



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 12:00 am BST

PDB ID : 1OW8
Title : Paxillin LD2 motif bound to the Focal Adhesion Targeting (FAT) domain of the Focal Adhesion Kinase
Authors : Hoellerer, M.K.; Noble, M.E.M.; Labesse, G.; Werner, J.M.; Arold, S.T.
Deposited on : 2003-03-28
Resolution : 2.85 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

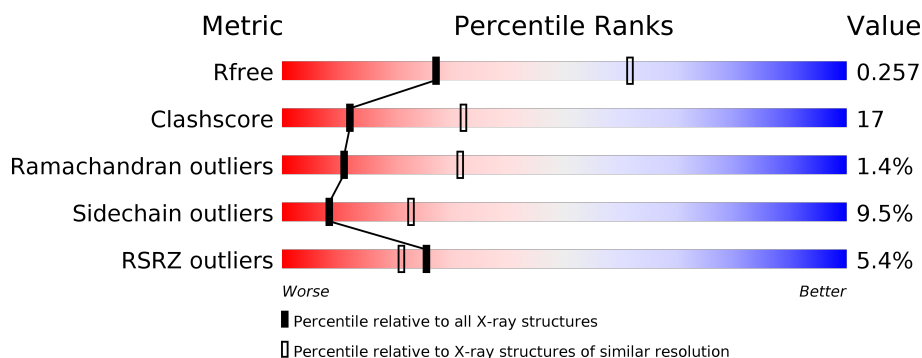
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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 on 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	161	<div> <div>54%</div> <div>25%</div> <div>• •</div> <div>17%</div> </div>
1	B	161	<div> <div>58%</div> <div>27%</div> <div>• •</div> <div>12%</div> </div>
1	C	161	<div> <div>4%</div> <div>55%</div> <div>29%</div> <div>• •</div> <div>12%</div> </div>
2	D	13	<div> <div>31%</div> <div>38%</div> <div>54%</div> <div>8%</div> </div>
2	F	13	<div> <div>92%</div> <div>62%</div> <div>31%</div> <div>8%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3472 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 Focal adhesion kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	134	Total	C	N	O	S	0	0	0
			1042	658	176	201	7			
1	B	141	Total	C	N	O	S	0	0	0
			1091	690	183	211	7			
1	C	142	Total	C	N	O	S	0	0	0
			1098	695	184	212	7			

- Molecule 2 is a protein called Paxillin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	12	Total	C	N	O	0	0	0
			100	63	16	21			
2	F	12	Total	C	N	O	0	0	0
			100	63	16	21			

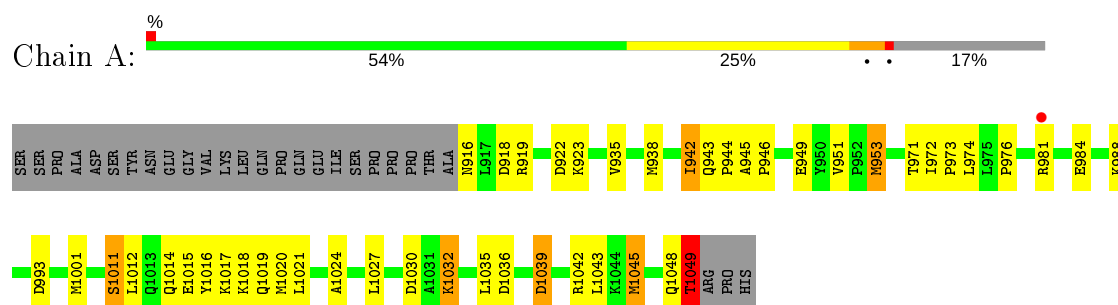
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	11	Total	O	0	0
			11	11		
3	B	18	Total	O	0	0
			18	18		
3	C	11	Total	O	0	0
			11	11		
3	D	1	Total	O	0	0
			1	1		

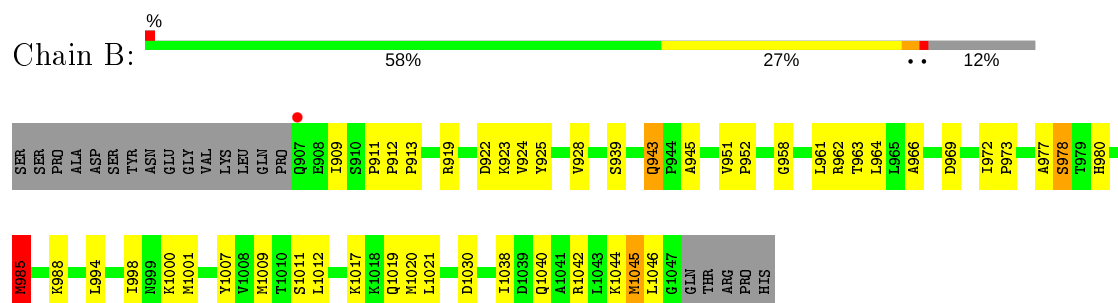
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

