Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 01:53 PM GMT

PDB ID	:	3VCM
Title	:	Crystal structure of human prorenin
Authors	:	Morales, R.; Watier, Y.; Bocskei, Z.
Deposited on	:	2012-01-04
Resolution	:	2.93 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:

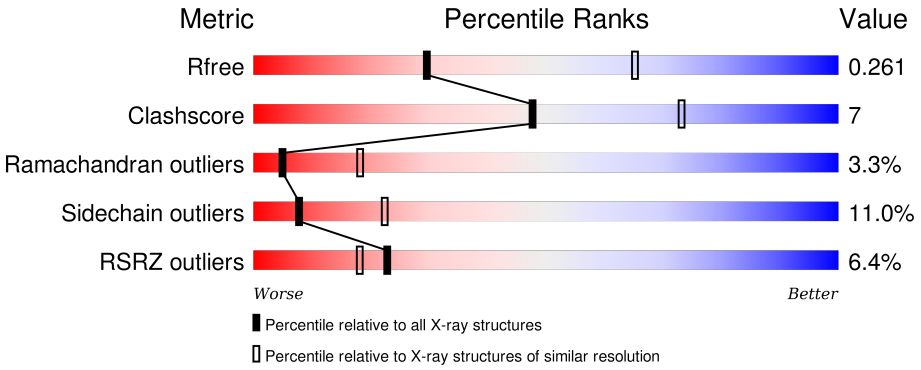
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.93 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	2057 (2.98-2.90)
Clashscore	102246	2308 (2.98-2.90)
Ramachandran outliers	100387	2245 (2.98-2.90)
Sidechain outliers	100360	2247 (2.98-2.90)
RSRZ outliers	91569	2065 (2.98-2.90)

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	335	10% 74% 21%
1	B	335	2% 77% 19%
2	P	43	5% 58% 16% 12% 12%
2	Q	43	5% 35% 19% 5% 42%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5738 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 prorenin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	335	Total	C	N	O	S	0	0	0
			2583	1652	417	500	14			
1	B	325	Total	C	N	O	S	0	0	0
			2514	1610	406	484	14			

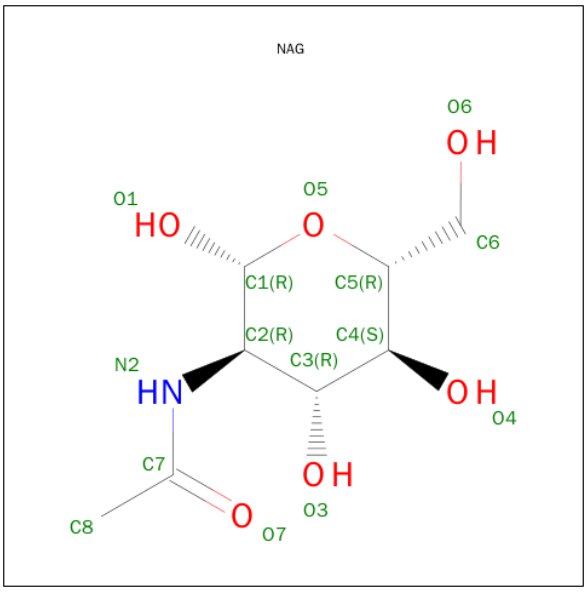
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	SER	DELETION	UNP P00797
A	?	-	GLU	DELETION	UNP P00797
A	?	-	ASN	DELETION	UNP P00797
A	?	-	SER	DELETION	UNP P00797
A	?	-	GLN	DELETION	UNP P00797
B	?	-	SER	DELETION	UNP P00797
B	?	-	GLU	DELETION	UNP P00797
B	?	-	ASN	DELETION	UNP P00797
B	?	-	SER	DELETION	UNP P00797
B	?	-	GLN	DELETION	UNP P00797

- Molecule 2 is a protein called prorenin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	38	Total	C	N	O	S	0	0	0
			319	202	62	52	3			
2	Q	25	Total	C	N	O	S	0	0	0
			211	134	40	35	2			

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 14 8 1 5	0	0

- Molecule 4 is water.

