Full wwPDB X-ray Structure Validation Report (i)

Jan 17, 2017 – 07:02 PM EST

PDB ID	:	5HQL
Title	:	Structure function studies of R. palustris RubisCO (A47V-M331A mutant; CABP-bound; no expression tag)
Authors	:	Arbing, M.A.; Shin, A.; Cascio, D.; Satagopan, S.; North, J.A.; Tabita, F.R.
Deposited on	:	2016-01-21
Resolution	:	2.53 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:

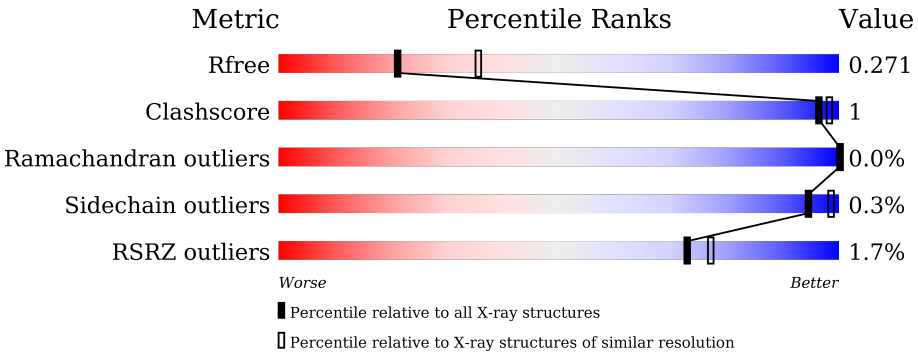
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028442

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 2.53 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	4241 (2.54-2.50)
Clashscore	102246	4968 (2.54-2.50)
Ramachandran outliers	100387	4873 (2.54-2.50)
Sidechain outliers	100360	4875 (2.54-2.50)
RSRZ outliers	91569	4253 (2.54-2.50)

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	461	2% 95%
1	B	461	% 95%
1	C	461	% 97%
1	D	461	3% 95%
1	E	461	% 96%
1	F	461	2% 93% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 41321 atoms, of which 19906 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.

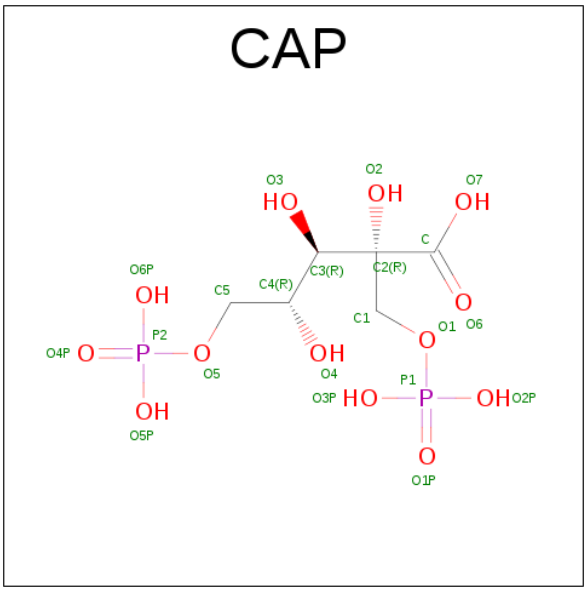
- Molecule 1 is a protein called Ribulose bisphosphate carboxylase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	456	Total	C	H	N	O	S	0	0	0
			6814	2221	3323	604	648	18			
1	B	457	Total	C	H	N	O	S	0	0	0
			6833	2226	3334	609	646	18			
1	C	456	Total	C	H	N	O	S	0	0	0
			6819	2222	3328	602	649	18			
1	D	455	Total	C	H	N	O	S	0	0	0
			6805	2217	3320	603	647	18			
1	E	457	Total	C	H	N	O	S	0	0	0
			6856	2230	3349	609	650	18			
1	F	454	Total	C	H	N	O	S	0	0	0
			6699	2190	3252	600	639	18			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	VAL	ALA	engineered mutation	UNP Q6N0W9
A	331	ALA	MET	engineered mutation	UNP Q6N0W9
B	47	VAL	ALA	engineered mutation	UNP Q6N0W9
B	331	ALA	MET	engineered mutation	UNP Q6N0W9
C	47	VAL	ALA	engineered mutation	UNP Q6N0W9
C	331	ALA	MET	engineered mutation	UNP Q6N0W9
D	47	VAL	ALA	engineered mutation	UNP Q6N0W9
D	331	ALA	MET	engineered mutation	UNP Q6N0W9
E	47	VAL	ALA	engineered mutation	UNP Q6N0W9
E	331	ALA	MET	engineered mutation	UNP Q6N0W9
F	47	VAL	ALA	engineered mutation	UNP Q6N0W9
F	331	ALA	MET	engineered mutation	UNP Q6N0W9

