W O R L D W I D E
wwPDB
PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Apr 11, 2016 – 11:39 AM EDT

PDB ID	:	5E0U
Title	:	Human PCNA variant (S228I) complexed with p21 at 1.9 Angstroms
Authors	:	Duffy, C.M.; Hilbert, B.J.; Kelch, B.A.
Deposited on	:	2015-09-29
Resolution	:	1.93 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027107
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)	:	rb-20027107

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 1.93 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.
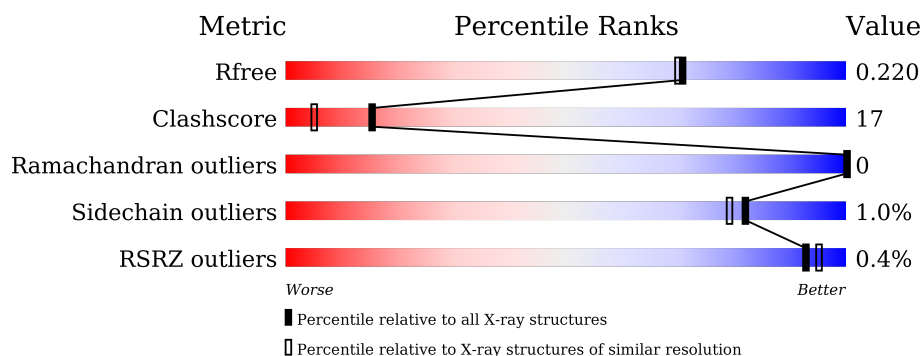
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2910 (1.96-1.92)
Clashscore	102246	3095 (1.96-1.92)
Ramachandran outliers	100387	3062 (1.96-1.92)
Sidechain outliers	100360	3062 (1.96-1.92)
RSRZ outliers	91569	2915 (1.96-1.92)

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	261	67% 30% ••
1	B	261	69% 28% ••
1	C	261	68% 30% •
2	D	23	48% 30% 22%
2	E	23	43% 35% • 17%
2	F	23	4% 35% 43% 22%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7085 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 Proliferating cell nuclear antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	255	Total 1965	C 1236	N 322	O 391	S 16	0	0	0
1	B	255	Total 1965	C 1236	N 322	O 391	S 16	0	0	0
1	C	255	Total 1965	C 1236	N 322	O 391	S 16	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	228	ILE	SER	engineered mutation	UNP P12004
B	228	ILE	SER	engineered mutation	UNP P12004
C	228	ILE	SER	engineered mutation	UNP P12004

- Molecule 2 is a protein called Cyclin-dependent kinase inhibitor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	18	Total 159	C 100	N 31	O 27	S 1	0	0	0
2	E	19	Total 171	C 106	N 35	O 29	S 1	0	0	0
2	F	18	Total 159	C 100	N 31	O 27	S 1	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	138	CYS	-	expression tag	UNP P38936
E	138	CYS	-	expression tag	UNP P38936
F	138	CYS	-	expression tag	UNP P38936

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	246	Total 246	O 246	0	0
3	B	200	Total 200	O 200	0	0
3	C	182	Total 182	O 182	0	0
3	D	24	Total 24	O 24	0	0
3	E	23	Total 23	O 23	0	0
3	F	26	Total 26	O 26	0	0