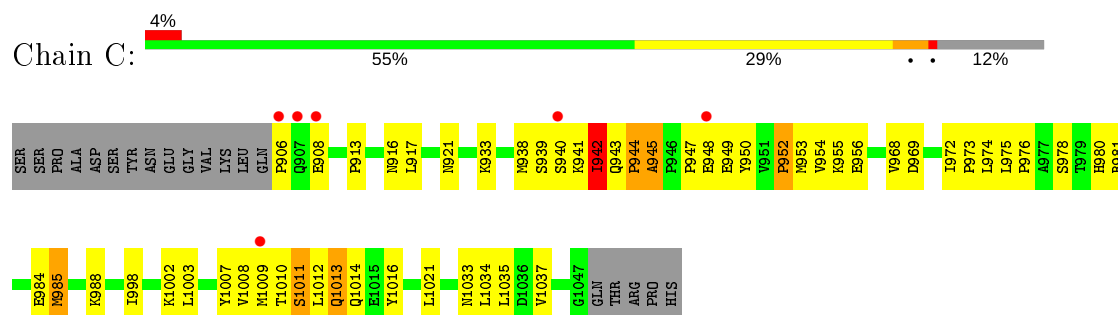
• Molecule 1: Focal adhesion kinase 1



• Molecule 1: Focal adhesion kinase 1



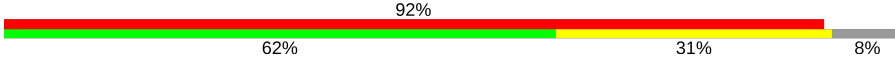
• Molecule 1: Focal adhesion kinase 1



• Molecule 2: Paxillin



● Molecule 2: Paxillin

Chain F:  92%
62% 31% 8%



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	87.98 Å 220.78 Å 97.37 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.50 – 2.85 25.42 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.3 (34.50-2.85) 99.5 (25.42-2.85)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 2.84 Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.235 , 0.275 0.224 , 0.257	Depositor DCC
R_{free} test set	1149 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	70.5	Xtriage
Anisotropy	0.445	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 55.9	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	0.94	EDS
Total number of atoms	3472	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.71% 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	0.51	0/1053	1.13	6/1424 (0.4%)
1	B	0.51	0/1105	1.09	3/1498 (0.2%)
1	C	0.51	0/1113	0.85	3/1509 (0.2%)
2	D	0.65	0/99	1.01	0/131
2	F	0.68	0/99	0.73	0/131
All	All	0.52	0/3469	1.02	12/4693 (0.3%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	922	ASP	CB-CG-OD2	8.82	126.24	118.30
1	A	1049	THR	CA-C-O	7.00	134.80	120.10
1	A	1039	ASP	CB-CG-OD2	6.99	124.59	118.30
1	A	922	ASP	CB-CG-OD2	6.89	124.50	118.30
1	A	1042	ARG	NE-CZ-NH2	-6.76	116.92	120.30
1	A	1030	ASP	CB-CG-OD2	6.50	124.15	118.30
1	A	1036	ASP	CB-CG-OD2	5.88	123.59	118.30
1	B	1030	ASP	CB-CG-OD2	5.49	123.24	118.30
1	C	945	ALA	N-CA-C	5.39	125.56	111.00
1	C	942	ILE	N-CA-C	5.38	125.52	111.00
1	C	917	LEU	CA-CB-CG	5.20	127.27	115.30
1	B	985	MET	CG-SD-CE	5.00	108.21	100.20

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	1042	0	1093	35	0
1	B	1091	0	1141	33	0
1	C	1098	0	1149	49	0
2	D	100	0	105	10	0
2	F	100	0	105	7	0
3	A	11	0	0	0	0
3	B	18	0	0	2	0
3	C	11	0	0	1	0
3	D	1	0	0	0	0
All	All	3472	0	3593	121	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 17.