- Molecule 2 is 2-CARBOXYARABINITOL-1,5-DIPHOSPHATE (three-letter code: CAP) (formula: $C_6H_{14}O_{13}P_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O P 21 6 13 2	0	0
2	B	1	Total C O P 21 6 13 2	0	0
2	C	1	Total C O P 21 6 13 2	0	0
2	D	1	Total C O P 21 6 13 2	0	0
2	E	1	Total C O P 21 6 13 2	0	0
2	F	1	Total C O P 21 6 13 2	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total Mg 1 1	0	0
3	E	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0
3	F	1	Total Mg 1 1	0	0

- Molecule 4 is water.

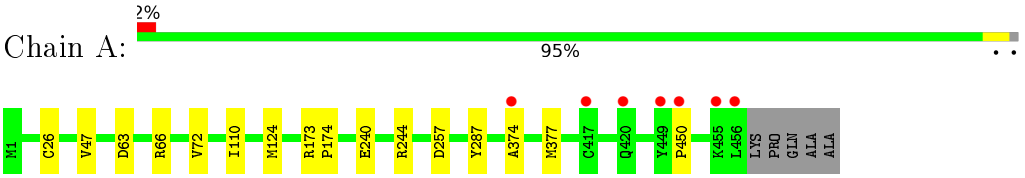
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	69	Total O 69 69	0	0
4	B	55	Total O 55 55	0	0
4	C	78	Total O 78 78	0	0
4	D	57	Total O 57 57	0	0
4	E	58	Total O 58 58	0	0
4	F	46	Total O 46 46	0	0

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 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.

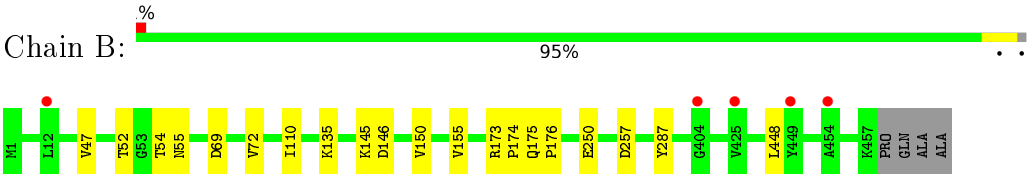
- Molecule 1: Ribulose bisphosphate carboxylase

Chain A:



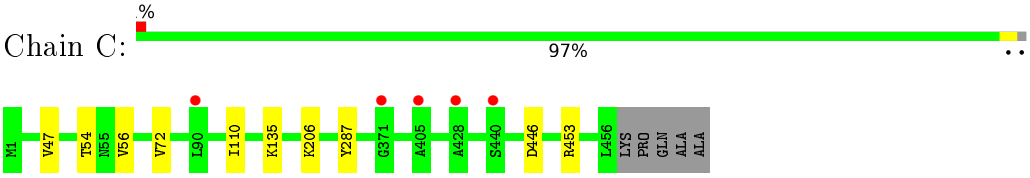
- Molecule 1: Ribulose bisphosphate carboxylase

Chain B:



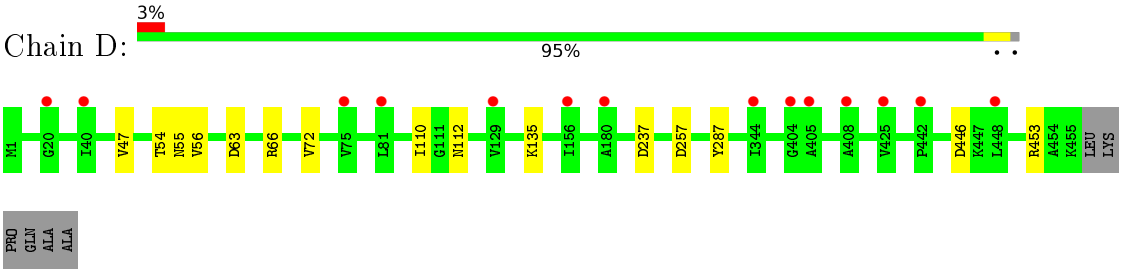
- Molecule 1: Ribulose bisphosphate carboxylase

Chain C:



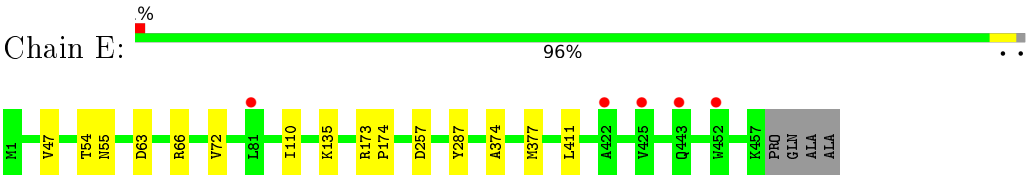
- Molecule 1: Ribulose bisphosphate carboxylase

Chain D:



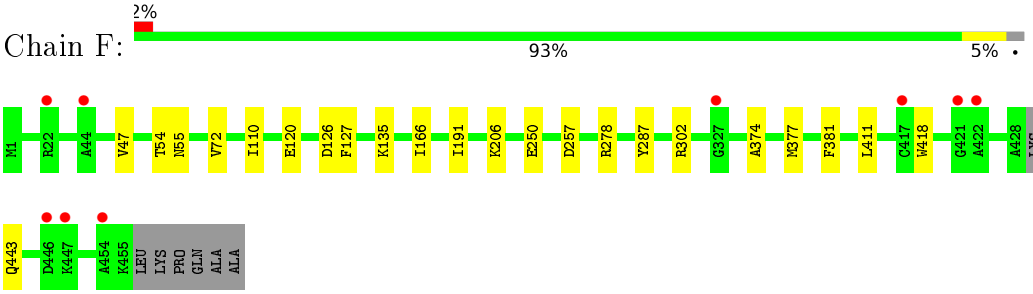
- Molecule 1: Ribulose bisphosphate carboxylase

Chain E:



• Molecule 1: Ribulose bisphosphate carboxylase

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	74.44Å 100.49Å 103.97Å 108.13° 113.66° 95.44°	Depositor
Resolution (Å)	87.96 – 2.53 87.97 – 2.53	Depositor EDS
% Data completeness (in resolution range)	90.9 (87.96-2.53) 79.3 (87.97-2.53)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.17 (at 2.51Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.213 , 0.259 0.235 , 0.271	Depositor DCC
R_{free} test set	7703 reflections (11.11%)	DCC
Wilson B-factor (Å^2)	37.3	Xtriage
Anisotropy	0.690	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 43.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	41321	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.70% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CAP, KCX

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	0.29	0/3567	0.52	0/4832
1	B	0.30	0/3575	0.53	0/4845
1	C	0.29	0/3567	0.51	0/4834
1	D	0.29	0/3561	0.51	0/4825
1	E	0.30	0/3583	0.53	0/4854
1	F	0.31	0/3521	0.52	0/4773
All	All	0.30	0/21374	0.52	0/28963

There are no bond length outliers.

There are no bond angle outliers.

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	3491	3323	3336	10	0
1	B	3499	3334	3349	13	0
1	C	3491	3328	3341	7	0
1	D	3485	3320	3335	11	0
1	E	3507	3349	3363	10	0
1	F	3447	3252	3264	15	0
2	A	21	0	7	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	21	0	8	0	0
2	C	21	0	8	0	0
2	D	21	0	8	0	0
2	E	21	0	9	0	0
2	F	21	0	8	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	69	0	0	0	0
4	B	55	0	0	0	0
4	C	78	0	0	0	0
4	D	57	0	0	0	0
4	E	58	0	0	0	0
4	F	46	0	0	0	0
All	All	21415	19906	20036	58	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 1.