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: Proliferating cell nuclear antigen
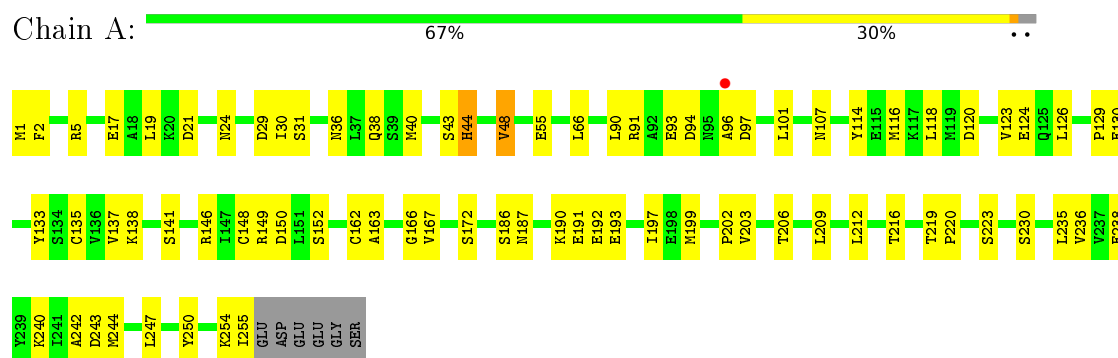
• Molecule 1: Proliferating cell nuclear antigen
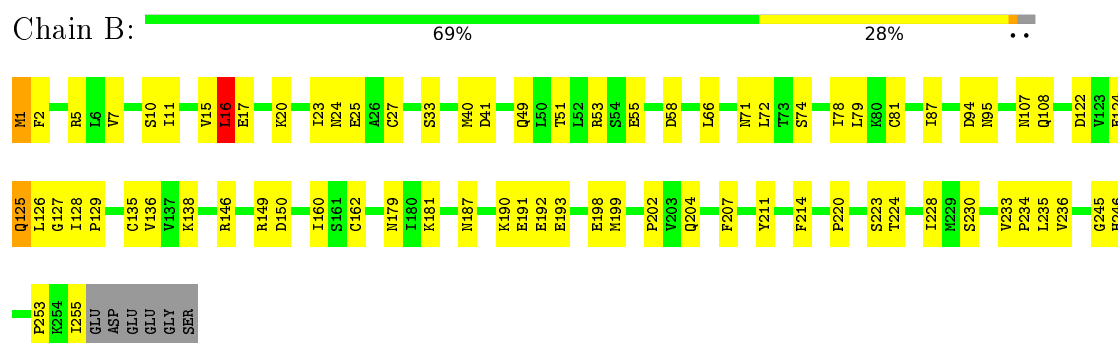
• Molecule 1: Proliferating cell nuclear antigen

• Molecule 2: Cyclin-dependent kinase inhibitor 1
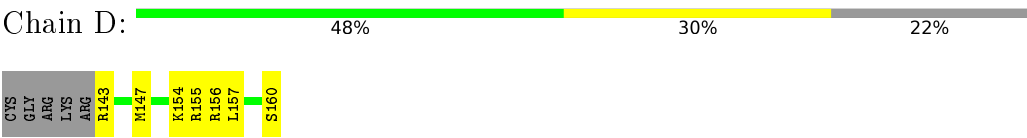
Chain D:

48%   30%   22%

CYS GLY ARG LYS ARG R143 M147 K154 R155 R156 L157 S160

• Molecule 2: Cyclin-dependent kinase inhibitor 1

Chain E:

43%   35%   •   17%

CYS GLY ARG LYS R142 S146 M147 S153 K154 R155 R156 L157 I158 F159 S160

• Molecule 2: Cyclin-dependent kinase inhibitor 1

Chain F:

