



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:44 AM UTC

PDB ID : 3RL7 / pdb_00003rl7
Title : Crystal structure of hDLG1-PDZ1 complexed with APC
Authors : Zhang, Z.; Li, H.; Wu, G.
Deposited on : 2011-04-19
Resolution : 2.30 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

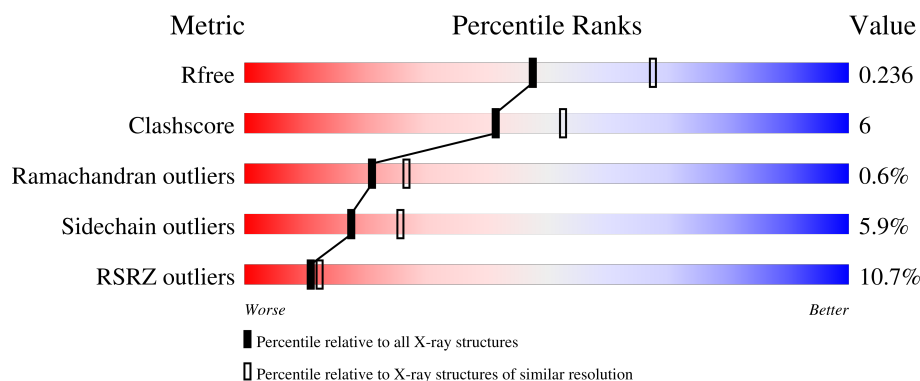
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	107	3% 67% 16% 16%
1	B	107	4% 68% 15% 17%
1	C	107	13% 72% 9% 19%
1	D	107	7% 71% 12% 14%
1	E	107	10% 71% 6% 23%

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Mol	Chain	Length	Quality of chain
1	F	107	4% 68% 11% 5% 15%
2	G	11	36% 45% 18% 36%
2	H	11	36% 9% 55%
2	I	11	36% 9% 27% 9% 55%
2	J	11	9% 36% 18% 45%
2	K	11	27% 36% 9% 55%
2	L	11	36% 18% 9% 9% 64%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4352 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 Disks large homolog 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	89	Total	C	N	O	S	0	0	0
			682	421	126	134	1			
1	A	90	Total	C	N	O	S	0	0	0
			686	424	124	137	1			
1	C	87	Total	C	N	O	S	0	0	0
			660	406	122	131	1			
1	D	92	Total	C	N	O	S	0	0	0
			705	435	129	139	2			
1	E	82	Total	C	N	O	S	0	0	0
			629	391	116	121	1			
1	F	91	Total	C	N	O	S	0	0	0
			694	429	125	138	2			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	211	MET	-	expression tag	UNP Q12959
B	212	GLY	-	expression tag	UNP Q12959
B	213	HIS	-	expression tag	UNP Q12959
B	214	HIS	-	expression tag	UNP Q12959
B	215	HIS	-	expression tag	UNP Q12959
B	216	HIS	-	expression tag	UNP Q12959
B	217	HIS	-	expression tag	UNP Q12959
B	218	HIS	-	expression tag	UNP Q12959
B	219	MET	-	expression tag	UNP Q12959
A	211	MET	-	expression tag	UNP Q12959
A	212	GLY	-	expression tag	UNP Q12959
A	213	HIS	-	expression tag	UNP Q12959
A	214	HIS	-	expression tag	UNP Q12959
A	215	HIS	-	expression tag	UNP Q12959
A	216	HIS	-	expression tag	UNP Q12959
A	217	HIS	-	expression tag	UNP Q12959
A	218	HIS	-	expression tag	UNP Q12959

