Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 04:54 PM GMT

PDB ID	:	4GK5
Title	:	Crystal structure of human Rev3-Rev7-Rev1-Polkappa complex
Authors	:	Tao, J.; Min, X.; Wei, X.
Deposited on	:	2012-08-10
Resolution	:	3.21 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

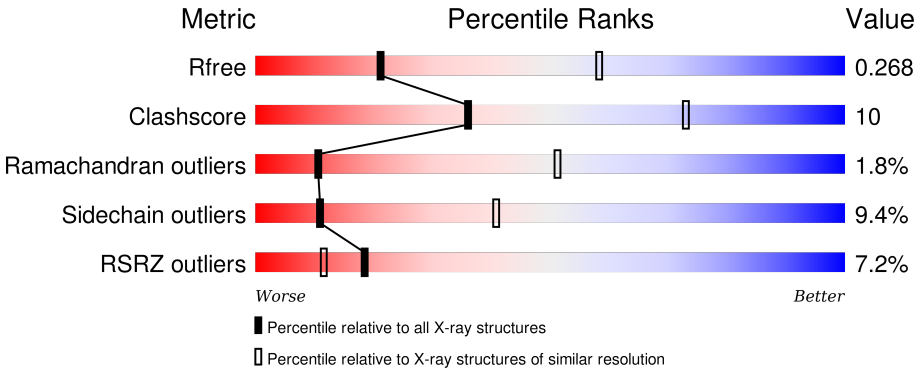
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.21 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}	91344	1095 (3.26-3.18)
Clashscore	102246	1046 (3.24-3.20)
Ramachandran outliers	100387	1026 (3.24-3.20)
Sidechain outliers	100360	1025 (3.24-3.20)
RSRZ outliers	91569	1100 (3.26-3.18)

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. 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 <=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	238	5% 58% 20% 5% 17%
1	B	238	5% 61% 16% • 20%
2	C	52	6% 19% 17% • 62%
2	D	52	8% 21% 15% • 62%
3	E	136	6% 54% 15% • 29%

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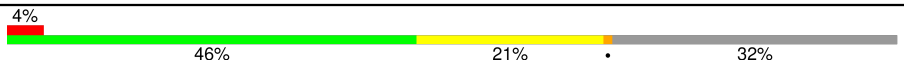
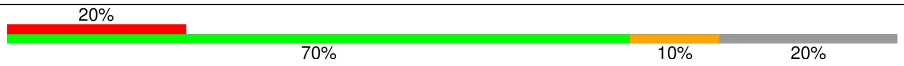
Mol	Chain	Length	Quality of chain
3	F	136	
4	G	10	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5058 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 Mitotic spindle assembly checkpoint protein MAD2B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	198	Total	C	N	O	S	0	0	0
			1605	1037	270	288	10			
1	B	190	Total	C	N	O	S	0	0	0
			1546	999	261	276	10			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	EXPRESSION TAG	UNP Q9UI95
A	-14	GLY	-	EXPRESSION TAG	UNP Q9UI95
A	-13	SER	-	EXPRESSION TAG	UNP Q9UI95
A	-12	SER	-	EXPRESSION TAG	UNP Q9UI95
A	-11	HIS	-	EXPRESSION TAG	UNP Q9UI95
A	-10	HIS	-	EXPRESSION TAG	UNP Q9UI95
A	-9	HIS	-	EXPRESSION TAG	UNP Q9UI95
A	-8	HIS	-	EXPRESSION TAG	UNP Q9UI95
A	-7	HIS	-	EXPRESSION TAG	UNP Q9UI95
A	-6	HIS	-	EXPRESSION TAG	UNP Q9UI95
A	-5	SER	-	EXPRESSION TAG	UNP Q9UI95
A	-4	GLN	-	EXPRESSION TAG	UNP Q9UI95
A	-3	ASP	-	EXPRESSION TAG	UNP Q9UI95
A	-2	PRO	-	EXPRESSION TAG	UNP Q9UI95
A	-1	ASN	-	EXPRESSION TAG	UNP Q9UI95
A	0	SER	-	EXPRESSION TAG	UNP Q9UI95
A	124	ALA	ARG	ENGINEERED MUTATION	UNP Q9UI95
A	212	GLY	-	EXPRESSION TAG	UNP Q9UI95
A	213	SER	-	EXPRESSION TAG	UNP Q9UI95
A	214	GLY	-	EXPRESSION TAG	UNP Q9UI95
A	215	SER	-	EXPRESSION TAG	UNP Q9UI95
A	216	GLY	-	EXPRESSION TAG	UNP Q9UI95
A	217	SER	-	EXPRESSION TAG	UNP Q9UI95
A	218	GLY	-	EXPRESSION TAG	UNP Q9UI95
A	219	SER	-	EXPRESSION TAG	UNP Q9UI95

