:NE2	2.31	0.63
2:E:478:PHE:HE1	2:F:481:GLU:HG3	1.63	0.63
1:B:136:ASN:OD1	1:B:138:GLN:NE2	2.32	0.63
1:A:136:ASN:OD1	1:A:138:GLN:NE2	2.33	0.61
1:A:78:GLN:NE2	1:A:92:GLU:OE1	2.34	0.60
1:B:45:PHE:HZ	1:B:61:ILE:HA	1.67	0.59
2:E:482:ARG:HH11	2:F:481:GLU:CD	2.10	0.59
1:B:45:PHE:N	1:B:48:LYS:O	2.25	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:VAL:HG21	1:A:132:LEU:HD21	1.85	0.59
1:A:130:ARG:HB2	1:A:135:TYR:HE1	1.68	0.58
1:B:121:PHE:HB2	1:B:143:LEU:HD22	1.84	0.58
1:B:7:THR:H	1:B:10:GLY:HA2	1.68	0.57
1:B:42:ARG:O	1:B:69:LEU:HA	2.03	0.57
1:A:77:MET:HB3	1:A:93:VAL:O	2.05	0.56
2:E:481:GLU:HG2	2:F:482:ARG:HA	1.86	0.56
1:B:90:THR:HG23	2:C:486:GLU:OE1	2.06	0.56
1:A:42:ARG:O	1:A:69:LEU:HA	2.05	0.56
1:B:45:PHE:HD2	1:B:50:LEU:HD21	1.71	0.55
2:F:456:LYS:O	2:F:459:GLU:HG2	2.06	0.55
2:E:488:ILE:HG21	2:F:489:HIS:HA	1.90	0.54
2:C:457:GLN:HG2	2:C:458:GLU:N	2.22	0.53
2:D:487:LYS:O	2:D:490:GLU:HG3	2.10	0.52
1:A:43:LEU:HA	1:A:68:HIS:O	2.09	0.52
1:B:148:ARG:NH1	1:B:148:ARG:HB3	2.25	0.51
2:E:498:GLN:HA	2:E:501:ILE:HG12	1.91	0.51
1:A:103:LYS:HB3	1:A:114:PRO:HB3	1.92	0.51
1:B:11:LYS:HA	1:B:11:LYS:HE2	1.93	0.50
1:A:72:ARG:HE	2:F:473:VAL:HG13	1.76	0.50
1:A:101:ASN:O	1:A:105:LYS:HG3	2.12	0.50
1:A:83:THR:HG22	1:A:85:THR:H	1.77	0.49
1:B:77:MET:HB3	1:B:93:VAL:O	2.12	0.49
1:B:102:VAL:HG21	1:B:132:LEU:HD21	1.94	0.49
1:A:83:THR:HB	1:A:87:LYS:O	2.12	0.49
2:C:446:GLN:O	2:C:450:MET:HG2	2.12	0.48
2:C:478:PHE:CD1	2:D:481:GLU:HG3	2.48	0.48
2:F:502:LEU:O	2:F:506:ASN:ND2	2.45	0.48
2:C:474:TYR:CD2	2:D:475:CYS:HB2	2.49	0.48
2:C:482:ARG:NH1	2:D:481:GLU:OE2	2.46	0.48
2:D:456:LYS:O	2:D:459:GLU:HG2	2.13	0.48
1:B:45:PHE:CZ	1:B:61:ILE:HA	2.46	0.48
1:B:73:LEU:HG	2:D:474:TYR:CD1	2.49	0.47
1:B:83:THR:HB	1:B:87:LYS:O	2.14	0.47
2:C:471:MET:HG2	2:D:467:LEU:HD11	1.96	0.47
2:D:487:LYS:O	2:D:491:GLU:HG3	2.14	0.47
1:B:130:ARG:HB2	1:B:135:TYR:HE1	1.80	0.47
1:A:72:ARG:HG3	2:F:477:ASP:OD2	2.14	0.47
2:C:501:ILE:HG13	2:C:502:LEU:N	2.30	0.47
1:A:73:LEU:HG	2:F:474:TYR:CD1	2.51	0.46
2:E:501:ILE:HG13	2:E:502:LEU:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:488:ILE:HD13	2:F:489:HIS:HB2	1.97	0.46