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Chain	Residue	Modelled	Actual	Comment	Reference
A	219	MET	-	expression tag	UNP Q12959
C	211	MET	-	expression tag	UNP Q12959
C	212	GLY	-	expression tag	UNP Q12959
C	213	HIS	-	expression tag	UNP Q12959
C	214	HIS	-	expression tag	UNP Q12959
C	215	HIS	-	expression tag	UNP Q12959
C	216	HIS	-	expression tag	UNP Q12959
C	217	HIS	-	expression tag	UNP Q12959
C	218	HIS	-	expression tag	UNP Q12959
C	219	MET	-	expression tag	UNP Q12959
D	211	MET	-	expression tag	UNP Q12959
D	212	GLY	-	expression tag	UNP Q12959
D	213	HIS	-	expression tag	UNP Q12959
D	214	HIS	-	expression tag	UNP Q12959
D	215	HIS	-	expression tag	UNP Q12959
D	216	HIS	-	expression tag	UNP Q12959
D	217	HIS	-	expression tag	UNP Q12959
D	218	HIS	-	expression tag	UNP Q12959
D	219	MET	-	expression tag	UNP Q12959
E	211	MET	-	expression tag	UNP Q12959
E	212	GLY	-	expression tag	UNP Q12959
E	213	HIS	-	expression tag	UNP Q12959
E	214	HIS	-	expression tag	UNP Q12959
E	215	HIS	-	expression tag	UNP Q12959
E	216	HIS	-	expression tag	UNP Q12959
E	217	HIS	-	expression tag	UNP Q12959
E	218	HIS	-	expression tag	UNP Q12959
E	219	MET	-	expression tag	UNP Q12959
F	211	MET	-	expression tag	UNP Q12959
F	212	GLY	-	expression tag	UNP Q12959
F	213	HIS	-	expression tag	UNP Q12959
F	214	HIS	-	expression tag	UNP Q12959
F	215	HIS	-	expression tag	UNP Q12959
F	216	HIS	-	expression tag	UNP Q12959
F	217	HIS	-	expression tag	UNP Q12959
F	218	HIS	-	expression tag	UNP Q12959
F	219	MET	-	expression tag	UNP Q12959

- Molecule 2 is a protein called 11-mer peptide from Adenomatous polyposis coli protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	G	7	Total	C	N	O	0	0	0
			54	35	7	12			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	H	5	Total	C	N	O	0	0	0
			33	21	5	7			
2	I	5	Total	C	N	O	0	0	0
			40	27	5	8			
2	J	6	Total	C	N	O	0	0	0
			48	32	6	10			
2	K	5	Total	C	N	O	0	0	0
			36	23	5	8			
2	L	4	Total	C	N	O	0	0	0
			28	18	4	6			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	54	Total	O	0	0
			54	54		
3	A	1	Total	O	0	0
			1	1		
3	C	1	Total	O	0	0
			1	1		
3	G	1	Total	O	0	0
			1	1		

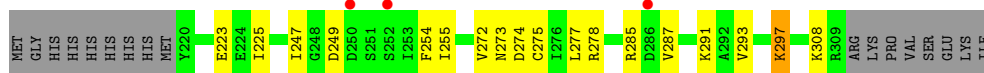
3 Residue-property plots [i](#)

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.