All (58) 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:B:257:ASP:OD2	1:D:135:LYS:NZ	2.19	0.75
1:A:63:ASP:OD1	1:A:66:ARG:NH1	2.20	0.74
1:D:63:ASP:OD1	1:D:66:ARG:NH1	2.20	0.74
1:B:135:LYS:NZ	1:D:257:ASP:OD2	2.22	0.72
1:E:257:ASP:OD2	1:F:135:LYS:NZ	2.29	0.62
1:A:374:ALA:HA	1:A:377:MET:CE	2.30	0.61
1:E:374:ALA:HA	1:E:377:MET:CE	2.34	0.58
1:F:377:MET:HE1	1:F:411:LEU:HA	1.85	0.57
1:F:374:ALA:HA	1:F:377:MET:CE	2.35	0.56
1:E:135:LYS:NZ	1:F:257:ASP:OD2	2.37	0.56
1:D:446:ASP:OD1	1:D:453:ARG:NH1	2.38	0.55
1:E:377:MET:HE1	1:E:411:LEU:HA	1.89	0.55
1:A:257:ASP:OD2	1:C:135:LYS:NZ	2.37	0.54
1:D:112:ASN:ND2	2:F:500:CAP:O7	2.39	0.54
1:F:443:GLN:H	1:F:443:GLN:CD	2.13	0.51
1:E:63:ASP:OD1	1:E:66:ARG:NH1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:145:LYS:HG3	1:B:155:VAL:HB	1.94	0.48
1:B:54:THR:OG1	1:B:55:ASN:N	2.45	0.48
1:B:146:ASP:O	1:B:150:VAL:HG23	2.14	0.47
1:A:374:ALA:HA	1:A:377:MET:HE3	1.95	0.47
1:C:110:ILE:HG23	1:C:110:ILE:O	2.14	0.47
1:A:26:CYS:SG	1:A:124:MET:CE	3.03	0.47
1:F:381:PHE:HB3	1:F:418:TRP:CE2	2.49	0.47
1:D:237:ASP:OD2	1:F:278:ARG:NH1	2.46	0.47
1:F:54:THR:OG1	1:F:55:ASN:N	2.45	0.47
1:D:47:VAL:HG21	1:D:72:VAL:HG23	1.97	0.47
1:B:173:ARG:HB3	1:B:174:PRO:HD2	1.98	0.46
1:F:47:VAL:HG21	1:F:72:VAL:HG23	1.98	0.46
1:B:175:GLN:HB3	1:B:176:PRO:HD3	1.98	0.45
1:E:54:THR:OG1	1:E:55:ASN:N	2.49	0.45
1:B:47:VAL:HG21	1:B:72:VAL:HG23	1.98	0.45
1:B:250:GLU:OE1	1:F:206:LYS:NZ	2.28	0.45
1:E:110:ILE:HG23	1:E:110:ILE:O	2.16	0.45
1:E:47:VAL:HG21	1:E:72:VAL:HG23	1.99	0.45
1:B:110:ILE:O	1:B:110:ILE:HG23	2.16	0.44
1:A:47:VAL:HG21	1:A:72:VAL:CG2	2.48	0.44
1:D:110:ILE:HG23	1:D:110:ILE:O	2.17	0.44
1:C:206:LYS:NZ	1:F:250:GLU:OE1	2.40	0.44
1:F:110:ILE:O	1:F:110:ILE:HG23	2.18	0.43
1:F:120:GLU:O	1:F:302:ARG:NH1	2.48	0.43
1:A:110:ILE:HG23	1:A:110:ILE:O	2.18	0.43
1:B:52:THR:OG1	1:B:69:ASP:OD1	2.24	0.42
1:D:54:THR:HG23	1:D:56:VAL:H	1.84	0.42
1:C:446:ASP:OD1	1:C:453:ARG:NH1	2.53	0.42
1:C:47:VAL:HG21	1:C:72:VAL:HG23	2.02	0.42
1:A:47:VAL:HG21	1:A:72:VAL:HG23	2.02	0.42
1:D:54:THR:OG1	1:D:55:ASN:N	2.50	0.42
1:E:173:ARG:HB3	1:E:174:PRO:HD2	2.02	0.41
1:C:47:VAL:HG21	1:C:72:VAL:CG2	2.50	0.41
1:F:166:ILE:HD11	1:F:191:ILE:HG21	2.02	0.41
1:C:54:THR:HG23	1:C:56:VAL:H	1.86	0.41
1:E:47:VAL:HG21	1:E:72:VAL:CG2	2.50	0.41
1:B:173:ARG:HB3	1:B:174:PRO:CD	2.50	0.41
1:D:47:VAL:HG21	1:D:72:VAL:CG2	2.50	0.41
1:A:240:GLU:OE2	1:A:244:ARG:NE	2.50	0.40
1:F:126:ASP:OD1	1:F:127:PHE:N	2.53	0.40
1:A:173:ARG:HB3	1:A:174:PRO:HD2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:448:LEU:N	1:B:448:LEU:HD12	2.36	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	453/461 (98%)	436 (96%)	16 (4%)	1 (0%)	52 74
1	B	454/461 (98%)	436 (96%)	18 (4%)	0	100 100
1	C	453/461 (98%)	439 (97%)	14 (3%)	0	100 100
1	D	452/461 (98%)	439 (97%)	13 (3%)	0	100 100
1	E	454/461 (98%)	438 (96%)	16 (4%)	0	100 100
1	F	449/461 (97%)	434 (97%)	15 (3%)	0	100 100
All	All	2715/2766 (98%)	2622 (97%)	92 (3%)	1 (0%)	100 100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	450	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	342/355 (96%)	341 (100%)	1 (0%)	94	98
1	B	343/355 (97%)	342 (100%)	1 (0%)	94	98
1	C	344/355 (97%)	343 (100%)	1 (0%)	94	98
1	D	343/355 (97%)	342 (100%)	1 (0%)	94	98
1	E	346/355 (98%)	345 (100%)	1 (0%)	94	98
1	F	333/355 (94%)	332 (100%)	1 (0%)	94	98
All	All	2051/2130 (96%)	2045 (100%)	6 (0%)	94	98