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Chain	Residue	Modelled	Actual	Comment	Reference
A	220	GLY	-	EXPRESSION TAG	UNP Q9UI95
A	221	SER	-	EXPRESSION TAG	UNP Q9UI95
A	222	HIS	-	EXPRESSION TAG	UNP Q9UI95
B	-15	MET	-	EXPRESSION TAG	UNP Q9UI95
B	-14	GLY	-	EXPRESSION TAG	UNP Q9UI95
B	-13	SER	-	EXPRESSION TAG	UNP Q9UI95
B	-12	SER	-	EXPRESSION TAG	UNP Q9UI95
B	-11	HIS	-	EXPRESSION TAG	UNP Q9UI95
B	-10	HIS	-	EXPRESSION TAG	UNP Q9UI95
B	-9	HIS	-	EXPRESSION TAG	UNP Q9UI95
B	-8	HIS	-	EXPRESSION TAG	UNP Q9UI95
B	-7	HIS	-	EXPRESSION TAG	UNP Q9UI95
B	-6	HIS	-	EXPRESSION TAG	UNP Q9UI95
B	-5	SER	-	EXPRESSION TAG	UNP Q9UI95
B	-4	GLN	-	EXPRESSION TAG	UNP Q9UI95
B	-3	ASP	-	EXPRESSION TAG	UNP Q9UI95
B	-2	PRO	-	EXPRESSION TAG	UNP Q9UI95
B	-1	ASN	-	EXPRESSION TAG	UNP Q9UI95
B	0	SER	-	EXPRESSION TAG	UNP Q9UI95
B	124	ALA	ARG	ENGINEERED MUTATION	UNP Q9UI95
B	212	GLY	-	EXPRESSION TAG	UNP Q9UI95
B	213	SER	-	EXPRESSION TAG	UNP Q9UI95
B	214	GLY	-	EXPRESSION TAG	UNP Q9UI95
B	215	SER	-	EXPRESSION TAG	UNP Q9UI95
B	216	GLY	-	EXPRESSION TAG	UNP Q9UI95
B	217	SER	-	EXPRESSION TAG	UNP Q9UI95
B	218	GLY	-	EXPRESSION TAG	UNP Q9UI95
B	219	SER	-	EXPRESSION TAG	UNP Q9UI95
B	220	GLY	-	EXPRESSION TAG	UNP Q9UI95
B	221	SER	-	EXPRESSION TAG	UNP Q9UI95
B	222	HIS	-	EXPRESSION TAG	UNP Q9UI95

- Molecule 2 is a protein called DNA polymerase zeta catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	20	Total	C	N	O	S	0	0	0
			151	95	25	29	2			
2	D	20	Total	C	N	O	S	0	0	0
			151	95	25	29	2			

- Molecule 3 is a protein called DNA repair protein REV1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	96	Total	C	N	O	S	0	0	0
			778	500	121	152	5			
3	F	93	Total	C	N	O	S	0	0	0
			756	487	118	146	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	1116	MET	-	EXPRESSION TAG	UNP Q9UBZ9
F	1116	MET	-	EXPRESSION TAG	UNP Q9UBZ9

- Molecule 4 is a protein called DNA polymerase kappa.