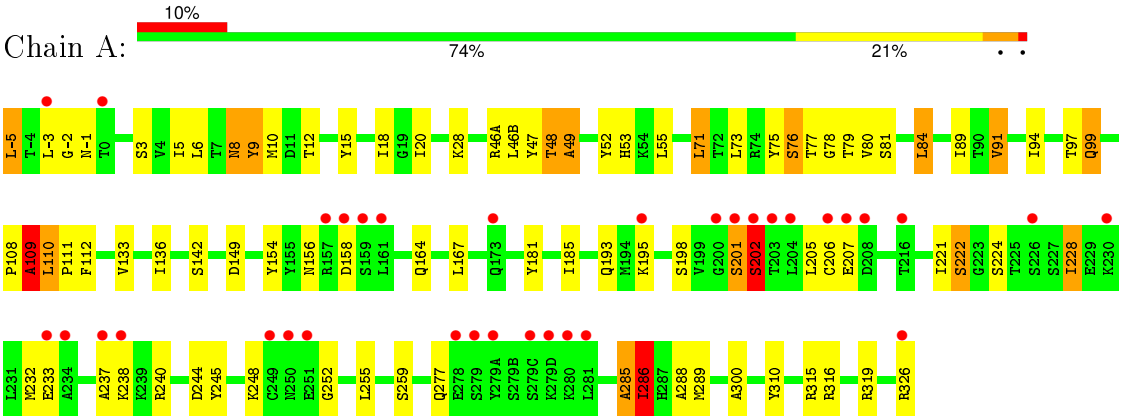
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	36	Total O 36 36	0	0
4	B	49	Total O 49 49	0	0
4	P	8	Total O 8 8	0	0
4	Q	4	Total O 4 4	0	0

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.

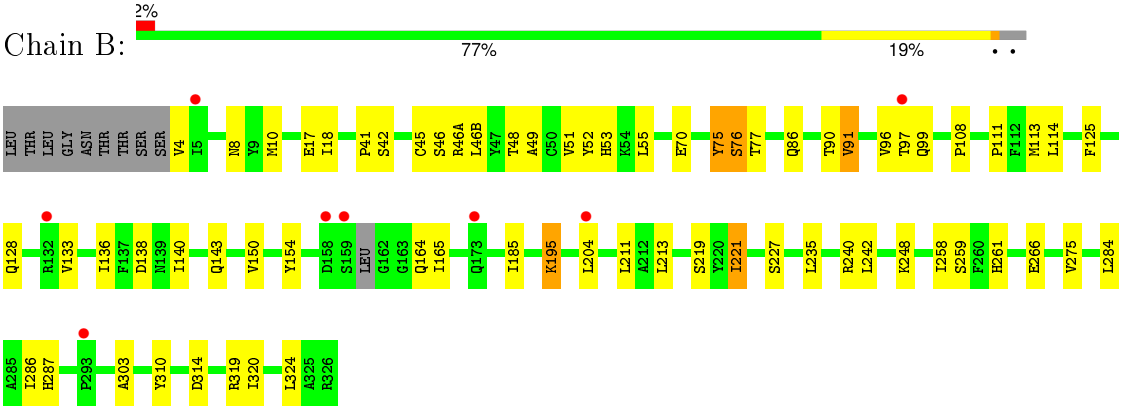
- Molecule 1: prorenin

Chain A:



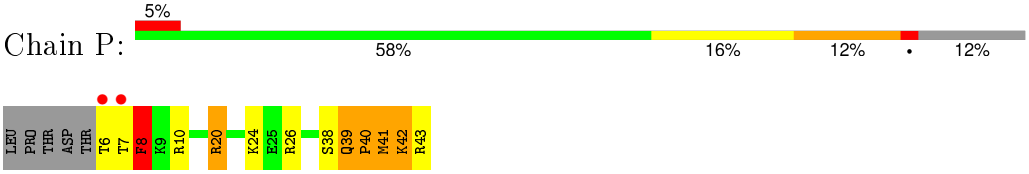
- Molecule 1: prorenin

Chain B:



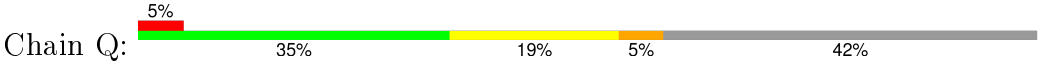
- Molecule 2: prorenin

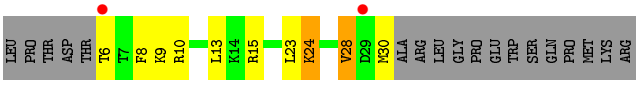
Chain P:



- Molecule 2: prorenin

Chain Q:




LEU
PRO
THR
ASP
THR
T6
T7
F8
K9
R10
L13
K14
R15
L23
K24
V28
D29
MSO
ALA
ARG
LEU
GLY
PRO
GLU
TRP
SER
GLN
PRO
MET
LYS
ARG

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, α, β, γ	104.42Å 104.42Å 237.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.53 – 2.93 36.48 – 2.93	Depositor EDS
% Data completeness (in resolution range)	100.0 (36.53-2.93) 100.0 (36.48-2.93)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.54 (at 2.95Å)	Xtriage
Refinement program	BUSTER 2.9.7	Depositor
R, R_{free}	0.212 , 0.248 0.222 , 0.261	Depositor DCC
R_{free} test set	1476 reflections (5.35%)	DCC
Wilson B-factor (Å^2)	47.6	Xtriage
Anisotropy	0.623	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 47.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 29067 reflections	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	5738	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 4.40% 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

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

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	0.39	0/2640	0.71	2/3576 (0.1%)
1	B	0.39	0/2571	0.70	1/3481 (0.0%)
2	P	0.48	0/325	0.87	0/431
2	Q	0.45	0/213	0.88	0/280
All	All	0.40	0/5749	0.72	3/7768 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	75	TYR	C-N-CA	7.59	140.67	121.70
1	A	201	SER	C-N-CA	7.54	140.56	121.70
1	A	109	ALA	C-N-CA	5.99	136.69	121.70

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	2583	0	2522	44	0
1	B	2514	0	2447	33	0
2	P	319	0	339	11	0
2	Q	211	0	229	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	14	0	13	0	0
4	A	36	0	0	0	0
4	B	49	0	0	0	0
4	P	8	0	0	0	0
4	Q	4	0	0	0	0
All	All	5738	0	5550	83	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 7.