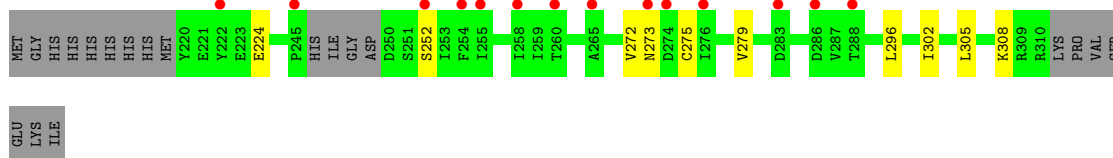
- Molecule 1: Disks large homolog 1



- Molecule 1: Disks large homolog 1



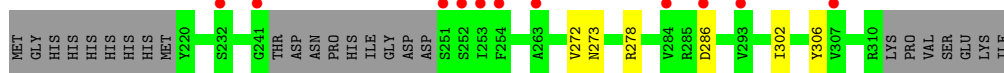
- Molecule 1: Disks large homolog 1



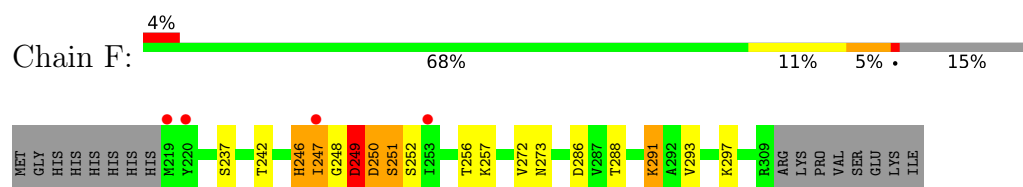
- Molecule 1: Disks large homolog 1



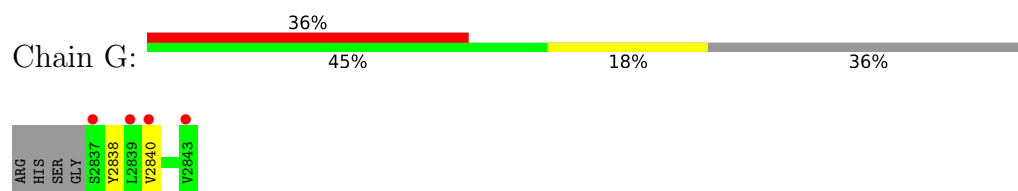
- Molecule 1: Disks large homolog 1



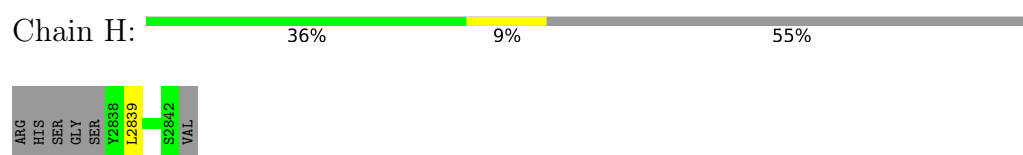
- Molecule 1: Disks large homolog 1



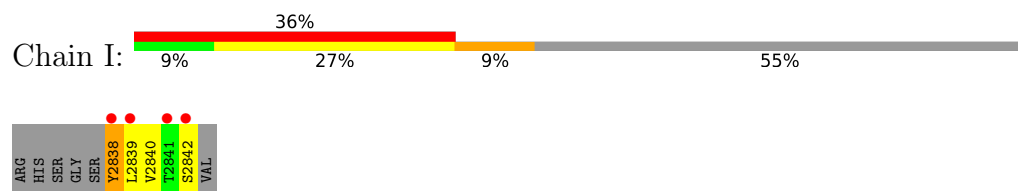
- Molecule 2: 11-mer peptide from Adenomatous polyposis coli protein



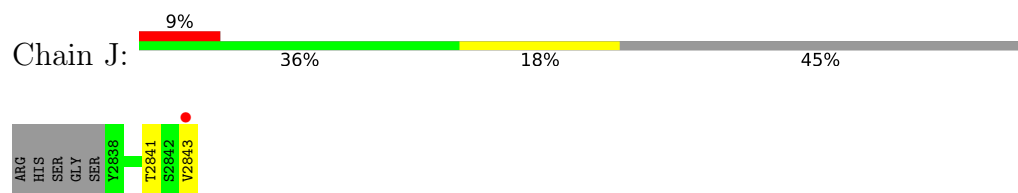
- Molecule 2: 11-mer peptide from Adenomatous polyposis coli protein



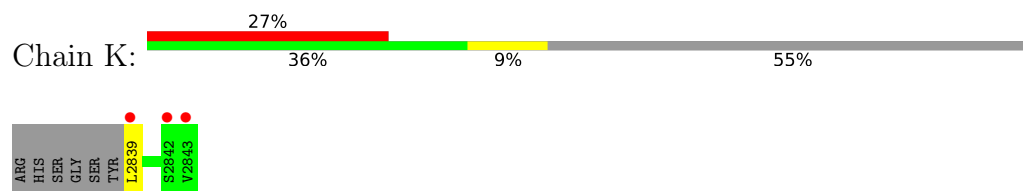
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ARG					
HIS					
SER					
GLY					
SER					
TYR					
L2839					
V2840					
T2841					
S2842					
VAL					