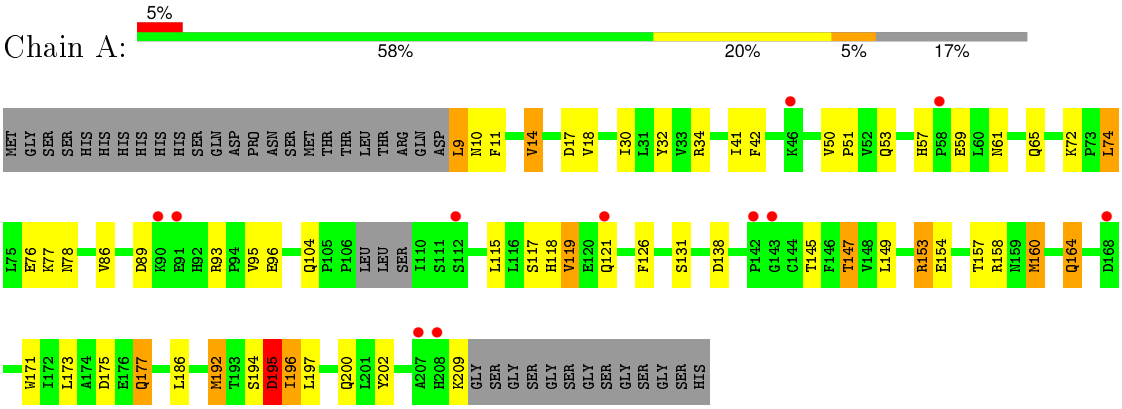
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	8	Total	C	N	O	0	0	0
			71	46	13	12			

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

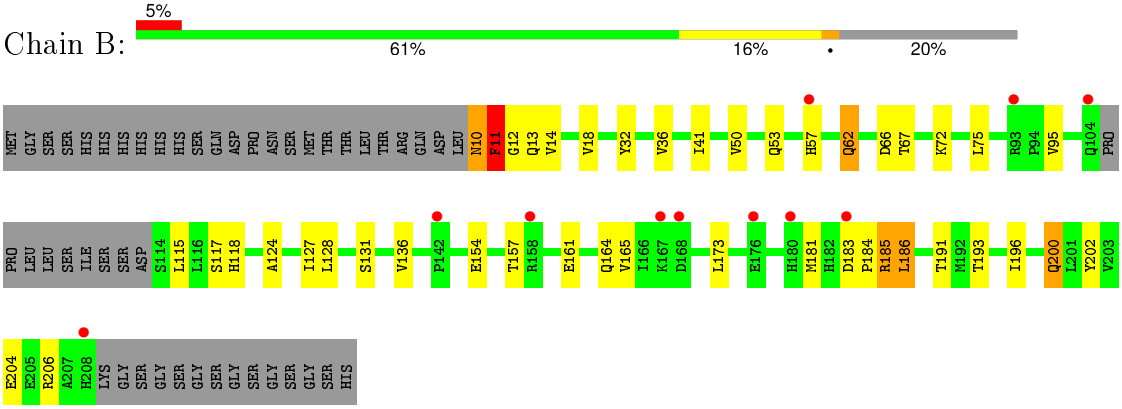
- Molecule 1: Mitotic spindle assembly checkpoint protein MAD2B

Chain A:



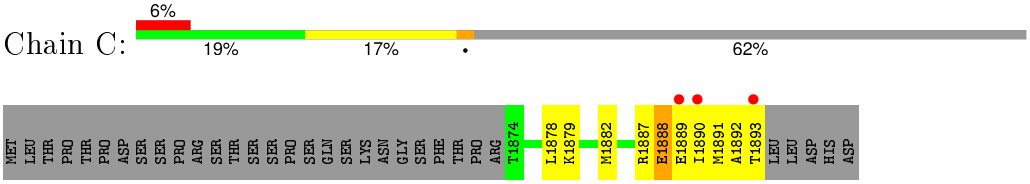
- Molecule 1: Mitotic spindle assembly checkpoint protein MAD2B

Chain B:



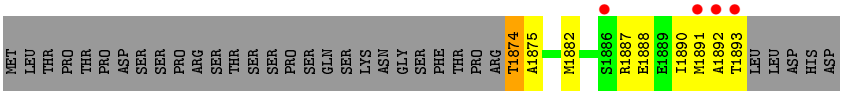
- Molecule 2: DNA polymerase zeta catalytic subunit

Chain C:

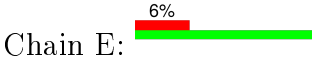


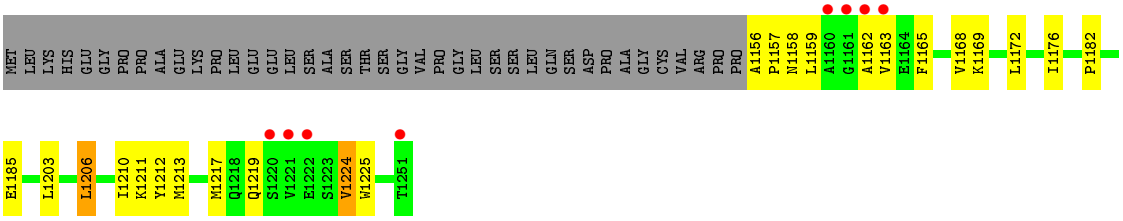
- Molecule 2: DNA polymerase zeta catalytic subunit