4%
35%   43%   22%

CYS GLY ARG LYS ARG R143 M147 F150 Y151 H152 S153 K154 R155 R156 L157 I158 F159 S160
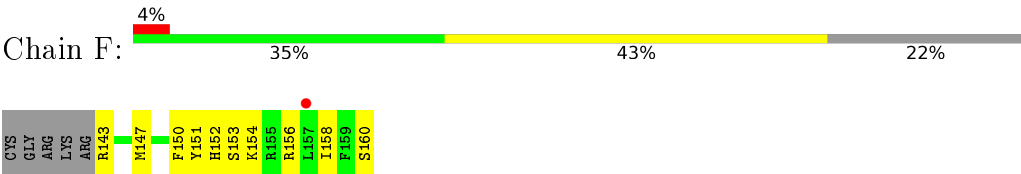
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, α, β, γ	143.29Å 143.29Å 41.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.44 – 1.93 34.44 – 1.93	Depositor EDS
% Data completeness (in resolution range)	99.8 (34.44-1.93) 99.8 (34.44-1.93)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.17 (at 1.92Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.162 , 0.221 0.162 , 0.220	Depositor DCC
R_{free} test set	1993 reflections (2.79%)	DCC
Wilson B-factor (Å^2)	28.1	Xtriage
Anisotropy	0.590	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 41.2	EDS
Estimated twinning fraction	0.477 for -h,-k,l 0.085 for h,-h-k,-l 0.085 for -k,-h,-l	Xtriage
L-test for twinning[2]	$< \lvert L \rvert > = 0.41, < L^2 > = 0.23$	Xtriage
Outliers	0 of 71743 reflections	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	7085	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< \lvert L \rvert >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	0.74	0/1991	0.81	2/2690 (0.1%)
1	B	0.74	1/1991 (0.1%)	0.83	3/2690 (0.1%)
1	C	0.65	0/1991	0.74	0/2690
2	D	0.80	0/162	0.80	0/214
2	E	0.61	0/174	0.72	0/228
2	F	0.67	0/162	0.65	0/214
All	All	0.71	1/6471 (0.0%)	0.79	5/8726 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	81	CYS	CB-SG	-5.29	1.73	1.81

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	49	GLN	CA-CB-CG	6.32	127.30	113.40
1	B	66	LEU	CA-CB-CG	5.95	128.98	115.30
1	B	16	LEU	CA-CB-CG	-5.49	102.67	115.30
1	A	19	LEU	CA-CB-CG	5.26	127.39	115.30
1	A	90	LEU	CA-CB-CG	-5.25	103.22	115.30

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	1965	0	1979	66	0
1	B	1965	0	1979	72	0
1	C	1965	0	1979	72	0
2	D	159	0	157	15	0
2	E	171	0	170	14	0
2	F	159	0	157	16	0
3	A	246	0	0	27	0
3	B	200	0	0	20	4
3	C	182	0	0	17	1
3	D	24	0	0	0	0
3	E	23	0	0	2	1
3	F	26	0	0	7	0
All	All	7085	0	6421	221	4