All (83) 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:8:ASN:HD21	1:B:10:MET:HG2	1.27	0.97
2:P:20:ARG:HG3	2:P:20:ARG:HH11	1.33	0.94
1:B:75:TYR:HB3	1:B:76:SER:HB2	1.55	0.88
1:B:76:SER:N	1:B:77:THR:HA	1.94	0.82
1:B:240:ARG:C	1:B:242:LEU:HA	2.03	0.80
1:A:109:ALA:HB3	1:A:110:LEU:HB3	1.71	0.73
1:B:49:ALA:HA	1:B:51:VAL:H	1.56	0.71
1:B:42:SER:O	1:B:45:CYS:HB2	1.91	0.70
2:Q:23:LEU:O	2:Q:24:LYS:HB2	1.91	0.70
2:P:20:ARG:HG3	2:P:20:ARG:NH1	2.01	0.69
1:A:18:ILE:HG22	1:A:91:VAL:HG13	1.75	0.69
1:A:185:ILE:HD11	1:A:193:GLN:HB2	1.74	0.68
1:A:201:SER:HB3	1:A:202:SER:HB2	1.76	0.67
1:B:18:ILE:HG22	1:B:91:VAL:HG13	1.80	0.64
1:A:232:MET:HG3	1:A:237:ALA:HB3	1.82	0.60
1:B:18:ILE:HG22	1:B:91:VAL:CG1	2.33	0.59
1:B:150:VAL:HG12	1:B:314:ASP:HA	1.84	0.59
1:A:76:SER:HB2	2:P:39:GLN:HG2	1.85	0.58
1:A:164:GLN:HE22	2:P:10:ARG:HH11	1.49	0.58
1:A:222:SER:HB3	1:A:300:ALA:HB3	1.85	0.56
1:B:76:SER:H	1:B:77:THR:HA	1.68	0.55
2:P:39:GLN:O	2:P:41:MET:N	2.39	0.55
1:A:285:ALA:HA	1:A:286:ILE:C	2.28	0.54
1:A:73:LEU:HB2	1:A:80:VAL:HB	1.90	0.54
1:A:285:ALA:HA	1:A:286:ILE:O	2.07	0.54
1:A:80:VAL:HG22	1:A:108:PRO:HD3	1.89	0.54
1:B:125:PHE:H	1:B:128:GLN:HE21	1.54	0.53
2:P:20:ARG:CG	2:P:20:ARG:HH11	2.13	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:46(A):ARG:O	1:B:46(B):LEU:CB	2.57	0.52
1:A:232:MET:HG2	1:A:245:TYR:CD1	2.46	0.51
2:P:7:THR:O	2:P:8:PHE:HB2	2.11	0.51
1:A:154:TYR:HB2	1:A:310:TYR:CE2	2.46	0.51
1:B:164:GLN:HE22	2:Q:10:ARG:HH11	1.60	0.50
1:B:41:PRO:HB2	1:B:55:LEU:HD23	1.94	0.49
1:A:9:TYR:HA	1:A:12:THR:OG1	2.13	0.49
1:A:97:THR:O	1:A:99:GLN:HA	2.12	0.48
2:Q:6:THR:HA	2:Q:8:PHE:H	1.78	0.48
1:A:110:LEU:HD22	1:B:51:VAL:HG21	1.96	0.47
1:A:77:THR:HA	1:A:78:GLY:HA2	1.59	0.47
1:A:110:LEU:HA	1:B:52:TYR:OH	2.14	0.47
1:B:8:ASN:ND2	1:B:10:MET:HG2	2.11	0.47
1:A:8:ASN:HA	2:P:42:LYS:HB2	1.97	0.47
1:A:49:ALA:HA	1:A:52:TYR:CD2	2.50	0.47
1:B:275:VAL:HG22	1:B:284:LEU:HD22	1.96	0.46
1:A:48:THR:O	1:A:49:ALA:HB3	2.15	0.46
1:A:71:LEU:HD22	1:A:84:LEU:HD13	1.96	0.46
1:B:108:PRO:HB2	1:B:111:PRO:HD2	1.96	0.46
1:A:84:LEU:HD21	1:A:133:VAL:HG11	1.97	0.46
1:A:99:GLN:HG3	1:A:136:ILE:HD12	1.97	0.45
1:A:53:HIS:HE1	1:A:112:PHE:O	1.99	0.45
1:A:20:ILE:HG12	1:A:89:ILE:HG12	1.97	0.45
1:A:221:ILE:O	1:A:286:ILE:HA	2.16	0.45
1:B:154:TYR:HB2	1:B:310:TYR:HE2	1.82	0.45
1:A:47:TYR:CD2	1:B:48:THR:HG22	2.52	0.45
1:A:201:SER:CA	1:A:202:SER:HB2	2.47	0.44
1:A:252:GLY:HA3	1:A:277:GLN:HE22	1.82	0.44
1:A:181:TYR:HB3	1:A:319:ARG:HD2	1.98	0.44
1:B:259:SER:HB2	1:B:266:GLU:HG2	1.99	0.44
1:A:201:SER:CB	1:A:202:SER:HB2	2.45	0.44
2:Q:23:LEU:HD22	2:Q:28:VAL:HG21	1.99	0.43
1:A:109:ALA:CB	1:A:110:LEU:HB3	2.46	0.43
1:A:164:GLN:HE22	2:P:10:ARG:HD3	1.84	0.43
1:A:149:ASP:HB2	1:A:316:ARG:HB2	2.01	0.43
1:B:195:LYS:HB2	1:B:261:HIS:HD2	1.84	0.43
1:A:75:TYR:CG	2:P:41:MET:HG3	2.53	0.43
1:B:195:LYS:HB2	1:B:261:HIS:CD2	2.54	0.42
2:P:39:GLN:O	2:P:40:PRO:C	2.57	0.42
1:B:136:ILE:O	1:B:140:ILE:HG13	2.20	0.42
1:A:110:LEU:HA	1:A:111:PRO:HA	1.86	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:TYR:CE2	1:A:28:LYS:HD3	2.55	0.42
1:B:154:TYR:HB2	1:B:310:TYR:CE2	2.55	0.42
1:A:94:ILE:HD12	1:A:167:LEU:HD13	2.01	0.42
1:A:-5:LEU:N	1:A:5:ILE:O	2.54	0.41
1:A:228:ILE:O	1:A:232:MET:HB2	2.20	0.41
1:B:314:ASP:HB3	1:B:319:ARG:HG2	2.01	0.41
1:B:46(A):ARG:HB3	1:B:51:VAL:HG12	2.02	0.41
1:A:198:SER:HB2	1:A:259:SER:HB2	2.03	0.41
1:B:219:SER:HA	1:B:303:ALA:HB3	2.02	0.41
1:B:235:LEU:HD11	1:B:258:ILE:HD11	2.02	0.41
1:B:221:ILE:HG22	1:B:286:ILE:HG23	2.03	0.40
1:B:53:HIS:HE1	1:B:113:MET:O	2.04	0.40
1:A:154:TYR:HB2	1:A:310:TYR:HE2	1.84	0.40
1:B:165:ILE:HD11	2:Q:13:LEU:HD21	2.04	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	327/335 (98%)	293 (90%)	19 (6%)	15 (5%)	3 10
1	B	317/335 (95%)	295 (93%)	21 (7%)	1 (0%)	46 78
2	P	36/43 (84%)	30 (83%)	1 (3%)	5 (14%)	0 0
2	Q	23/43 (54%)	20 (87%)	1 (4%)	2 (9%)	1 2
All	All	703/756 (93%)	638 (91%)	42 (6%)	23 (3%)	5 18