Chain D:

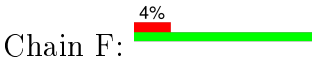


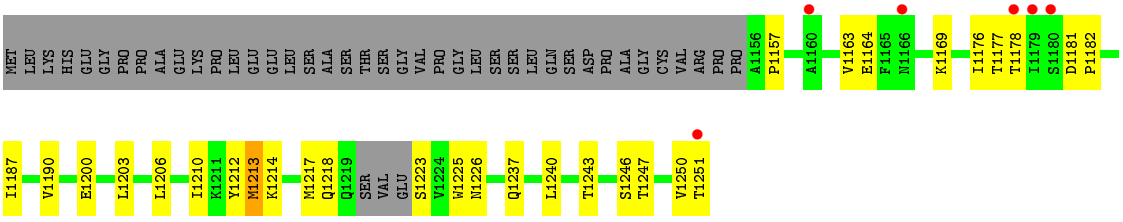
• Molecule 3: DNA repair protein REV1



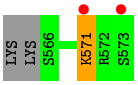


• Molecule 3: DNA repair protein REV1





• Molecule 4: DNA polymerase kappa



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	120.00Å 72.76Å 104.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.21 30.16 – 3.21	Depositor EDS
% Data completeness (in resolution range)	99.0 (20.00-3.21) 99.2 (30.16-3.21)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.10 (at 3.24Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.232 , 0.281 0.226 , 0.268	Depositor DCC
R_{free} test set	772 reflections (5.30%)	DCC
Wilson B-factor (Å^2)	90.0	Xtriage
Anisotropy	0.369	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 46.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 15469 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	5058	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.91% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.63	0/1640	0.87	2/2228 (0.1%)
1	B	0.51	0/1579	0.76	0/2144
2	C	0.68	0/153	0.86	0/207
2	D	0.52	0/153	0.87	0/207
3	E	0.62	0/789	0.82	0/1070
3	F	0.53	0/766	0.74	0/1037
4	G	0.77	0/72	1.02	0/92
All	All	0.58	0/5152	0.81	2/6985 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	153	ARG	NE-CZ-NH1	6.00	123.30	120.30
1	A	153	ARG	NE-CZ-NH2	-5.43	117.59	120.30

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	1605	0	1640	38	0
1	B	1546	0	1577	24	0
2	C	151	0	160	5	0
2	D	151	0	160	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	778	0	789	19	0
3	F	756	0	768	13	0
4	G	71	0	70	1	0
All	All	5058	0	5164	98	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 10.

