Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 08:12 AM GMT

PDB ID	:	3DPU
Title	:	RocCOR domain tandem of Rab family protein (Roco)
Authors	:	Gotthardt, K.; Weyand, M.; Kortholt, A.; Van Haastert, P.J.M.; Wittinghofer, A.
Deposited on	:	2008-07-09
Resolution	:	2.90 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:

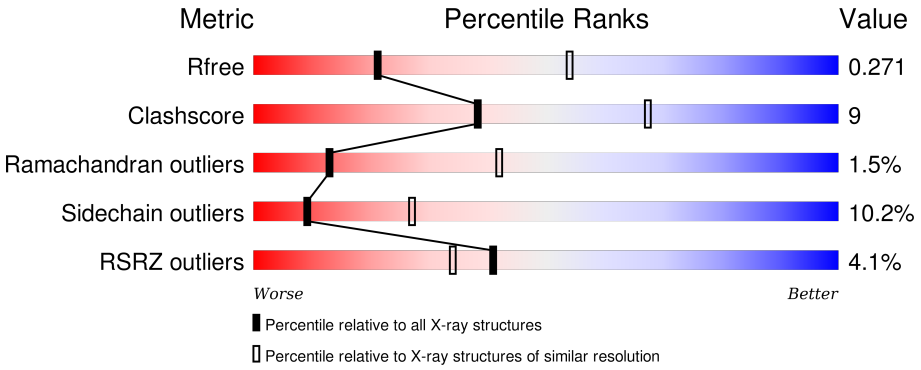
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.90 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	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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	535	4% 66% 21% • 9%
1	B	535	2% 47% 12% • 39%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 6235 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 Rab family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	485	Total	C	N	O	S	0	0	0
			3695	2379	603	696	17			
1	B	328	Total	C	N	O	S	0	0	0
			2540	1640	414	475	11			

There are 2 discrepancies between the modelled and reference sequences:

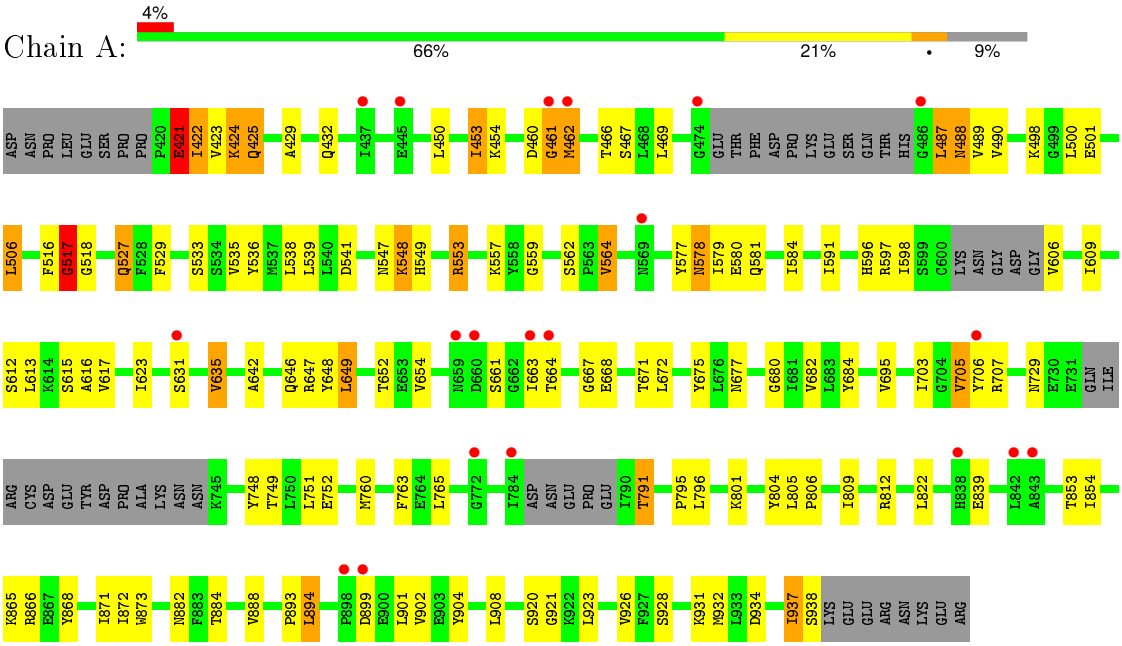
Chain	Residue	Modelled	Actual	Comment	Reference
A	917	ARG	GLU	ENGINEERED	UNP Q8KC98
B	917	ARG	GLU	ENGINEERED	UNP Q8KC98

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.