All (121) 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:D:5:LEU:HA	2:D:8:LEU:HD12	1.54	0.89
1:C:985:MET:CE	1:C:985:MET:HA	2.09	0.82
1:C:955:LYS:HA	2:F:12:LEU:HD13	1.62	0.81
2:F:5:LEU:HA	2:F:8:LEU:HD12	1.62	0.80
1:A:1014:GLN:HE21	1:A:1018:LYS:NZ	1.82	0.78
1:A:918:ASP:HB3	1:B:1045:MET:CE	2.16	0.76
1:C:985:MET:HA	1:C:985:MET:HE2	1.71	0.73
1:B:978:SER:HB3	3:B:35:HOH:O	1.90	0.71
1:C:942:ILE:O	1:C:943:GLN:C	2.29	0.70
1:B:985:MET:HG3	1:C:1012:LEU:HG	1.75	0.68
1:C:969:ASP:HA	1:C:972:ILE:HD12	1.78	0.66
1:C:945:ALA:HB1	1:C:949:GLU:HB2	1.77	0.66
2:F:2:LEU:HD11	2:F:5:LEU:HD23	1.78	0.66
1:C:943:GLN:HB2	1:C:944:PRO:CD	2.27	0.64
2:D:2:LEU:HD11	2:D:5:LEU:HD23	1.81	0.63
1:C:955:LYS:CA	2:F:12:LEU:HD13	2.28	0.63
1:C:943:GLN:CB	1:C:944:PRO:CD	2.77	0.63
1:A:918:ASP:HB3	1:B:1045:MET:HE2	1.82	0.61
1:C:976:PRO:O	1:C:980:HIS:CD2	2.54	0.61
1:A:945:ALA:O	1:A:1017:LYS:NZ	2.33	0.61
1:B:966:ALA:O	1:B:969:ASP:HB2	1.99	0.61
1:A:974:LEU:HD13	1:B:973:PRO:HB2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:943:GLN:HB2	1:C:944:PRO:HD2	1.83	0.61
1:C:947:PRO:HG3	1:C:950:TYR:OH	2.01	0.60
1:A:1011:SER:C	1:A:1012:LEU:HD23	2.23	0.59
1:B:1011:SER:OG	1:C:985:MET:HG2	2.02	0.59
1:C:972:ILE:N	1:C:973:PRO:CD	2.65	0.59
1:A:1032:LYS:HG3	2:D:9:LEU:HD11	1.83	0.59
1:B:1012:LEU:HG	1:C:985:MET:HG3	1.85	0.58
1:A:943:GLN:HB3	1:A:944:PRO:HD3	1.86	0.57
1:C:972:ILE:HA	1:C:975:LEU:HD12	1.86	0.56
1:A:1012:LEU:N	1:A:1012:LEU:HD23	2.21	0.56
1:A:1048:GLN:HG2	1:A:1049:THR:H	1.68	0.56
1:A:972:ILE:HB	1:A:973:PRO:HD3	1.88	0.56
1:C:921:ASN:HB2	3:C:53:HOH:O	2.06	0.56
2:D:2:LEU:HD12	2:D:5:LEU:HB3	1.88	0.55
1:B:951:VAL:HB	1:B:952:PRO:HD3	1.89	0.55
2:F:2:LEU:HD12	2:F:5:LEU:HB3	1.89	0.54
1:A:1014:GLN:HE21	1:A:1018:LYS:HZ2	1.53	0.54
1:A:1014:GLN:HE21	1:A:1018:LYS:CE	2.21	0.54
1:A:1032:LYS:HD3	1:A:1032:LYS:O	2.08	0.53
1:A:935:VAL:HG13	1:A:1024:ALA:HB1	1.90	0.53
1:B:958:GLY:C	1:B:962:ARG:NH1	2.62	0.53
2:F:2:LEU:CD1	2:F:5:LEU:HD23	2.38	0.53
1:A:946:PRO:HG2	1:A:949:GLU:HG3	1.90	0.53
1:B:1000:LYS:HD2	1:B:1019:GLN:CB	2.39	0.53
1:B:1000:LYS:HD2	1:B:1019:GLN:HB3	1.90	0.53
1:A:938:MET:HG3	1:A:953:MET:HB3	1.91	0.53
2:D:2:LEU:CD1	2:D:5:LEU:HD23	2.40	0.52
1:A:1014:GLN:NE2	1:A:1018:LYS:NZ	2.55	0.52
1:A:919:ARG:NH2	1:A:1039:ASP:OD2	2.37	0.52
1:C:942:ILE:HG23	1:C:943:GLN:N	2.24	0.51
1:C:968:VAL:HG21	1:C:1034:LEU:HD21	1.91	0.51
1:B:1045:MET:HE3	1:B:1045:MET:HA	1.92	0.51
1:A:951:VAL:HG22	1:A:1001:MET:SD	2.51	0.51
1:A:1032:LYS:HG3	2:D:9:LEU:CD1	2.41	0.51
1:C:950:TYR:HA	1:C:953:MET:HB2	1.93	0.51
1:A:1032:LYS:CG	2:D:9:LEU:HD11	2.41	0.50
1:B:1045:MET:CE	1:B:1045:MET:HA	2.41	0.50
1:C:1010:THR:HG22	1:C:1011:SER:H	1.75	0.50
1:A:942:ILE:HG21	1:A:1021:LEU:HD21	1.94	0.50
1:C:938:MET:HG2	1:C:939:SER:N	2.25	0.50
1:C:968:VAL:HG12	1:C:972:ILE:HD11	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:993:ASP:HB2	1:A:1027:LEU:HD13	1.95	0.49