All (98) 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:32:TYR:CE2	1:A:53:GLN:HG3	2.21	0.75
2:D:1874:THR:OG1	2:D:1875:ALA:N	2.24	0.71
1:A:32:TYR:CD2	1:A:53:GLN:HG3	2.31	0.66
1:A:138:ASP:HB2	1:A:209:LYS:HE2	1.77	0.66
3:E:1156:ALA:N	3:E:1157:PRO:CD	2.58	0.66
3:E:1158:ASN:HB3	3:E:1163:VAL:HG22	1.78	0.65
1:A:126:PHE:HE1	1:A:192:MET:HG2	1.63	0.63
2:D:1888:GLU:CD	2:D:1888:GLU:H	2.02	0.63
1:A:164:GLN:HA	1:A:164:GLN:HE21	1.63	0.62
1:B:181:MET:HE1	1:B:204:GLU:HB3	1.82	0.61
2:D:1890:ILE:C	2:D:1892:ALA:H	2.05	0.60
3:F:1176:ILE:HA	3:F:1225:TRP:CH2	2.36	0.60
3:F:1157:PRO:HG3	3:F:1200:GLU:HG3	1.83	0.60
1:A:164:GLN:NE2	1:A:164:GLN:HA	2.18	0.59
1:B:32:TYR:CD2	1:B:53:GLN:HG3	2.37	0.59
3:F:1206:LEU:HG	3:F:1210:ILE:HD12	1.85	0.59
3:E:1172:LEU:HD13	3:E:1213:MET:CE	2.33	0.59
1:B:186:LEU:HD21	1:B:202:TYR:CD2	2.38	0.59
1:B:200:GLN:NE2	3:F:1203:LEU:H	2.02	0.58
1:A:164:GLN:HE22	1:A:171:TRP:H	1.51	0.58
1:A:11:PHE:O	1:A:76:GLU:O	2.21	0.57
3:F:1214:LYS:O	3:F:1218:GLN:HG3	2.05	0.57
2:C:1890:ILE:O	2:C:1892:ALA:N	2.38	0.56
1:B:11:PHE:HD2	1:B:12:GLY:H	1.52	0.55
2:C:1888:GLU:OE1	2:C:1888:GLU:N	2.39	0.55
1:A:173:LEU:HD23	2:C:1878:LEU:HD23	1.89	0.53
1:A:57:HIS:HE1	1:A:59:GLU:HB2	1.74	0.53
1:B:36:VAL:O	2:D:1887:ARG:NH1	2.42	0.53
1:A:149:LEU:HD23	2:C:1879:LYS:HB3	1.91	0.52
1:B:191:THR:HG23	1:B:200:GLN:HG3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:1187:ILE:O	3:F:1190:VAL:HB	2.10	0.51
1:B:62:GLN:HA	1:B:62:GLN:NE2	2.25	0.50
1:B:10:ASN:HB3	1:B:13:GLN:HB3	1.92	0.50
1:B:183:ASP:CG	1:B:185:ARG:HH12	2.15	0.50
1:A:126:PHE:CE1	1:A:192:MET:HG2	2.44	0.50
1:A:50:VAL:HB	1:A:51:PRO:HD2	1.94	0.49
1:B:66:ASP:O	1:B:67:THR:C	2.51	0.49
1:A:96:GLU:OE2	1:A:209:LYS:NZ	2.45	0.49
3:E:1169:LYS:HG2	3:E:1212:TYR:CE2	2.48	0.49
3:E:1172:LEU:HD13	3:E:1213:MET:HE3	1.95	0.48
1:A:74:LEU:N	1:A:74:LEU:HD23	2.28	0.48
1:B:57:HIS:CE1	2:D:1890:ILE:HG12	2.48	0.48
3:E:1176:ILE:HG22	3:E:1176:ILE:O	2.13	0.48
1:B:184:PRO:HG2	3:F:1246:SER:HB3	1.96	0.48
3:E:1156:ALA:N	3:E:1157:PRO:HD2	2.28	0.47
1:A:195:ASP:HB3	1:A:196:ILE:HD13	1.94	0.47
1:B:72:LYS:O	1:B:75:LEU:HB2	2.15	0.47
3:E:1159:LEU:O	3:E:1162:ALA:HB3	2.15	0.47
3:F:1237:GLN:HE21	3:F:1247:THR:HB	1.79	0.47
1:A:118:HIS:O	1:A:119:VAL:C	2.53	0.47
1:A:200:GLN:NE2	3:E:1203:LEU:H	2.13	0.46
3:E:1224:VAL:HG12	3:E:1225:TRP:N	2.30	0.46
1:A:86:VAL:HB	1:A:147:THR:HG23	1.97	0.46