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	287	TYR
1	B	287	TYR
1	C	287	TYR
1	D	287	TYR
1	E	287	TYR
1	F	287	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

6 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	KCX	A	192	1,3	9,11,12	0.67	0	8,12,14	1.24	2 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	KCX	B	192	1,3	9,11,12	0.69	0	8,12,14	0.98	1 (12%)
1	KCX	C	192	1,3	9,11,12	0.78	0	8,12,14	0.98	1 (12%)
1	KCX	D	192	1,3	9,11,12	0.67	0	8,12,14	0.99	1 (12%)
1	KCX	E	192	1,3	9,11,12	0.67	0	8,12,14	1.04	1 (12%)
1	KCX	F	192	1,3	9,11,12	0.69	0	8,12,14	1.10	1 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KCX	A	192	1,3	-	0/8/10/12	0/0/0/0
1	KCX	B	192	1,3	-	0/8/10/12	0/0/0/0
1	KCX	C	192	1,3	-	0/8/10/12	0/0/0/0
1	KCX	D	192	1,3	-	0/8/10/12	0/0/0/0
1	KCX	E	192	1,3	-	0/8/10/12	0/0/0/0
1	KCX	F	192	1,3	-	0/8/10/12	0/0/0/0

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	192	KCX	O-C-CA	-2.48	119.07	125.72
1	A	192	KCX	O-C-CA	-2.25	119.68	125.72
1	D	192	KCX	O-C-CA	-2.24	119.70	125.72
1	E	192	KCX	O-C-CA	-2.24	119.70	125.72
1	F	192	KCX	O-C-CA	-2.13	120.00	125.72
1	C	192	KCX	O-C-CA	-2.12	120.04	125.72
1	A	192	KCX	CE-NZ-CX	2.29	125.13	121.92