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	-3	LEU

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Mol	Chain	Res	Type
1	A	-2	GLY
1	A	-1	ASN
1	A	8	ASN
1	A	202	SER
1	A	285	ALA
1	A	288	ALA
1	B	76	SER
2	P	40	PRO
2	P	41	MET
1	A	286	ILE
2	P	8	PHE
2	P	38	SER
2	Q	24	LYS
1	A	49	ALA
1	A	109	ALA
2	P	42	LYS
1	A	110	LEU
1	A	224	SER
1	A	46(B)	LEU
1	A	289	MET
2	Q	28	VAL
1	A	156	ASN

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	285/285 (100%)	252 (88%)	33 (12%)	7 20
1	B	276/285 (97%)	251 (91%)	25 (9%)	12 33
2	P	35/40 (88%)	28 (80%)	7 (20%)	1 4
2	Q	24/40 (60%)	21 (88%)	3 (12%)	6 16
All	All	620/650 (95%)	552 (89%)	68 (11%)	8 22

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-5	LEU
1	A	3	SER
1	A	6	LEU
1	A	9	TYR
1	A	10	MET
1	A	46(A)	ARG
1	A	48	THR
1	A	55	LEU
1	A	71	LEU
1	A	76	SER
1	A	79	THR
1	A	81	SER
1	A	84	LEU
1	A	91	VAL
1	A	99	GLN
1	A	142	SER
1	A	158	ASP
1	A	195	LYS
1	A	202	SER
1	A	205	LEU
1	A	206	CYS
1	A	207	GLU
1	A	222	SER
1	A	228	ILE
1	A	233	GLU
1	A	238	LYS
1	A	240	ARG
1	A	244	ASP
1	A	248	LYS
1	A	255	LEU
1	A	286	ILE
1	A	315	ARG
1	A	326	ARG
1	B	4	VAL
1	B	17	GLU
1	B	46	SER
1	B	70	GLU
1	B	86	GLN
1	B	90	THR
1	B	91	VAL
1	B	96	VAL
1	B	97	THR
1	B	99	GLN