1:B:181:MET:HE2	1:B:184:PRO:HB3	1.96	0.46
3:E:1182:PRO:HD2	3:E:1224:VAL:HG11	1.97	0.46
1:A:194:SER:OG	1:A:197:LEU:O	2.31	0.46
1:B:193:THR:O	1:B:193:THR:HG22	2.15	0.46
1:A:57:HIS:CE1	1:A:59:GLU:HB2	2.50	0.45
1:A:78:ASN:O	1:A:153:ARG:HD2	2.16	0.45
3:F:1163:VAL:HG12	3:F:1164:GLU:N	2.32	0.45
1:A:9:LEU:HD22	1:A:10:ASN:H	1.81	0.45
1:B:181:MET:CE	1:B:184:PRO:HB3	2.47	0.45
1:A:164:GLN:HE22	1:A:171:TRP:N	2.15	0.45
3:E:1172:LEU:CD1	3:E:1213:MET:CE	2.95	0.45
3:E:1165:PHE:O	3:E:1168:VAL:HB	2.17	0.45
3:E:1206:LEU:C	3:E:1206:LEU:HD12	2.37	0.44
2:D:1887:ARG:HB3	2:D:1888:GLU:OE2	2.17	0.44
1:B:185:ARG:O	1:B:204:GLU:HA	2.18	0.44
3:E:1172:LEU:HD22	3:E:1213:MET:HE2	1.99	0.44
1:B:50:VAL:HG11	1:B:128:LEU:HD21	1.99	0.44
1:A:10:ASN:ND2	1:A:77:LYS:HA	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:1213:MET:O	3:E:1217:MET:HB2	2.17	0.44
3:E:1211:LYS:O	3:E:1212:TYR:C	2.56	0.44
1:A:11:PHE:H	1:A:78:ASN:HB2	1.82	0.44
3:F:1181:ASP:HA	3:F:1182:PRO:HD3	1.86	0.44
2:D:1890:ILE:C	2:D:1892:ALA:N	2.70	0.43
1:A:186:LEU:HD11	1:A:202:TYR:CD2	2.53	0.43
1:B:32:TYR:CE2	1:B:53:GLN:HG3	2.54	0.43
3:E:1182:PRO:CD	3:E:1224:VAL:HG11	2.48	0.43
1:A:14:VAL:O	1:A:18:VAL:HG23	2.18	0.43
1:B:157:THR:O	1:B:161:GLU:HG3	2.19	0.43
1:A:160:MET:CE	1:A:173:LEU:HG	2.48	0.43
4:G:571:LYS:HD2	4:G:571:LYS:HA	1.79	0.43
1:A:61:ASN:O	1:A:65:GLN:HB2	2.19	0.42
1:A:14:VAL:HA	1:A:17:ASP:OD2	2.19	0.42
1:B:124:ALA:O	1:B:127:ILE:HB	2.19	0.42
1:A:175:ASP:OD2	1:A:177:GLN:HB3	2.20	0.42
1:A:160:MET:O	1:A:164:GLN:HB2	2.20	0.42
1:A:173:LEU:HD23	2:C:1878:LEU:CD2	2.50	0.42
1:A:30:ILE:O	1:A:34:ARG:HG2	2.20	0.41
1:B:95:VAL:HG12	1:B:206:ARG:HE	1.84	0.41
1:A:89:ASP:OD2	1:A:93:ARG:NH2	2.53	0.41
3:F:1169:LYS:HG3	3:F:1212:TYR:CE2	2.56	0.41
1:A:17:ASP:HA	1:A:72:LYS:HE2	2.02	0.40
3:F:1213:MET:HG2	3:F:1217:MET:SD	2.62	0.40
3:E:1210:ILE:HA	3:E:1210:ILE:HD13	1.94	0.40
1:A:41:ILE:HG13	1:A:42:PHE:CD2	2.56	0.40
1:B:200:GLN:HE21	3:F:1203:LEU:H	1.69	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	194/238 (82%)	186 (96%)	6 (3%)	2 (1%)	19 64
1	B	186/238 (78%)	164 (88%)	18 (10%)	4 (2%)	8 45
2	C	18/52 (35%)	12 (67%)	4 (22%)	2 (11%)	0 3
2	D	18/52 (35%)	13 (72%)	4 (22%)	1 (6%)	2 18
3	E	94/136 (69%)	89 (95%)	5 (5%)	0	100 100
3	F	89/136 (65%)	76 (85%)	11 (12%)	2 (2%)	8 45
4	G	6/10 (60%)	4 (67%)	2 (33%)	0	100 100
All	All	605/862 (70%)	544 (90%)	50 (8%)	11 (2%)	11 51