4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, α , β , γ	105.63Å 105.63Å 50.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.30 50.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-2.30) 99.9 (50.00-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.98 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.193 , 0.231 0.204 , 0.236	Depositor DCC
R_{free} test set	1392 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	29.5	Xtriage
Anisotropy	0.295	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 22.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	0.166 for -h,-k,l 0.226 for h,-h-k,-l 0.135 for -k,-h,-l	Xtriage
Reported twinning fraction	0.262 for H, K, L 0.239 for h+k,-k,-l 0.261 for -h,-k,l 0.238 for K, H, -L	Depositor
Outliers	0 of 28157 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4352	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 29.43 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.5529e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.46	0/693	0.80	0/934
1	B	0.45	0/688	0.76	0/925
1	C	0.51	0/664	0.77	0/892
1	D	0.46	0/712	0.82	0/958
1	E	0.42	0/633	0.74	0/848
1	F	0.48	0/701	0.93	3/944 (0.3%)
2	G	0.45	0/54	0.66	0/72
2	H	0.55	0/32	0.91	0/43
2	I	0.38	0/40	0.47	0/54
2	J	0.42	0/48	0.72	0/64
2	K	0.58	0/35	0.66	0/46
2	L	0.45	0/27	0.44	0/36
All	All	0.47	0/4327	0.80	3/5816 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	246	HIS	N-CA-C	9.54	121.67	110.41
1	F	246	HIS	CB-CA-C	-6.00	101.39	111.24
1	F	251	SER	N-CA-C	-5.93	106.29	112.93

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	686	0	682	12	0
1	B	682	0	678	7	0
1	C	660	0	662	8	0
1	D	705	0	704	7	0
1	E	629	0	641	2	0
1	F	694	0	691	19	0
2	G	54	0	54	2	0
2	H	33	0	33	1	0
2	I	40	0	40	4	0
2	J	48	0	49	3	0
2	K	36	0	40	0	0
2	L	28	0	31	1	0
3	A	1	0	0	0	0
3	B	54	0	0	0	0
3	C	1	0	0	0	0
3	G	1	0	0	0	0
All	All	4352	0	4305	55	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 (55) 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:F:249:ASP:HB2	1:F:250:ASP:HA	1.58	0.83
1:B:243:ASP:OD2	1:B:288:THR:HG23	1.81	0.79
1:D:245:PRO:HD2	2:I:2838:TYR:HB2	1.63	0.78
1:F:247:ILE:HG22	1:F:248:GLY:H	1.50	0.76
1:F:248:GLY:O	1:F:249:ASP:HB3	1.83	0.75
1:F:247:ILE:HG22	1:F:248:GLY:N	2.02	0.75
1:F:249:ASP:CB	1:F:250:ASP:HA	2.20	0.68
1:C:272:VAL:O	1:C:273:ASN:HB2	1.94	0.67
1:F:246:HIS:O	1:F:246:HIS:ND1	2.29	0.66
1:F:247:ILE:CG2	1:F:248:GLY:H	2.05	0.62
2:H:2839:LEU:HD21	2:I:2840:VAL:HG21	1.83	0.60