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Mol	Chain	Res	Type
1	B	114	LEU
1	B	133	VAL
1	B	138	ASP
1	B	143	GLN
1	B	185	ILE
1	B	195	LYS
1	B	204	LEU
1	B	211	LEU
1	B	213	LEU
1	B	221	ILE
1	B	227	SER
1	B	248	LYS
1	B	287	HIS
1	B	320	ILE
1	B	324	LEU
2	P	6	THR
2	P	8	PHE
2	P	20	ARG
2	P	24	LYS
2	P	26	ARG
2	P	39	GLN
2	P	43	ARG
2	Q	9	LYS
2	Q	15	ARG
2	Q	30	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	164	GLN
1	A	261	HIS
1	A	277	GLN
1	A	318	ASN
1	B	8	ASN
1	B	13	GLN
1	B	53	HIS
1	B	67	ASN
1	B	128	GLN
1	B	143	GLN
1	B	164	GLN
1	B	183	ASN
1	B	261	HIS

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Mol	Chain	Res	Type
1	B	318	ASN
2	P	39	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)

1 ligand is 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	$\#\|Z\| > 2$
3	NAG	A	401	1	14,14,15	1.18	1 (7%)	15,19,21	1.11	1 (6%)

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
3	NAG	A	401	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	NAG	C1-C2	2.55	1.56	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	401	NAG	C1-O5-C5	2.88	115.90	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	335/335 (100%)	0.28	34 (10%) 9 6	23, 47, 87, 103	0
1	B	325/335 (97%)	-0.02	8 (2%) 61 58	24, 42, 63, 98	0
2	P	38/43 (88%)	0.16	2 (5%) 30 26	31, 50, 75, 80	0
2	Q	25/43 (58%)	0.13	2 (8%) 15 11	33, 47, 73, 83	0
All	All	723/756 (95%)	0.13	46 (6%) 23 18	23, 45, 79, 103	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	279(D)	LYS	5.4
1	B	158	ASP	5.3
1	A	203	THR	5.1
1	A	202	SER	4.6
2	P	6	THR	4.5
1	A	279	SER	4.0
1	A	279(A)	TYR	3.7
1	A	201	SER	3.6
1	A	158	ASP	3.3
1	A	159	SER	3.0
1	A	249	CYS	3.0
1	A	237	ALA	2.9
1	A	250	ASN	2.9
1	A	280	LYS	2.9
1	B	159	SER	2.9
2	Q	6	THR	2.9
1	A	279(C)	SER	2.8
1	A	251	GLU	2.8
2	Q	29	ASP	2.7
1	A	200	GLY	2.7
1	A	278	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	157	ARG	2.5
1	A	281	LEU	2.5
1	A	208	ASP	2.4
1	A	207	GLU	2.4
1	A	173	GLN	2.4
1	A	0	THR	2.3
1	A	230	LYS	2.3
1	A	326	ARG	2.3
2	P	7	THR	2.3
1	A	-3	LEU	2.3
1	B	97	THR	2.2
1	A	234	ALA	2.2
1	A	238	LYS	2.2
1	A	226	SER	2.2
1	A	216	THR	2.2
1	A	206	CYS	2.2
1	B	173	GLN	2.2
1	A	204	LEU	2.1
1	B	204	LEU	2.1
1	A	161	LEU	2.0
1	B	5	ILE	2.0
1	B	132	ARG	2.0
1	B	293	PRO	2.0
1	A	195	LYS	2.0
1	A	233	GLU	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)

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
3	NAG	A	401	14/15	0.90	0.21	0.63	50,55,58,59	0

6.5 Other polymers (i)

There are no such residues in this entry.