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 (221) 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:146:ARG:NH1	1:A:150:ASP:OD2	1.74	1.19
1:A:130:GLU:OE2	3:A:301:HOH:O	1.68	1.10
1:B:190:LYS:NZ	3:B:301:HOH:O	1.90	1.04
1:A:40:MET:SD	3:A:390:HOH:O	2.20	0.99
1:A:40:MET:HE3	2:D:147:MET:HB2	1.45	0.97
1:B:146:ARG:HH11	1:B:149:ARG:HH22	1.14	0.94
1:A:1:MET:N	1:A:94:ASP:OD1	2.01	0.93
1:B:181:LYS:NZ	3:B:302:HOH:O	2.03	0.91
1:B:17:GLU:OE1	1:B:20:LYS:NZ	2.03	0.90
1:C:131:GLN:NE2	3:C:304:HOH:O	2.02	0.90
1:C:150:ASP:OD2	3:C:302:HOH:O	1.92	0.87
1:B:53:ARG:NH2	3:B:303:HOH:O	2.08	0.86
1:C:41:ASP:OD2	1:C:43:SER:OG	1.94	0.86
1:B:199:MET:HE2	1:B:202:PRO:HA	1.57	0.85
1:B:146:ARG:NH1	1:B:149:ARG:HH22	1.72	0.85
1:A:24:ASN:O	3:A:304:HOH:O	1.94	0.84
1:C:8:GLN:OE1	3:C:303:HOH:O	1.93	0.84
1:A:38:GLN:HE22	1:A:126:LEU:H	1.25	0.84
1:A:55:GLU:OE2	3:A:305:HOH:O	1.95	0.83
1:A:172:SER:O	3:A:306:HOH:O	1.96	0.82
1:B:129:PRO:HB3	2:D:157:LEU:HD13	1.65	0.79
2:F:151:TYR:OH	3:F:202:HOH:O	2.03	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:GLY:O	3:A:308:HOH:O	2.03	0.76
2:F:143:ARG:NH1	3:F:203:HOH:O	2.09	0.76
1:A:120:ASP:OD1	2:D:160:SER:N	2.19	0.76
1:A:97:ASP:OD2	3:A:309:HOH:O	2.04	0.76
1:C:1:MET:N	1:C:94:ASP:OD1	2.19	0.75
1:B:71:ASN:ND2	3:B:308:HOH:O	2.19	0.75
2:E:142:ARG:NH2	3:E:202:HOH:O	2.20	0.75
1:C:64:ARG:NH2	3:C:314:HOH:O	2.20	0.74
1:C:117:LYS:NZ	3:C:313:HOH:O	2.20	0.73
1:B:246:HIS:ND1	3:B:309:HOH:O	2.20	0.73
1:C:17:GLU:OE1	1:C:20:LYS:NZ	2.16	0.73
1:C:40:MET:HE3	2:F:147:MET:HB2	1.69	0.73
1:C:120:ASP:OD1	2:F:160:SER:N	2.22	0.71
1:B:146:ARG:HH11	1:B:149:ARG:NH2	1.88	0.71
1:B:228:ILE:HB	1:B:236:VAL:HB	1.72	0.71
1:C:133:TYR:OH	3:C:305:HOH:O	2.08	0.71
1:A:24:ASN:OD1	3:A:312:HOH:O	2.10	0.70
1:A:203:VAL:O	3:A:310:HOH:O	2.09	0.70
1:C:148:CYS:O	1:C:152:SER:OG	2.05	0.69
1:C:230:SER:OG	3:C:306:HOH:O	2.10	0.69
1:C:168:LYS:NZ	1:C:179:ASN:OD1	2.26	0.68
1:C:126:LEU:HD13	2:F:151:TYR:HB2	1.75	0.68
1:B:149:ARG:NH2	1:B:150:ASP:OD1	2.26	0.68
1:B:10:SER:OG	3:B:305:HOH:O	2.12	0.67
1:C:255:ILE:N	2:F:143:ARG:O	2.25	0.67
1:A:40:MET:CE	2:D:147:MET:HB2	2.24	0.67
1:B:129:PRO:HD3	2:D:155:ARG:NH1	2.10	0.66
1:C:93:GLU:OE1	3:C:308:HOH:O	2.12	0.66
1:B:41:ASP:O	3:B:306:HOH:O	2.13	0.66
1:C:245:GLY:O	3:C:307:HOH:O	2.12	0.66
1:B:1:MET:N	1:B:94:ASP:OD1	2.16	0.65
1:C:49:GLN:NE2	1:C:51:THR:OG1	2.31	0.64
1:C:138:LYS:NZ	3:C:317:HOH:O	2.29	0.63
1:C:40:MET:CE	2:F:147:MET:HB2	2.29	0.63