1:E:272:VAL:O	1:E:273:ASN:HB2	2.04	0.56
1:A:255:ILE:HG12	1:A:274:ASP:HB2	1.86	0.56
1:F:248:GLY:O	1:F:249:ASP:CB	2.53	0.54
1:B:286:ASP:OD1	1:A:285:ARG:NH1	2.40	0.54
1:C:296:LEU:HD21	1:C:305:LEU:HD21	1.90	0.54
1:A:275:CYS:HB2	1:A:308:LYS:HG2	1.89	0.53
1:B:288:THR:HG22	1:B:290:SER:H	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:277:LEU:HD21	1:D:308:LYS:HD3	1.91	0.52
1:A:254:PHE:HA	1:A:274:ASP:O	2.10	0.52
1:F:272:VAL:O	1:F:273:ASN:HB2	2.11	0.51
1:F:288:THR:OG1	1:F:291:LYS:HG2	2.12	0.50
1:F:293:VAL:O	1:F:297:LYS:HG2	2.12	0.50
1:A:272:VAL:O	1:A:273:ASN:HB2	2.11	0.50
1:A:287:VAL:HB	1:A:291:LYS:HB2	1.92	0.50
1:F:256:THR:HB	2:G:2838:TYR:HB2	1.96	0.48
1:F:246:HIS:O	1:F:247:ILE:HB	2.14	0.48
1:D:246:HIS:C	1:D:248:GLY:N	2.68	0.47
1:D:272:VAL:O	1:D:273:ASN:HB2	2.15	0.47
1:F:246:HIS:O	1:F:246:HIS:CG	2.63	0.47
1:D:278:ARG:HB2	1:D:306:TYR:HB2	1.97	0.46
1:C:252:SER:HB2	1:C:275:CYS:SG	2.55	0.46
1:A:293:VAL:CG1	1:A:297:LYS:HE2	2.46	0.46
1:D:237:SER:HA	2:I:2842:SER:HA	1.97	0.45
1:B:275:CYS:O	1:B:307:VAL:HA	2.16	0.45
1:F:246:HIS:O	1:F:247:ILE:CB	2.63	0.45
1:A:277:LEU:HD21	1:A:308:LYS:HD3	1.99	0.44
1:B:277:LEU:HD21	1:B:308:LYS:HE3	2.00	0.44
1:A:247:ILE:CD1	1:F:252:SER:OG	2.65	0.44
1:A:255:ILE:CG1	1:A:274:ASP:HB2	2.48	0.43
1:B:285:ARG:HB3	1:A:285:ARG:NH1	2.33	0.43
2:I:2838:TYR:HB3	2:I:2839:LEU:H	1.64	0.43
1:C:296:LEU:HD13	2:J:2843:VAL:HG11	2.00	0.43
1:F:246:HIS:C	1:F:247:ILE:HG12	2.43	0.43
1:F:237:SER:HB2	1:F:257:LYS:HB3	2.01	0.42
1:C:296:LEU:HB3	2:J:2843:VAL:HG11	2.00	0.42
1:E:278:ARG:HB3	1:E:306:TYR:HB2	2.01	0.42
1:F:242:THR:HA	1:F:251:SER:HB2	2.01	0.42
1:B:272:VAL:O	1:B:273:ASN:HB2	2.20	0.42
1:D:244:ASN:O	1:D:247:ILE:HG12	2.20	0.42
1:C:279:VAL:HG21	1:C:296:LEU:HG	2.03	0.41
1:A:223:GLU:OE1	1:A:225:ILE:HD11	2.21	0.41
1:C:275:CYS:HB3	1:C:308:LYS:HG2	2.02	0.41
1:C:296:LEU:HB3	2:J:2843:VAL:CG1	2.50	0.41
2:G:2840:VAL:HG21	2:L:2839:LEU:HD23	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	88/107 (82%)	84 (96%)	4 (4%)	0	100	100
1	B	85/107 (79%)	81 (95%)	4 (5%)	0	100	100
1	C	83/107 (78%)	78 (94%)	5 (6%)	0	100	100
1	D	90/107 (84%)	84 (93%)	5 (6%)	1 (1%)	11	13
1	E	78/107 (73%)	72 (92%)	6 (8%)	0	100	100
1	F	89/107 (83%)	79 (89%)	8 (9%)	2 (2%)	5	4
2	G	5/11 (46%)	5 (100%)	0	0	100	100
2	H	3/11 (27%)	3 (100%)	0	0	100	100
2	I	3/11 (27%)	3 (100%)	0	0	100	100
2	J	4/11 (36%)	4 (100%)	0	0	100	100
2	K	3/11 (27%)	3 (100%)	0	0	100	100
2	L	2/11 (18%)	2 (100%)	0	0	100	100
All	All	533/708 (75%)	498 (93%)	32 (6%)	3 (1%)	21	27