2:E:499:LEU:HD21	2:F:498:GLN:HG2	1.97	0.46
1:B:119:LEU:O	1:B:126:LEU:HG	2.17	0.45
2:E:460:ASP:O	2:E:463:THR:HB	2.15	0.45
1:B:2:GLN:HA	1:B:16:GLU:HA	1.97	0.45
1:B:56:LEU:O	1:B:61:ILE:N	2.32	0.45
2:C:499:LEU:HD11	2:D:498:GLN:NE2	2.32	0.45
1:B:44:ILE:HD12	1:B:68:HIS:HB2	1.99	0.45
2:C:481:GLU:HG2	2:D:482:ARG:HA	1.99	0.44
2:C:498:GLN:HA	2:C:501:ILE:HG12	1.99	0.44
2:E:504:LYS:HA	2:E:504:LYS:HD2	1.76	0.44
1:A:45:PHE:N	1:A:48:LYS:O	2.48	0.44
2:F:463:THR:O	2:F:466:VAL:HG13	2.18	0.44
1:A:100:GLU:HG3	1:A:128:ASP:O	2.18	0.43
1:A:92:GLU:OE2	2:E:482:ARG:NH2	2.52	0.43
2:E:474:TYR:CD2	2:F:475:CYS:HB2	2.53	0.43
2:E:489:HIS:CE1	2:E:493:GLU:HG3	2.54	0.43
2:C:488:ILE:HG21	2:D:489:HIS:HA	2.00	0.43
2:C:477:ASP:HB3	2:D:478:PHE:CE1	2.54	0.42
1:B:12:THR:O	1:B:13:ILE:HD13	2.20	0.42
1:A:7:THR:HG22	1:A:8:LEU:H	1.84	0.42
2:E:468:ARG:O	2:E:471:MET:HG3	2.19	0.42
1:A:119:LEU:O	1:A:126:LEU:HG	2.20	0.42
1:B:73:LEU:HD13	2:C:478:PHE:CG	2.55	0.42
2:C:488:ILE:HD13	2:D:489:HIS:HB2	2.01	0.42
2:D:499:LEU:HD22	2:D:499:LEU:HA	1.86	0.42
1:A:91:LEU:HD21	1:A:106:ILE:HG13	2.00	0.42
2:F:487:LYS:O	2:F:491:GLU:HG3	2.19	0.42
1:A:36:ILE:HA	1:A:37:PRO:HD3	1.89	0.41
1:A:134:ASP:C	1:A:136:ASN:H	2.28	0.41
2:E:478:PHE:CD1	2:F:481:GLU:HG3	2.54	0.41
1:B:113:PRO:HA	1:B:114:PRO:HD3	1.91	0.41
1:B:1:MET:N	1:B:17:VAL:O	2.43	0.41
1:B:72:ARG:HG3	2:D:477:ASP:OD2	2.21	0.41
2:E:481:GLU:HG2	2:F:482:ARG:CA	2.50	0.41
2:F:437:GLU:H	2:F:437:GLU:CD	2.29	0.41
2:F:490:GLU:O	2:F:491:GLU:C	2.64	0.41
1:B:36:ILE:HA	1:B:37:PRO:HD3	1.84	0.40
1:A:112:ILE:HA	1:A:113:PRO:HD3	1.82	0.40
1:A:93:VAL:HG12	1:A:105:LYS:HE3	2.03	0.40
2:E:449:GLU:O	2:E:453:THR:HG23	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:489:HIS:O	2:F:493:GLU:HG2	2.21	0.40
2:E:474:TYR:CE2	2:F:475:CYS:HB2	2.55	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	135/152 (89%)	126 (93%)	8 (6%)	1 (1%)	18	53
1	B	149/152 (98%)	138 (93%)	11 (7%)	0	100	100
2	C	70/97 (72%)	70 (100%)	0	0	100	100
2	D	70/97 (72%)	69 (99%)	1 (1%)	0	100	100
2	E	67/97 (69%)	67 (100%)	0	0	100	100
2	F	74/97 (76%)	74 (100%)	0	0	100	100
All	All	565/692 (82%)	544 (96%)	20 (4%)	1 (0%)	43	76