1:C:972:ILE:N	1:C:973:PRO:HD3	2.28	0.48
1:C:985:MET:HA	1:C:985:MET:HE3	1.95	0.48
1:C:938:MET:HE1	1:C:954:VAL:HG22	1.93	0.48
1:B:985:MET:HE3	1:B:988:LYS:HD2	1.96	0.48
1:A:1015:GLU:HG3	1:A:1019:GLN:HE21	1.79	0.48
1:C:943:GLN:CB	1:C:944:PRO:HD3	2.43	0.48
1:A:976:PRO:HD3	1:A:1045:MET:HG2	1.96	0.48
1:B:919:ARG:HD2	1:B:925:TYR:CD2	2.49	0.47
1:A:1048:GLN:HG2	1:A:1049:THR:N	2.29	0.47
1:C:972:ILE:HG22	1:C:980:HIS:CE1	2.49	0.47
1:C:952:PRO:C	1:C:954:VAL:N	2.66	0.47
2:D:6:ASP:HA	2:D:9:LEU:HD12	1.95	0.47
1:C:942:ILE:HG21	1:C:1021:LEU:HD21	1.97	0.47
1:B:943:GLN:O	1:B:1017:LYS:NZ	2.46	0.47
1:A:976:PRO:HD3	1:A:1045:MET:CG	2.44	0.47
1:B:939:SER:CB	1:B:1021:LEU:HD22	2.44	0.47
1:B:945:ALA:O	1:B:1017:LYS:NZ	2.37	0.47
1:C:955:LYS:HA	2:F:12:LEU:CD1	2.38	0.47
1:B:1038:ILE:O	1:B:1038:ILE:HG22	2.13	0.47
1:B:911:PRO:O	1:B:912:PRO:C	2.52	0.47
1:C:939:SER:HA	1:C:1021:LEU:HD22	1.97	0.47
1:B:924:VAL:O	1:B:928:VAL:HG23	2.16	0.46
1:C:1003:LEU:HD13	1:C:1016:TYR:CE1	2.51	0.46
1:B:1042:ARG:O	1:B:1046:LEU:HG	2.16	0.46
2:D:8:LEU:O	2:D:11:GLU:N	2.49	0.46
1:C:968:VAL:O	1:C:972:ILE:CD1	2.65	0.45
1:C:998:ILE:CG2	1:C:1002:LYS:HE2	2.46	0.45
1:C:1010:THR:HG22	1:C:1011:SER:N	2.31	0.45
1:A:1014:GLN:C	1:A:1016:TYR:N	2.70	0.45
1:A:1020:MET:O	1:A:1021:LEU:C	2.56	0.44
1:B:985:MET:CE	1:B:988:LYS:HD2	2.48	0.44
1:C:1033:ASN:O	1:C:1037:VAL:HG23	2.18	0.44
1:B:972:ILE:HB	1:B:973:PRO:HD3	1.99	0.44
1:C:1007:TYR:O	1:C:1013:GLN:HB2	2.18	0.44
1:C:942:ILE:CG2	1:C:943:GLN:N	2.80	0.44
1:A:1045:MET:HA	1:A:1045:MET:CE	2.48	0.43
1:B:963:THR:O	1:B:964:LEU:C	2.55	0.43
1:C:952:PRO:O	1:C:954:VAL:N	2.51	0.43
1:A:971:THR:O	1:A:971:THR:HG22	2.17	0.43
1:C:976:PRO:O	1:C:980:HIS:HD2	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:968:VAL:O	1:C:972:ILE:HD12	2.18	0.43
1:B:994:LEU:O	1:B:998:ILE:HG13	2.17	0.43
2:D:8:LEU:O	2:D:9:LEU:C	2.57	0.43
1:B:977:ALA:HA	1:B:980:HIS:CD2	2.55	0.42
1:B:1001:MET:HA	1:B:1020:MET:SD	2.59	0.42
1:A:972:ILE:N	1:A:973:PRO:CD	2.82	0.42
1:C:998:ILE:HG22	1:C:1002:LYS:HE2	2.02	0.42
1:C:948:GLU:C	1:C:949:GLU:HG3	2.40	0.42
1:C:969:ASP:O	1:C:973:PRO:HD3	2.20	0.42
1:A:1043:LEU:HA	1:A:1043:LEU:HD23	1.80	0.42
1:C:998:ILE:HG22	1:C:1002:LYS:CE	2.50	0.42
1:C:952:PRO:O	1:C:955:LYS:N	2.53	0.41
1:B:909:ILE:HD12	3:B:19:HOH:O	2.21	0.41
1:B:1007:TYR:OH	1:C:988:LYS:HG2	2.21	0.41
1:A:1014:GLN:HE21	1:A:1018:LYS:HE3	1.85	0.41
1:B:961:LEU:O	1:B:961:LEU:HD12	2.21	0.41
1:B:912:PRO:O	1:B:913:PRO:C	2.60	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	132/161 (82%)	127 (96%)	4 (3%)	1 (1%)	19	46
1	B	139/161 (86%)	133 (96%)	6 (4%)	0	100	100
1	C	140/161 (87%)	120 (86%)	15 (11%)	5 (4%)	3	11
2	D	10/13 (77%)	8 (80%)	2 (20%)	0	100	100
2	F	10/13 (77%)	10 (100%)	0	0	100	100
All	All	431/509 (85%)	398 (92%)	27 (6%)	6 (1%)	11	31