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	249	ASP
1	F	247	ILE
1	D	248	GLY

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	73/89 (82%)	70 (96%)	3 (4%)	27	41
1	B	72/89 (81%)	67 (93%)	5 (7%)	14	20
1	C	70/89 (79%)	68 (97%)	2 (3%)	37	55
1	D	75/89 (84%)	69 (92%)	6 (8%)	11	15
1	E	66/89 (74%)	64 (97%)	2 (3%)	36	53
1	F	74/89 (83%)	70 (95%)	4 (5%)	20	29
2	G	7/10 (70%)	7 (100%)	0	100	100
2	H	4/10 (40%)	4 (100%)	0	100	100
2	I	5/10 (50%)	4 (80%)	1 (20%)	1	1
2	J	6/10 (60%)	5 (83%)	1 (17%)	2	2
2	K	5/10 (50%)	4 (80%)	1 (20%)	1	1
2	L	4/10 (40%)	2 (50%)	2 (50%)	0	0
All	All	461/594 (78%)	434 (94%)	27 (6%)	18	26

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	221	GLU
1	B	246	HIS
1	B	260	THR
1	B	297	LYS
1	B	302	ILE
1	A	249	ASP
1	A	278	ARG
1	A	297	LYS
1	C	224	GLU
1	C	302	ILE
1	D	224	GLU
1	D	246	HIS
1	D	247	ILE
1	D	275	CYS
1	D	297	LYS
1	D	302	ILE
1	E	286	ASP
1	E	302	ILE
1	F	249	ASP
1	F	250	ASP
1	F	286	ASP
1	F	291	LYS

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Mol	Chain	Res	Type
2	I	2838	TYR
2	J	2841	THR
2	K	2839	LEU
2	L	2839	LEU
2	L	2841	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	231	ASN
1	A	266	GLN
1	D	244	ASN
1	E	266	GLN
1	F	244	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](#)

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

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	90/107 (84%)	0.70	3 (3%) 49 51	27, 32, 42, 45	0
1	B	89/107 (83%)	0.70	4 (4%) 38 40	27, 32, 42, 47	0
1	C	87/107 (81%)	1.15	14 (16%) 4 5	31, 38, 47, 53	0
1	D	92/107 (85%)	0.93	8 (8%) 16 17	27, 34, 43, 47	0
1	E	82/107 (76%)	1.14	11 (13%) 7 8	38, 44, 49, 50	0
1	F	91/107 (85%)	0.80	4 (4%) 39 41	34, 38, 44, 48	0
2	G	7/11 (63%)	2.44	4 (57%) 0 0	57, 58, 59, 59	0
2	H	5/11 (45%)	1.18	0 100 100	37, 38, 43, 50	0
2	I	5/11 (45%)	2.40	4 (80%) 0 0	53, 54, 55, 57	0
2	J	6/11 (54%)	1.67	1 (16%) 4 5	45, 47, 50, 53	0
2	K	5/11 (45%)	2.75	3 (60%) 0 0	65, 65, 73, 75	0
2	L	4/11 (36%)	4.60	4 (100%) 0 0	76, 82, 84, 93	0
All	All	563/708 (79%)	0.99	60 (10%) 11 12	27, 37, 49, 93	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	252	SER	5.9
2	L	2842	SER	5.9
1	C	252	SER	5.7
1	D	220	TYR	5.4
2	L	2839	LEU	4.9
2	L	2840	VAL	4.4
2	G	2843	VAL	4.4
1	E	241	GLY	4.3
2	K	2839	LEU	3.9
1	D	219	MET	3.6
2	J	2843	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	263	ALA	3.5
1	C	260	THR	3.4
2	L	2841	THR	3.2
2	K	2843	VAL	3.2
1	F	219	MET	3.2
2	K	2842	SER	3.1
1	F	247	ILE	3.0
2	I	2839	LEU	2.8
1	C	265	ALA	2.8
2	G	2837	SER	2.7
1	A	250	ASP	2.7
1	C	255	ILE	2.7
1	D	299	ALA	2.7
2	I	2838	TYR	2.6
1	A	252	SER	2.6
1	D	309	ARG	2.6
1	E	307	VAL	2.6
1	B	260	THR	2.6
1	E	253	ILE	2.6
2	G	2840	VAL	2.5
1	F	220	TYR	2.5
1	B	219	MET	2.5
1	C	258	ILE	2.4
2	G	2839	LEU	2.4
2	I	2841	THR	2.4
1	C	276	ILE	2.4
1	B	220	TYR	2.4
1	C	222	TYR	2.3
1	A	286	ASP	2.3
1	D	268	GLY	2.3
1	C	288	THR	2.2
1	E	263	ALA	2.2
1	E	293	VAL	2.2
1	C	254	PHE	2.2
1	C	273	ASN	2.2
1	D	282	VAL	2.2
2	I	2842	SER	2.2
1	E	284	VAL	2.1
1	E	286	ASP	2.1
1	F	253	ILE	2.1
1	C	286	ASP	2.1
1	D	252	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	232	SER	2.1
1	E	251	SER	2.1
1	E	254	PHE	2.1
1	B	258	ILE	2.0
1	C	245	PRO	2.0
1	C	274	ASP	2.0
1	C	283	ASP	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.