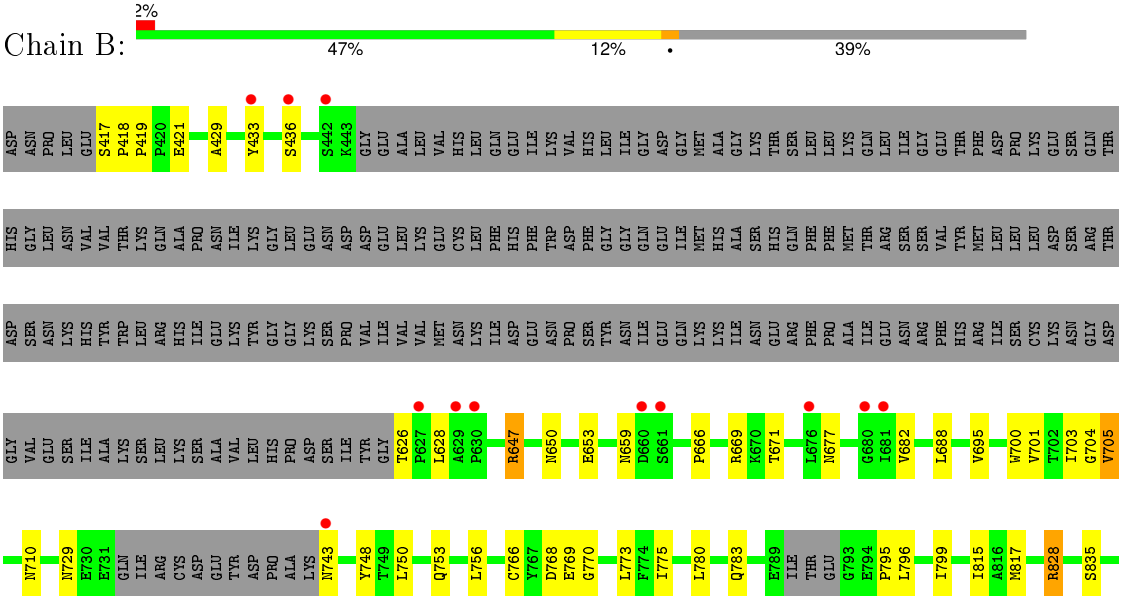
- Molecule 1: Rab family protein

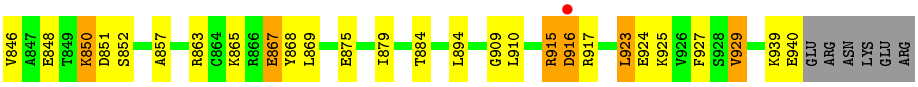
Chain A:



- Molecule 1: Rab family protein

Chain B:




V846
A847
E848
T849
K850
D851
S852
A857
R863
C864
K865
R866
E867
Y868
L869
E875
I879
T884
L894
G909
L910
R915
D916
R917
L923
E924
K925
V926
F927
S928
V929
K939
E940
GLU
ARG
ASN
LYS
GLU
ARG

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	83.20Å 106.10Å 139.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.67 – 2.90 47.66 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.67-2.90) 98.5 (47.66-2.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	3.90 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.230 , 0.270 0.230 , 0.271	Depositor DCC
R_{free} test set	1374 reflections (5.26%)	DCC
Wilson B-factor (Å^2)	54.3	Xtriage
Anisotropy	0.390	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 51.1	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 27475 reflections	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	6235	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.02% 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	0.45	0/3772	0.62	2/5135 (0.0%)
1	B	0.48	0/2592	0.63	0/3527
All	All	0.46	0/6364	0.63	2/8662 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

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	506	LEU	CA-CB-CG	5.51	127.97	115.30
1	A	518	GLY	N-CA-C	-5.29	99.87	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	517	GLY	Peptide

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	3695	0	3490	78	0
1	B	2540	0	2456	36	0
All	All	6235	0	5946	111	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 9.