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	916	ASN
1	C	942	ILE
1	C	908	GLU
1	A	1011	SER
1	C	944	PRO
1	C	952	PRO

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	117/141 (83%)	106 (91%)	11 (9%)	8	23
1	B	123/141 (87%)	115 (94%)	8 (6%)	17	41
1	C	124/141 (88%)	107 (86%)	17 (14%)	3	9
2	D	12/13 (92%)	11 (92%)	1 (8%)	11	29
2	F	12/13 (92%)	12 (100%)	0	100	100
All	All	388/449 (86%)	351 (90%)	37 (10%)	8	23

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	916	ASN
1	A	923	LYS
1	A	942	ILE
1	A	953	MET
1	A	981	ARG
1	A	984	GLU
1	A	988	LYS
1	A	1032	LYS
1	A	1035	LEU
1	A	1045	MET
1	A	1049	THR
1	B	923	LYS

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Mol	Chain	Res	Type
1	B	943	GLN
1	B	978	SER
1	B	985	MET
1	B	1009	MET
1	B	1040	GLN
1	B	1044	LYS
1	B	1045	MET
1	C	906	PRO
1	C	913	PRO
1	C	933	LYS
1	C	940	SER
1	C	941	LYS
1	C	956	GLU
1	C	974	LEU
1	C	978	SER
1	C	981	ARG
1	C	984	GLU
1	C	985	MET
1	C	1008	VAL
1	C	1009	MET
1	C	1011	SER
1	C	1013	GLN
1	C	1014	GLN
1	C	1035	LEU
2	D	3	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	916	ASN
1	A	927	ASN
1	A	1013	GLN
1	A	1014	GLN
1	B	927	ASN
1	B	1014	GLN
1	C	927	ASN
1	C	980	HIS
1	C	1033	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 carbohydrates 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	134/161 (83%)	-0.31	1 (0%) 87 87	41, 64, 90, 104	0
1	B	141/161 (87%)	-0.44	1 (0%) 87 87	40, 59, 76, 123	0
1	C	142/161 (88%)	-0.02	6 (4%) 36 31	51, 76, 120, 132	0
2	D	12/13 (92%)	1.08	4 (33%) 0 0	83, 90, 112, 118	0
2	F	12/13 (92%)	5.34	12 (100%) 0 0	118, 134, 138, 147	0
All	All	441/509 (86%)	-0.07	24 (5%) 25 21	40, 68, 119, 147	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	13	ASN	10.1
2	F	12	LEU	7.1
2	F	2	LEU	6.0
2	F	6	ASP	5.4
2	F	10	LEU	5.2
2	F	4	GLU	5.1
2	F	3	SER	4.8
2	F	8	LEU	4.7
2	F	9	LEU	4.5
1	B	907	GLN	4.3
2	F	7	ARG	4.2
1	C	908	GLU	4.2
1	C	1009	MET	4.1
2	F	5	LEU	3.8
2	D	3	SER	3.2
2	F	11	GLU	3.2
1	C	906	PRO	3.2
1	C	907	GLN	2.8
2	D	13	ASN	2.7
1	C	948	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
2	D	7	ARG	2.5
1	C	940	SER	2.0
2	D	4	GLU	2.0
1	A	981	ARG	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 carbohydrates 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.