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	CAP	A	500	3	14,20,20	1.07	0	16,31,31	1.88	6 (37%)
2	CAP	B	500	3	14,20,20	1.13	0	16,31,31	1.92	6 (37%)
2	CAP	C	500	3	14,20,20	1.08	0	16,31,31	1.85	6 (37%)
2	CAP	D	500	3	14,20,20	1.11	0	16,31,31	1.92	7 (43%)
2	CAP	E	500	3	14,20,20	1.16	0	16,31,31	2.00	8 (50%)
2	CAP	F	500	3	14,20,20	1.13	0	16,31,31	1.96	7 (43%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CAP	A	500	3	-	0/23/29/29	0/0/0/0
2	CAP	B	500	3	-	0/23/29/29	0/0/0/0
2	CAP	C	500	3	-	0/23/29/29	0/0/0/0
2	CAP	D	500	3	-	0/23/29/29	0/0/0/0
2	CAP	E	500	3	-	0/23/29/29	0/0/0/0
2	CAP	F	500	3	-	0/23/29/29	0/0/0/0

There are no bond length outliers.

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	500	CAP	O5P-P2-O4P	-2.23	103.36	110.63
2	F	500	CAP	O5P-P2-O4P	-2.16	103.58	110.63
2	E	500	CAP	O2P-P1-O1P	-2.12	103.71	110.63
2	D	500	CAP	O6P-P2-O4P	-2.01	104.07	110.63
2	F	500	CAP	O6P-P2-O5	2.26	113.31	106.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	500	CAP	O3P-P1-O1	2.33	113.53	106.72
2	C	500	CAP	O6P-P2-O5	2.35	113.59	106.72
2	A	500	CAP	O3P-P1-O1	2.37	113.65	106.72
2	C	500	CAP	O3P-P1-O1	2.38	113.67	106.72
2	E	500	CAP	O3P-P1-O1	2.38	113.68	106.72
2	E	500	CAP	O2P-P1-O1	2.39	113.69	106.72
2	A	500	CAP	O6P-P2-O5	2.39	113.70	106.72
2	B	500	CAP	O5P-P2-O5	2.40	113.73	106.72
2	A	500	CAP	O5P-P2-O5	2.41	113.75	106.72
2	B	500	CAP	O2P-P1-O1	2.44	113.86	106.72
2	C	500	CAP	O2P-P1-O1	2.51	114.05	106.72
2	E	500	CAP	O5P-P2-O5	2.52	114.09	106.72
2	D	500	CAP	O2P-P1-O1	2.54	114.14	106.72
2	F	500	CAP	O2P-P1-O1	2.55	114.18	106.72
2	C	500	CAP	O5P-P2-O5	2.58	114.27	106.72
2	D	500	CAP	O6P-P2-O5	2.62	114.38	106.72
2	A	500	CAP	O2P-P1-O1	2.62	114.38	106.72
2	C	500	CAP	O5-P2-O4P	2.64	113.73	107.08
2	D	500	CAP	O1-P1-O1P	2.65	113.76	107.08
2	F	500	CAP	O3P-P1-O1	2.67	114.52	106.72
2	B	500	CAP	O6P-P2-O5	2.68	114.53	106.72
2	D	500	CAP	O5-P2-O4P	2.68	113.83	107.08
2	D	500	CAP	O5P-P2-O5	2.71	114.64	106.72
2	D	500	CAP	O3P-P1-O1	2.71	114.64	106.72
2	F	500	CAP	O1-P1-O1P	2.73	113.96	107.08
2	A	500	CAP	O1-P1-O1P	2.76	114.03	107.08
2	B	500	CAP	O1-P1-O1P	2.87	114.30	107.08
2	F	500	CAP	O5-P2-O4P	2.88	114.33	107.08
2	A	500	CAP	O5-P2-O4P	2.90	114.38	107.08
2	E	500	CAP	O5-P2-O4P	2.91	114.41	107.08
2	C	500	CAP	O1-P1-O1P	2.93	114.45	107.08
2	E	500	CAP	O6P-P2-O5	2.96	115.35	106.72
2	F	500	CAP	O5P-P2-O5	2.97	115.38	106.72
2	B	500	CAP	O5-P2-O4P	2.98	114.57	107.08
2	E	500	CAP	O1-P1-O1P	3.09	114.86	107.08