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	46	ALA

5.3.2 Protein sidechains [i](#)

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	85/136 (62%)	73 (86%)	12 (14%)	3	16
1	B	92/136 (68%)	76 (83%)	16 (17%)	2	10
2	C	35/83 (42%)	26 (74%)	9 (26%)	0	3
2	D	37/83 (45%)	25 (68%)	12 (32%)	0	1
2	E	36/83 (43%)	29 (81%)	7 (19%)	1	8
2	F	41/83 (49%)	31 (76%)	10 (24%)	1	4
All	All	326/604 (54%)	260 (80%)	66 (20%)	1	7

All (66) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	3	ILE
1	B	11	LYS
1	B	12	THR
1	B	13	ILE
1	B	17	VAL
1	B	18	GLU
1	B	49	GLN
1	B	69	LEU
1	B	78	GLN
1	B	83	THR
1	B	87	LYS
1	B	90	THR
1	B	99	ILE
1	B	107	GLN
1	B	112	ILE
1	B	115	ASP
2	C	437	GLU
2	C	452	GLN
2	C	453	THR
2	C	457	GLN
2	C	476	SER
2	C	481	GLU
2	C	482	ARG
2	C	495	LEU
2	C	499	LEU
2	D	459	GLU
2	D	462	GLU
2	D	466	VAL
2	D	467	LEU
2	D	471	MET

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Mol	Chain	Res	Type
2	D	482	ARG
2	D	490	GLU
2	D	495	LEU
2	D	497	LEU
2	D	499	LEU
2	D	503	LEU
2	D	507	ASN
1	A	7	THR
1	A	50	LEU
1	A	78	GLN
1	A	83	THR
1	A	84	LEU
1	A	87	LYS
1	A	107	GLN
1	A	112	ILE
1	A	115	ASP
1	A	116	GLN
1	A	138	GLN
1	A	148	ARG
2	E	454	LEU
2	E	476	SER
2	E	481	GLU
2	E	495	LEU
2	E	499	LEU
2	E	504	LYS
2	E	505	GLU
2	F	459	GLU
2	F	462	GLU
2	F	466	VAL
2	F	467	LEU
2	F	471	MET
2	F	476	SER
2	F	495	LEU
2	F	497	LEU
2	F	499	LEU
2	F	507	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	40	GLN
1	B	138	GLN

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Mol	Chain	Res	Type
1	A	144	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](#)

There are no ligands in this entry.

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	141/152 (92%)	-0.87	2 (1%) 73 51	25, 68, 149, 163	0
1	B	151/152 (99%)	-0.79	3 (1%) 65 41	23, 72, 159, 176	0
2	C	72/97 (74%)	-0.96	0 100 100	29, 67, 127, 134	0
2	D	72/97 (74%)	-0.91	0 100 100	37, 71, 145, 153	0
2	E	69/97 (71%)	-0.94	0 100 100	26, 64, 123, 139	0
2	F	76/97 (78%)	-0.97	0 100 100	36, 75, 129, 145	0
All	All	581/692 (83%)	-0.89	5 (0%) 81 61	23, 70, 145, 176	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	51	GLU	2.8
1	B	52	ASP	2.2
1	B	4	PHE	2.2
1	B	53	GLY	2.1
1	A	32	ASP	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 [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.