1:A:93:GLU:H	1:A:96:ALA:HB2	1.64	0.62
1:B:125:GLN:HG3	2:E:156:ARG:HD2	1.79	0.62
1:B:199:MET:HG2	3:B:335:HOH:O	1.99	0.62
1:A:242:ALA:O	3:A:315:HOH:O	2.16	0.61
1:B:255:ILE:HB	2:E:142:ARG:N	2.15	0.61
1:C:131:GLN:NE2	3:C:320:HOH:O	2.34	0.61
1:B:1:MET:HG2	1:B:2:PHE:N	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:CYS:O	1:A:152:SER:OG	2.13	0.60
1:C:212:LEU:O	1:C:216:THR:HG23	2.01	0.60
1:C:10:SER:HA	1:C:13:LYS:HD3	1.84	0.60
1:B:95:ASN:HB2	3:B:463:HOH:O	2.01	0.59
1:B:124:GLU:HG2	2:E:153:SER:HB2	1.83	0.59
1:A:36:ASN:HB3	3:A:472:HOH:O	2.02	0.59
1:A:5:ARG:NH1	3:A:313:HOH:O	2.11	0.59
1:C:14:LYS:O	3:C:311:HOH:O	2.17	0.59
1:B:187:ASN:HB3	3:B:434:HOH:O	2.02	0.59
1:A:138:LYS:NZ	1:A:191:GLU:OE2	2.31	0.59
2:F:143:ARG:NH2	3:F:207:HOH:O	2.32	0.59
1:B:122:ASP:OD2	3:B:307:HOH:O	2.16	0.58
1:B:129:PRO:HA	2:D:155:ARG:O	2.02	0.58
1:A:187:ASN:ND2	3:A:327:HOH:O	2.36	0.57
1:C:230:SER:HB3	1:C:233:VAL:CG2	2.35	0.57
1:A:91:ARG:HD3	3:A:329:HOH:O	2.04	0.57
1:A:101:LEU:HD11	1:A:116:MET:HE2	1.86	0.57
1:A:238:GLU:OE2	1:A:240:LYS:HE2	2.04	0.57
1:B:128:ILE:O	2:D:154:LYS:HE2	2.05	0.57
1:B:107:ASN:ND2	3:B:304:HOH:O	2.09	0.57
1:A:243:ASP:HB3	3:A:315:HOH:O	2.06	0.56
1:C:124:GLU:OE2	2:F:153:SER:OG	2.20	0.56
1:C:192:GLU:N	1:C:192:GLU:OE1	2.37	0.56
1:B:124:GLU:CG	2:E:153:SER:HB2	2.36	0.56
1:B:138:LYS:HE2	1:B:191:GLU:OE2	2.05	0.56
1:B:135:CYS:SG	3:B:477:HOH:O	2.41	0.55
1:C:133:TYR:CD2	1:C:230:SER:HB2	2.41	0.55
1:B:7:VAL:HA	1:B:87:ILE:HG12	1.89	0.55
1:C:255:ILE:HG23	2:F:143:ARG:NH2	2.22	0.55
1:B:53:ARG:NH1	3:B:320:HOH:O	2.30	0.54
1:B:211:TYR:O	1:B:214:PHE:HB2	2.07	0.54
2:E:146:SER:OG	3:E:201:HOH:O	2.19	0.54
1:B:125:GLN:N	2:E:154:LYS:O	2.39	0.54
1:B:5:ARG:HB2	3:B:353:HOH:O	2.08	0.53
1:B:125:GLN:HG3	2:E:156:ARG:CD	2.37	0.53
1:B:16:LEU:HD13	1:B:79:LEU:CD1	2.39	0.53
1:C:190:LYS:NZ	1:C:192:GLU:OE2	2.42	0.53
1:A:31:SER:HB3	3:A:464:HOH:O	2.09	0.53
1:C:133:TYR:HB3	1:C:229:MET:O	2.09	0.53
1:A:118:LEU:HB2	2:D:160:SER:HB3	1.90	0.52
1:B:51:THR:O	1:B:245:GLY:HA3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:152:HIS:N	3:F:201:HOH:O	1.98	0.52
1:C:164:LYS:HG3	1:C:199:MET:HE2	1.91	0.52
1:B:129:PRO:CB	2:D:157:LEU:HD13	2.37	0.52
1:A:107:ASN:ND2	3:A:338:HOH:O	2.42	0.52
1:B:25:GLU:OE2	3:B:308:HOH:O	2.19	0.52
1:B:5:ARG:NE	1:B:58:ASP:OD2	2.41	0.52
1:B:192:GLU:HB2	1:B:223:SER:HB3	1.92	0.51
1:C:60:TYR:O	3:C:312:HOH:O	2.20	0.51
1:A:163:ALA:N	3:A:308:HOH:O	2.44	0.50