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	500	CAP	1	0

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	455/461 (98%)	0.21	7 (1%)	76	80	24, 44, 74, 104	0
1	B	456/461 (98%)	0.14	5 (1%)	82	85	26, 43, 69, 95	0
1	C	455/461 (98%)	0.14	5 (1%)	82	85	24, 40, 61, 89	0
1	D	454/461 (98%)	0.23	14 (3%)	52	58	25, 44, 67, 86	0
1	E	456/461 (98%)	0.14	5 (1%)	82	85	22, 41, 64, 82	0
1	F	453/461 (98%)	0.24	11 (2%)	62	67	24, 46, 77, 108	0
All	All	2729/2766 (98%)	0.18	47 (1%)	73	77	22, 43, 70, 108	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	455	LYS	4.1
1	C	428	ALA	3.3
1	F	327	GLY	3.0
1	B	404	GLY	3.0
1	F	435	ALA	2.9
1	E	425	VAL	2.9
1	D	40	ILE	2.9
1	F	421	GLY	2.9
1	D	75	VAL	2.8
1	F	446	ASP	2.8
1	D	20	GLY	2.7
1	A	456	LEU	2.7
1	F	22	ARG	2.7
1	D	129	VAL	2.7
1	F	422	ALA	2.6
1	D	448	LEU	2.6
1	E	422	ALA	2.5
1	C	90	LEU	2.4
1	B	425	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	425	VAL	2.4
1	E	81	LEU	2.4
1	D	408	ALA	2.4
1	B	454	ALA	2.4
1	C	440	SER	2.3
1	E	452	TRP	2.3
1	F	417	CYS	2.3
1	D	81	LEU	2.3
1	D	180	ALA	2.3
1	A	417	CYS	2.3
1	D	344	ILE	2.3
1	A	420	GLN	2.2
1	F	44	ALA	2.2
1	D	442	PRO	2.2
1	D	405	ALA	2.2
1	F	454	ALA	2.2
1	A	450	PRO	2.2
1	B	449	TYR	2.2
1	C	371	GLY	2.2
1	D	156	ILE	2.2
1	F	430	ASP	2.2
1	E	443	GLN	2.2
1	B	12	LEU	2.2
1	C	405	ALA	2.1
1	A	374	ALA	2.1
1	D	404	GLY	2.1
1	F	447	LYS	2.0
1	A	449	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
1	KCX	D	192	12/13	0.91	0.13	-	42,48,55,58	0
1	KCX	F	192	12/13	0.90	0.15	-	35,37,44,44	0
1	KCX	B	192	12/13	0.91	0.16	-	33,36,41,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
1	KCX	E	192	12/13	0.91	0.15	-	29,36,41,46	0
1	KCX	C	192	12/13	0.88	0.14	-	32,40,45,50	0
1	KCX	A	192	12/13	0.91	0.13	-	35,40,44,46	0

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	CAP	E	500	21/21	0.95	0.14	-0.02	26,38,43,43	0
2	CAP	F	500	21/21	0.90	0.16	-0.06	45,48,61,62	0
2	CAP	B	500	21/21	0.95	0.14	-0.15	30,34,37,39	0
2	CAP	A	500	21/21	0.91	0.16	-0.19	47,54,57,57	0
2	CAP	D	500	21/21	0.95	0.13	-0.70	50,51,53,53	0
2	CAP	C	500	21/21	0.95	0.14	-1.13	34,47,48,49	0
3	MG	A	501	1/1	0.77	0.13	-1.65	50,50,50,50	0
3	MG	D	501	1/1	0.89	0.08	-2.25	54,54,54,54	0
3	MG	F	501	1/1	0.97	0.10	-2.35	35,35,35,35	0
3	MG	B	501	1/1	0.91	0.07	-3.21	39,39,39,39	0
3	MG	E	501	1/1	0.93	0.06	-3.92	30,30,30,30	0
3	MG	C	501	1/1	0.94	0.07	-4.07	35,35,35,35	0

6.5 Other polymers (i)

There are no such residues in this entry.