All (111) 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:729:ASN:HD21	1:B:748:TYR:H	1.11	0.94
1:A:631:SER:HB3	1:A:663:ILE:HD11	1.55	0.88
1:A:421:GLU:HG3	1:A:422:ILE:N	1.95	0.79
1:A:578:ASN:HD22	1:A:579:ILE:H	1.31	0.76
1:A:487:LEU:HD13	1:A:706:TYR:CE1	2.22	0.75
1:A:549:HIS:O	1:A:553:ARG:HG2	1.94	0.68
1:A:812:ARG:HH12	1:A:882:ASN:ND2	1.93	0.66
1:A:453:ILE:CD1	1:A:535:VAL:HG23	2.26	0.66
1:A:553:ARG:NH1	1:B:850:LYS:HD2	2.13	0.64
1:A:487:LEU:HG	1:A:488:ASN:N	2.13	0.62
1:B:417:SER:N	1:B:418:PRO:HD2	2.15	0.61
1:B:875:GLU:O	1:B:879:ILE:HG12	2.00	0.61
1:A:577:TYR:O	1:A:597:ARG:NH1	2.34	0.60
1:A:469:LEU:HD21	1:A:490:VAL:HG21	1.82	0.60
1:A:553:ARG:O	1:A:557:LYS:HG2	2.02	0.59
1:A:453:ILE:HD11	1:A:535:VAL:HG23	1.86	0.58
1:B:429:ALA:HA	1:B:671:THR:HG21	1.84	0.58
1:A:421:GLU:HG2	1:A:675:TYR:HE1	1.69	0.58
1:B:701:VAL:O	1:B:705:VAL:HG12	2.02	0.58
1:A:729:ASN:HD21	1:A:748:TYR:H	1.50	0.58
1:B:917:ARG:HG3	1:B:917:ARG:HH11	1.69	0.58
1:A:578:ASN:HD21	1:A:581:GLN:HE21	1.51	0.57
1:B:729:ASN:HD21	1:B:748:TYR:N	1.94	0.56
1:A:596:HIS:HE1	1:A:612:SER:OG	1.89	0.56
1:B:939:LYS:O	1:B:940:GLU:CB	2.54	0.56
1:A:804:TYR:O	1:A:806:PRO:HD3	2.07	0.54
1:A:921:GLY:O	1:B:909:GLY:HA3	2.08	0.54
1:A:453:ILE:HD12	1:A:535:VAL:HG23	1.89	0.54
1:A:642:ALA:HB1	1:A:649:LEU:HD11	1.88	0.54
1:A:763:PHE:HB3	1:A:765:LEU:HD23	1.90	0.54
1:A:937:ILE:O	1:A:938:SER:CB	2.56	0.53
1:B:682:VAL:HG13	1:B:695:VAL:HG13	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:893:PRO:HA	1:A:901:LEU:HD23	1.91	0.52
1:A:536:TYR:CE1	1:A:559:GLY:HA3	2.45	0.52
1:B:795:PRO:HA	1:B:865:LYS:HE2	1.92	0.52
1:B:769:GLU:HB2	1:B:775:ILE:HD12	1.92	0.52
1:A:462:MET:CE	1:A:462:MET:HA	2.39	0.52
1:A:462:MET:HA	1:A:462:MET:HE2	1.92	0.52
1:A:796:LEU:HB2	1:A:865:LYS:HD2	1.92	0.52
1:A:937:ILE:O	1:A:938:SER:HB3	2.11	0.51
1:A:682:VAL:HG13	1:A:695:VAL:HG13	1.93	0.51
1:A:425:GLN:N	1:A:425:GLN:HE21	2.09	0.50
1:B:417:SER:N	1:B:418:PRO:CD	2.74	0.50
1:A:873:TRP:HZ3	1:A:937:ILE:HD11	1.75	0.50
1:A:460:ASP:O	1:A:461:GLY:C	2.50	0.50
1:A:635:VAL:CG2	1:A:672:LEU:HD21	2.42	0.49
1:A:667:GLY:O	1:A:671:THR:HG23	2.11	0.49
1:A:423:VAL:C	1:A:425:GLN:H	2.16	0.49
1:A:904:TYR:CE2	1:A:908:LEU:HD11	2.47	0.49
1:A:578:ASN:HD21	1:A:581:GLN:NE2	2.10	0.49
1:B:769:GLU:HB2	1:B:775:ILE:CD1	2.43	0.49
1:A:424:LYS:C	1:A:425:GLN:HE21	2.16	0.49
1:A:801:LYS:O	1:A:888:VAL:HA	2.13	0.49
1:A:928:SER:HB3	1:A:931:LYS:HB2	1.94	0.49
1:B:863:ARG:O	1:B:867:GLU:HB2	2.12	0.48
1:A:432:GLN:OE1	1:A:668:GLU:HB3	2.12	0.48
1:B:659:ASN:OD1	1:B:669:ARG:NH2	2.46	0.48