1:C:23:ILE:HG13	1:C:72:LEU:HD12	1.93	0.50
1:C:165:ASP:OD1	1:C:165:ASP:N	2.35	0.50
2:D:155:ARG:NH2	2:D:157:LEU:HD11	2.26	0.50
1:A:254:LYS:NZ	3:A:303:HOH:O	1.89	0.50
1:A:93:GLU:N	1:A:96:ALA:HB2	2.27	0.50
1:A:133:TYR:CD1	1:A:230:SER:HB2	2.47	0.50
3:A:310:HOH:O	1:C:131:GLN:OE1	2.20	0.50
1:C:40:MET:HE1	1:C:44:HIS:HB3	1.93	0.50
1:A:167:VAL:HA	3:A:308:HOH:O	2.11	0.50
1:C:112:SER:HB3	1:C:114:TYR:HE2	1.76	0.49
1:C:90:LEU:HD22	1:C:99:LEU:HD21	1.94	0.49
1:B:211:TYR:HA	1:B:214:PHE:HD2	1.76	0.49
1:C:200:ASN:ND2	3:C:330:HOH:O	2.45	0.49
1:B:108:GLN:NE2	3:C:314:HOH:O	2.43	0.48
1:C:125:GLN:O	3:F:204:HOH:O	2.19	0.48
1:C:164:LYS:O	1:C:184:GLN:NE2	2.46	0.48
1:C:51:THR:O	1:C:245:GLY:HA3	2.13	0.48
1:B:192:GLU:HA	1:B:224:THR:CG2	2.44	0.47
1:C:121:LEU:HB2	2:F:158:ILE:HB	1.95	0.47
1:B:7:VAL:HG23	1:B:58:ASP:HB2	1.96	0.47
1:C:164:LYS:HG2	1:C:199:MET:HB3	1.95	0.47
2:E:142:ARG:HA	2:E:142:ARG:HD2	1.46	0.47
1:B:136:VAL:HB	1:B:198:GLU:HB2	1.96	0.47
1:A:141:SER:HB2	1:A:219:THR:HG23	1.95	0.47
1:A:190:LYS:HD3	1:A:193:GLU:OE2	2.14	0.47
1:B:230:SER:HB3	1:B:233:VAL:CG2	2.44	0.47
1:A:186:SER:HB3	3:A:322:HOH:O	2.14	0.47
1:B:160:ILE:O	1:B:204:GLN:HA	2.15	0.47
1:C:11:ILE:O	1:C:15:VAL:HG23	2.15	0.46
1:A:114:TYR:OH	3:A:302:HOH:O	1.86	0.46
1:C:146:ARG:HD2	1:C:150:ASP:OD2	2.16	0.46
1:B:179:ASN:ND2	3:B:329:HOH:O	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:133:TYR:CG	1:C:228:ILE:HG22	2.51	0.46
1:C:13:LYS:HE2	1:C:84:ASN:OD1	2.16	0.46
1:C:192:GLU:HA	1:C:224:THR:HG21	1.97	0.46
1:A:192:GLU:HB2	1:A:223:SER:HB3	1.97	0.46
1:C:123:VAL:HB	2:F:156:ARG:HG3	1.97	0.46
1:B:125:GLN:O	2:E:154:LYS:N	2.48	0.45
1:A:244:MET:HE2	1:A:244:MET:HB2	1.84	0.45
1:A:137:VAL:HG22	1:A:197:ILE:HG12	1.98	0.45
1:A:152:SER:HA	1:A:209:LEU:HD13	1.97	0.45
1:A:206:THR:HG22	1:A:254:LYS:HD3	1.97	0.45
1:A:236:VAL:HG22	1:A:250:TYR:CD2	2.51	0.45
1:B:234:PRO:HA	1:B:253:PRO:HD3	1.98	0.45
1:A:30:ILE:HB	1:A:66:LEU:HB2	1.98	0.45
1:C:112:SER:HB3	1:C:114:TYR:CE2	2.51	0.45
1:B:138:LYS:HE3	1:B:191:GLU:HG2	1.98	0.45
1:B:74:SER:O	1:B:78:ILE:HG13	2.16	0.45
1:A:146:ARG:HD2	1:A:150:ASP:OD2	2.17	0.45
1:C:234:PRO:HD3	2:F:150:PHE:CD2	2.52	0.45
1:A:17:GLU:OE1	3:A:316:HOH:O	2.21	0.44
1:B:129:PRO:HD3	2:D:155:ARG:HH11	1.83	0.44
1:C:159:VAL:HG22	1:C:206:THR:OG1	2.18	0.44
2:F:156:ARG:NH2	3:F:206:HOH:O	2.31	0.44
1:B:27:CYS:SG	2:E:158:ILE:HG12	2.58	0.44
1:C:170:SER:HB3	3:C:423:HOH:O	2.17	0.44
1:A:133:TYR:HD1	1:A:230:SER:HB2	1.83	0.43