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	1891	MET
2	D	1891	MET
1	A	119	VAL
1	B	118	HIS
1	B	131	SER
2	C	1889	GLU
1	A	195	ASP
1	B	11	PHE
3	F	1178	THR
1	B	18	VAL
3	F	1250	VAL

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	186/219 (85%)	166 (89%)	20 (11%)	8 34
1	B	178/219 (81%)	162 (91%)	16 (9%)	12 43
2	C	18/49 (37%)	14 (78%)	4 (22%)	1 6
2	D	18/49 (37%)	15 (83%)	3 (17%)	3 13
3	E	90/123 (73%)	86 (96%)	4 (4%)	35 74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	F	87/123 (71%)	80 (92%)	7 (8%)	15 52
4	G	8/10 (80%)	7 (88%)	1 (12%)	6 26
All	All	585/792 (74%)	530 (91%)	55 (9%)	11 41

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LEU
1	A	14	VAL
1	A	74	LEU
1	A	95	VAL
1	A	104	GLN
1	A	115	LEU
1	A	117	SER
1	A	121	GLN
1	A	131	SER
1	A	145	THR
1	A	147	THR
1	A	154	GLU
1	A	157	THR
1	A	158	ARG
1	A	160	MET
1	A	164	GLN
1	A	177	GLN
1	A	192	MET
1	A	195	ASP
1	A	196	ILE
1	B	10	ASN
1	B	11	PHE
1	B	14	VAL
1	B	41	ILE
1	B	62	GLN
1	B	115	LEU
1	B	117	SER
1	B	136	VAL
1	B	154	GLU
1	B	164	GLN
1	B	165	VAL
1	B	173	LEU
1	B	185	ARG
1	B	186	LEU

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Mol	Chain	Res	Type
1	B	196	ILE
1	B	200	GLN
2	C	1882	MET
2	C	1887	ARG
2	C	1888	GLU
2	C	1893	THR
2	D	1874	THR
2	D	1882	MET
2	D	1893	THR
3	E	1185	GLU
3	E	1206	LEU
3	E	1219	GLN
3	E	1224	VAL
3	F	1177	THR
3	F	1213	MET
3	F	1223	SER
3	F	1226	ASN
3	F	1240	LEU
3	F	1243	THR
3	F	1251	THR
4	G	571	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	164	GLN
1	A	200	GLN
1	B	10	ASN
1	B	62	GLN
1	B	104	GLN
1	B	118	HIS
1	B	121	GLN
1	B	200	GLN
3	F	1189	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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

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, 95^{th} 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	198/238 (83%)	0.26	11 (5%) 28 17	26, 41, 63, 76	0
1	B	190/238 (79%)	0.28	11 (5%) 26 16	38, 59, 76, 80	0
2	C	20/52 (38%)	0.70	3 (15%) 3 2	32, 50, 81, 82	0
2	D	20/52 (38%)	0.88	4 (20%) 1 1	45, 63, 78, 79	0
3	E	96/136 (70%)	0.21	8 (8%) 14 8	26, 44, 65, 71	0
3	F	93/136 (68%)	0.20	6 (6%) 22 13	47, 68, 80, 81	0
4	G	8/10 (80%)	1.50	2 (25%) 1 1	50, 55, 59, 62	0
All	All	625/862 (72%)	0.30	45 (7%) 18 11	26, 53, 76, 82	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	1891	MET	5.5
1	A	90	LYS	4.6
3	E	1221	VAL	4.1
1	B	142	PRO	4.1
3	F	1179	ILE	3.7
3	F	1251	THR	3.7
3	F	1160	ALA	3.6
2	D	1892	ALA	3.5
1	B	104	GLN	3.4
4	G	573	SER	3.4
1	A	208	HIS	3.3
3	E	1251	THR	3.2
3	E	1161	GLY	3.0
3	E	1162	ALA	3.0
3	E	1220	SER	3.0
2	C	1893	THR	3.0
2	C	1889	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	112	SER	2.9
1	A	207	ALA	2.8
3	F	1178	THR	2.7
3	E	1160	ALA	2.6
1	B	183	ASP	2.6
1	A	142	PRO	2.5
1	B	158	ARG	2.5
1	B	176	GLU	2.5
1	A	168	ASP	2.5
3	E	1163	VAL	2.5
4	G	571	LYS	2.4
1	A	58	PRO	2.4
2	D	1886	SER	2.4
1	B	208	HIS	2.4
1	B	167	LYS	2.4
2	C	1890	ILE	2.4
1	B	57	HIS	2.3
1	B	168	ASP	2.3
1	B	93	ARG	2.3
1	A	143	GLY	2.3
1	A	91	GLU	2.3
1	A	121	GLN	2.2
3	E	1222	GLU	2.2
3	F	1180	SER	2.1
1	A	46	LYS	2.1
2	D	1893	THR	2.1
3	F	1166	ASN	2.0
1	B	180	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 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.