1:B:917:ARG:HG3	1:B:917:ARG:NH1	2.28	0.48
1:A:902:VAL:HG11	1:A:932:MET:HE1	1.96	0.47
1:A:564:VAL:HG22	1:A:591:ILE:HG12	1.96	0.47
1:A:421:GLU:CG	1:A:422:ILE:N	2.72	0.47
1:B:677:ASN:HA	1:B:682:VAL:O	2.15	0.47
1:A:646:GLN:O	1:A:648:TYR:N	2.47	0.47
1:A:805:LEU:HD11	1:A:854:ILE:HD11	1.96	0.47
1:B:647:ARG:HG2	1:B:700:TRP:CD1	2.50	0.47
1:B:666:PRO:HA	1:B:669:ARG:HD2	1.96	0.46
1:A:635:VAL:HG22	1:A:672:LEU:HD21	1.97	0.46
1:A:796:LEU:HD12	1:A:865:LYS:HB3	1.98	0.45
1:A:894:LEU:HD12	1:A:932:MET:HE1	1.99	0.45
1:B:835:SER:HB2	1:B:868:TYR:CZ	2.52	0.45
1:A:579:ILE:O	1:A:581:GLN:N	2.50	0.45
1:A:703:ILE:O	1:A:707:ARG:HG3	2.16	0.45
1:B:916:ASP:HA	1:B:929:VAL:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:453:ILE:HD13	1:A:454:LYS:N	2.32	0.45
1:B:796:LEU:O	1:B:857:ALA:HA	2.17	0.45
1:B:419:PRO:HB3	1:B:626:THR:HG21	1.98	0.44
1:B:923:LEU:O	1:B:925:LYS:N	2.50	0.44
1:A:429:ALA:HA	1:A:671:THR:HG21	1.99	0.44
1:A:596:HIS:HB3	1:A:598:ILE:HD13	2.00	0.44
1:A:535:VAL:HG22	1:A:616:ALA:HB1	1.99	0.44
1:B:704:GLY:HA3	1:B:756:LEU:HD21	2.00	0.44
1:A:553:ARG:CZ	1:B:850:LYS:HD2	2.48	0.44
1:A:606:VAL:HA	1:A:609:ILE:HD12	2.00	0.44
1:A:498:LYS:O	1:A:501:GLU:CD	2.56	0.43
1:A:460:ASP:OD2	1:A:547:ASN:ND2	2.51	0.43
1:B:780:LEU:O	1:B:828:ARG:NH1	2.51	0.43
1:A:920:SER:OG	1:A:923:LEU:HB2	2.18	0.43
1:A:553:ARG:HG2	1:A:553:ARG:H	1.70	0.43
1:B:915:ARG:HG2	1:B:916:ASP:H	1.83	0.43
1:A:791:THR:HA	1:A:795:PRO:HG2	2.00	0.43
1:A:806:PRO:HB2	1:A:809:ILE:HG12	2.01	0.42
1:A:613:LEU:O	1:A:617:VAL:HG23	2.19	0.42
1:A:529:PHE:HD2	1:A:680:GLY:HA3	1.84	0.42
1:A:749:THR:N	1:A:752:GLU:OE2	2.35	0.42
1:A:529:PHE:CD2	1:A:680:GLY:HA3	2.55	0.42
1:A:868:TYR:O	1:A:871:ILE:HG13	2.20	0.42
1:A:527:GLN:H	1:A:527:GLN:HG3	1.39	0.42
1:A:516:PHE:O	1:A:517:GLY:O	2.38	0.42
1:A:791:THR:HA	1:A:795:PRO:CG	2.51	0.41
1:A:548:LYS:HD2	1:A:584:ILE:HD11	2.02	0.41
1:A:866:ARG:HD3	1:A:934:ASP:O	2.20	0.41
1:B:433:TYR:O	1:B:436:SER:HB2	2.20	0.41
1:A:868:TYR:O	1:A:872:ILE:HG12	2.21	0.41
1:B:768:ASP:OD2	1:B:770:GLY:HA3	2.21	0.41
1:B:766:CYS:HB2	1:B:775:ILE:O	2.20	0.40
1:A:677:ASN:HB2	1:A:684:TYR:HB3	2.03	0.40
1:A:705:VAL:HB	1:A:760:MET:SD	2.61	0.40
1:B:917:ARG:HA	1:B:927:PHE:O	2.21	0.40
1:B:650:ASN:OD1	1:B:653:GLU:HG3	2.21	0.40
1:A:613:LEU:HD23	1:A:613:LEU:HA	1.81	0.40
1:B:750:LEU:O	1:B:753:GLN:HG2	2.21	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	475/535 (89%)	445 (94%)	19 (4%)	11 (2%)	8 30
1	B	320/535 (60%)	305 (95%)	14 (4%)	1 (0%)	46 79
All	All	795/1070 (74%)	750 (94%)	33 (4%)	12 (2%)	13 42