1:B:11:ILE:O	1:B:15:VAL:HG23	2.18	0.43
1:B:207:PHE:CZ	1:B:235:LEU:HB2	2.53	0.43
1:C:16:LEU:HD11	1:C:75:MET:SD	2.58	0.43
1:C:154:ILE:O	1:C:173:GLY:HA3	2.18	0.43
3:B:439:HOH:O	2:E:155:ARG:HB2	2.17	0.43
1:C:138:LYS:HE3	1:C:191:GLU:HG2	2.00	0.43
1:A:255:ILE:HG23	2:D:143:ARG:N	2.34	0.43
1:A:24:ASN:ND2	3:A:350:HOH:O	2.49	0.43
1:C:230:SER:HB3	1:C:233:VAL:HG21	2.00	0.43
1:A:212:LEU:O	1:A:216:THR:HG23	2.19	0.43
1:B:17:GLU:CD	1:B:20:LYS:NZ	2.69	0.43
1:B:40:MET:HE2	1:B:126:LEU:HD11	2.00	0.43
1:A:48:VAL:HG12	1:A:247:LEU:HD11	2.01	0.43
2:F:154:LYS:N	3:F:204:HOH:O	2.10	0.43
1:C:135:CYS:SG	1:C:162:CYS:HB3	2.59	0.43
1:B:129:PRO:CD	2:D:155:ARG:NH1	2.79	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:GLY:HA2	1:A:197:ILE:HD12	2.00	0.42
1:A:2:PHE:O	1:A:91:ARG:HA	2.19	0.42
1:B:127:GLY:CA	2:D:155:ARG:HD3	2.49	0.42
2:E:157:LEU:HA	2:E:157:LEU:HD23	1.81	0.42
1:A:123:VAL:HG12	1:A:124:GLU:N	2.34	0.42
1:A:129:PRO:HA	1:B:55:GLU:OE2	2.20	0.42
1:C:138:LYS:NZ	1:C:191:GLU:O	2.47	0.42
1:A:199:MET:CE	1:A:202:PRO:HA	2.49	0.42
1:C:73:THR:HG22	1:C:77:LYS:HE3	2.01	0.42
1:B:192:GLU:HG2	1:B:193:GLU:HG3	2.01	0.42
1:B:16:LEU:HD13	1:B:79:LEU:HD11	2.01	0.42
1:C:40:MET:HG3	1:C:47:LEU:HD12	2.00	0.42
1:C:164:LYS:HE3	1:C:164:LYS:HB3	1.88	0.41
1:A:135:CYS:SG	1:A:162:CYS:HB3	2.60	0.41
1:A:123:VAL:HG12	1:A:124:GLU:H	1.85	0.41
1:C:175:LEU:O	3:C:315:HOH:O	2.22	0.41
1:B:107:ASN:O	1:B:108:GLN:HB3	2.20	0.41
1:B:162:CYS:SG	3:B:477:HOH:O	2.13	0.41
1:C:216:THR:O	1:C:219:THR:OG1	2.17	0.41
1:C:136:VAL:HG22	1:C:228:ILE:HG23	2.02	0.41
1:A:219:THR:N	1:A:220:PRO:HD2	2.36	0.41
1:A:235:LEU:O	1:A:250:TYR:HA	2.20	0.41
1:A:29:ASP:OD1	2:D:156:ARG:NH2	2.48	0.41
1:A:40:MET:HE1	1:A:44:HIS:HB3	2.03	0.41
1:C:244:MET:HB3	1:C:244:MET:HE3	1.71	0.41
1:A:21:ASP:HB2	3:A:405:HOH:O	2.21	0.41
1:B:220:PRO:HG2	3:B:376:HOH:O	2.21	0.41
1:B:23:ILE:HG13	1:B:72:LEU:HD12	2.02	0.41
1:C:23:ILE:HD13	1:C:39:SER:HB3	2.03	0.41
1:A:149:ARG:NH2	3:A:319:HOH:O	2.27	0.40
1:C:101:LEU:HD12	1:C:101:LEU:N	2.36	0.40
1:A:43:SER:O	1:A:44:HIS:HB2	2.21	0.40
1:B:24:ASN:C	1:B:25:GLU:HG3	2.42	0.40
1:C:90:LEU:HB3	1:C:99:LEU:HD11	2.03	0.40
1:B:40:MET:CE	2:E:147:MET:HB2	2.52	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:390:HOH:O	3:E:202:HOH:O[1_554]	2.03	0.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:434:HOH:O	3:B:444:HOH:O[3_555]	2.03	0.17
3:B:302:HOH:O	3:C:366:HOH:O[3_555]	2.14	0.06
3:B:495:HOH:O	3:B:498:HOH:O[1_556]	2.16	0.04

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	253/261 (97%)	249 (98%)	4 (2%)	0	100	100
1	B	253/261 (97%)	250 (99%)	3 (1%)	0	100	100
1	C	253/261 (97%)	250 (99%)	3 (1%)	0	100	100
2	D	16/23 (70%)	16 (100%)	0	0	100	100
2	E	17/23 (74%)	17 (100%)	0	0	100	100
2	F	16/23 (70%)	16 (100%)	0	0	100	100
All	All	808/852 (95%)	798 (99%)	10 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	223/228 (98%)	221 (99%)	2 (1%)	84	82
1	B	223/228 (98%)	219 (98%)	4 (2%)	66	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	223/228 (98%)	223 (100%)	0	100	100
2	D	18/22 (82%)	18 (100%)	0	100	100
2	E	19/22 (86%)	18 (95%)	1 (5%)	28	12
2	F	18/22 (82%)	18 (100%)	0	100	100
All	All	724/750 (96%)	717 (99%)	7 (1%)	82	79

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	HIS
1	A	48	VAL
1	B	1	MET
1	B	16	LEU
1	B	33	SER
1	B	125	GLN
2	E	142	ARG

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

Mol	Chain	Res	Type
1	A	246	HIS
1	C	95	ASN
1	C	131	GLN

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 (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	255/261 (97%)	-0.71	1 (0%)	93	95	16, 25, 39, 74	0
1	B	255/261 (97%)	-0.73	0	100	100	18, 25, 41, 69	0
1	C	255/261 (97%)	-0.65	1 (0%)	93	95	21, 30, 55, 87	0
2	D	18/23 (78%)	-0.66	0	100	100	19, 23, 36, 37	0
2	E	19/23 (82%)	-0.67	0	100	100	27, 32, 40, 42	0
2	F	18/23 (78%)	-0.15	1 (5%)	28	36	28, 36, 63, 66	0
All	All	820/852 (96%)	-0.68	3 (0%)	93	95	16, 28, 50, 87	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	133	TYR	3.0
1	A	96	ALA	2.2
2	F	157	LEU	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 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.