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	647	ARG
1	A	822	LEU
1	A	884	THR
1	A	424	LYS
1	A	461	GLY
1	A	517	GLY
1	A	839	GLU
1	A	580	GLU
1	A	937	ILE
1	B	924	GLU
1	A	421	GLU
1	A	422	ILE

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	375/482 (78%)	338 (90%)	37 (10%)	10 29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	263/482 (55%)	235 (89%)	28 (11%)	8 25
All	All	638/964 (66%)	573 (90%)	65 (10%)	9 27

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	421	GLU
1	A	425	GLN
1	A	450	LEU
1	A	453	ILE
1	A	462	MET
1	A	466	THR
1	A	467	SER
1	A	487	LEU
1	A	488	ASN
1	A	489	VAL
1	A	500	LEU
1	A	506	LEU
1	A	527	GLN
1	A	533	SER
1	A	538	LEU
1	A	539	LEU
1	A	541	ASP
1	A	548	LYS
1	A	553	ARG
1	A	562	SER
1	A	564	VAL
1	A	578	ASN
1	A	615	SER
1	A	623	ILE
1	A	635	VAL
1	A	649	LEU
1	A	652	THR
1	A	654	VAL
1	A	661	SER
1	A	664	THR
1	A	705	VAL
1	A	751	LEU
1	A	791	THR
1	A	853	THR
1	A	894	LEU
1	A	899	ASP

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Mol	Chain	Res	Type
1	A	926	VAL
1	B	421	GLU
1	B	628	LEU
1	B	647	ARG
1	B	688	LEU
1	B	703	ILE
1	B	705	VAL
1	B	710	ASN
1	B	743	ASN
1	B	773	LEU
1	B	783	GLN
1	B	799	ILE
1	B	815	ILE
1	B	817	MET
1	B	828	ARG
1	B	846	VAL
1	B	848	GLU
1	B	850	LYS
1	B	851	ASP
1	B	852	SER
1	B	867	GLU
1	B	869	LEU
1	B	884	THR
1	B	894	LEU
1	B	910	LEU
1	B	915	ARG
1	B	916	ASP
1	B	923	LEU
1	B	929	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	425	GLN
1	A	451	GLN
1	A	547	ASN
1	A	549	HIS
1	A	574	ASN
1	A	578	ASN
1	A	596	HIS
1	A	659	ASN
1	A	729	ASN

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Mol	Chain	Res	Type
1	A	779	ASN
1	A	859	GLN
1	A	880	ASN
1	A	882	ASN
1	B	710	ASN
1	B	716	ASN
1	B	729	ASN
1	B	779	ASN
1	B	820	GLN
1	B	885	ASN

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	485/535 (90%)	0.20	20 (4%)	41	34	39, 49, 61, 70	0
1	B	328/535 (61%)	0.13	13 (3%)	42	35	38, 52, 60, 66	0
All	All	813/1070 (75%)	0.17	33 (4%)	41	34	38, 50, 61, 70	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	664	THR	4.3
1	B	627	PRO	3.1
1	A	462	MET	3.0
1	A	486	GLY	3.0
1	A	663	ILE	2.9
1	A	838	HIS	2.9
1	A	706	TYR	2.9
1	B	681	ILE	2.9
1	B	436	SER	2.8
1	A	445	GLU	2.8
1	B	680	GLY	2.8
1	A	437	ILE	2.7
1	A	461	GLY	2.6
1	A	898	PRO	2.6
1	A	784	ILE	2.6
1	B	676	LEU	2.5
1	A	842	LEU	2.5
1	B	442	SER	2.4
1	B	629	ALA	2.4
1	B	630	PRO	2.4
1	B	743	ASN	2.3
1	A	474	GLY	2.3
1	A	843	ALA	2.3
1	A	660	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	659	ASN	2.3
1	B	916	ASP	2.2
1	A	772	GLY	2.2
1	B	660	ASP	2.1
1	B	661	SER	2.1
1	A	569	ASN	2.1
1	A	899	ASP	2.0
1	B	433	TYR	2.0
1	A	631	SER	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.