

Full wwPDB X-ray Structure Validation Report (i)

Aug 19, 2023 – 11:48 PM EDT

PDB ID	:	2F8V
Title	:	Structure of full length telethonin in complex with the N-terminus of titin
Authors	:	Pinotsis, N.; Petoukhov, M.; Lange, S.; Svergun, D.; Zou, P.; Gautel, M.;
		Wilmanns, M.
Deposited on	:	2005-12-04
Resolution	:	2.75 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 https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\;DIFFRACTION$

The reported resolution of this entry is 2.75 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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	٨	001	.% ■				
	A	201		70%		22%	• •
		2.04	.% _				
1	В	201		61%		30%	7% •
			20%				
1	С	201		68%		22%	5% 5%
			15%				
1	D	201		62%		29%	5% •
			.%				
2	Т	167	28%	20%	• •	47%	



Mol	Chain	Length		Quality of chain				
			18%					
2	Y	167	31%	16% • •	47%			

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	А	601	-	-	Х	-
3	SO4	В	602	-	-	Х	-



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7409 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.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	1 A	104	Total	С	Ν	0	\mathbf{S}	0	0	0
		194	1455	911	249	294	1	0	0	0
1	р	107	Total	С	Ν	0	S	0	0	0
1	ГВ	197	1479	925	252	300	2	0	0	0
1	C	101	Total	С	Ν	0	S	0	0	0
1		191	1437	901	246	289	1	0	0	0
1	Л	102	Total	С	Ν	0	S	0	1	0
	195	1462	915	252	294	1	0		U	

• Molecule 1 is a protein called N2B-Titin Isoform.

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	197	THR	-	cloning artifact	UNP Q8WZ42
А	198	ARG	-	cloning artifact	UNP Q8WZ42
А	199	GLU	-	cloning artifact	UNP Q8WZ42
А	200	GLU	-	cloning artifact	UNP Q8WZ42
А	201	PHE	-	cloning artifact	UNP Q8WZ42
В	197	THR	-	cloning artifact	UNP Q8WZ42
В	198	ARG	-	cloning artifact	UNP Q8WZ42
В	199	GLU	-	cloning artifact	UNP Q8WZ42
В	200	GLU	-	cloning artifact	UNP Q8WZ42
В	201	PHE	-	cloning artifact	UNP Q8WZ42
С	197	THR	-	cloning artifact	UNP Q8WZ42
С	198	ARG	-	cloning artifact	UNP Q8WZ42
С	199	GLU	-	cloning artifact	UNP Q8WZ42
С	200	GLU	-	cloning artifact	UNP Q8WZ42
С	201	PHE	-	cloning artifact	UNP Q8WZ42
D	197	THR	-	cloning artifact	UNP Q8WZ42
D	198	ARG	-	cloning artifact	UNP Q8WZ42
D	199	GLU	-	cloning artifact	UNP Q8WZ42
D	200	GLU	-	cloning artifact	UNP Q8WZ42
D	201	PHE	_	cloning artifact	UNP Q8WZ42





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
0	т	00	Total	С	Ν	0	\mathbf{S}	0	1	0
2	1	00	743	458	134	147	4	0	1	0
0	V	00	Total	С	Ν	0	S	6	0	0
Z	I	00	729	447	132	146	4	0	0	0

• Molecule 2 is a protein called Telethonin.

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Т	8	SER	CYS	engineered mutation	UNP O15273
Т	15	SER	CYS	engineered mutation	UNP O15273
Т	38	SER	CYS	engineered mutation	UNP O15273
Т	57	SER	CYS	engineered mutation	UNP O15273
Т	127	SER	CYS	engineered mutation	UNP O15273
Y	8	SER	CYS	engineered mutation	UNP O15273
Y	15	SER	CYS	engineered mutation	UNP O15273
Y	38	SER	CYS	engineered mutation	UNP O15273
Y	57	SER	CYS	engineered mutation	UNP 015273
Y	127	SER	CYS	engineered mutation	UNP O15273

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0



Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	D	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	33	Total O 33 33	0	0
4	В	24	Total O 24 24	0	0
4	Т	8	Total O 8 8	0	0
4	С	10	Total O 10 10	0	0
4	D	3	Total O 3 3	0	0
4	Y	1	Total O 1 1	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: N2B-Titin Isoform





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	112.51Å 46.88Å 128.03Å	Depositor
a, b, c, α , β , γ	90.00° 98.30° 90.00°	Depositor
Bosolution (Å)	23.90 - 2.75	Depositor
Resolution (A)	23.93 - 2.75	EDS
% Data completeness	$100.0\ (23.90-2.75)$	Depositor
(in resolution range)	95.9(23.93-2.75)	EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.73 (at 2.76\AA)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
B B.	0.267 , 0.287	Depositor
$\mathbf{n}, \mathbf{n}_{free}$	0.265 , 0.283	DCC
R_{free} test set	1063 reflections $(3.16%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	47.6	Xtriage
Anisotropy	0.938	Xtriage
Bulk solvent $k_{sol}(e/A^3), B_{sol}(A^2)$	0.29, 53.1	EDS
L-test for $twinning^2$	$ < L >=0.50, < L^2>=0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	7409	wwPDB-VP
Average B, all atoms $(Å^2)$	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.85% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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).

Mal	Chain	Bo	nd lengths	Bond angles		
IVIOI	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.57	0/1481	0.78	3/2020~(0.1%)	
1	В	0.64	0/1505	0.83	1/2052~(0.0%)	
1	С	0.41	0/1463	0.66	1/1995~(0.1%)	
1	D	0.45	0/1488	0.70	0/2029	
2	Т	0.62	0/760	0.83	3/1026~(0.3%)	
2	Y	0.82	1/744~(0.1%)	0.81	6/1003~(0.6%)	
All	All	0.57	1/7441~(0.0%)	0.76	14/10125~(0.1%)	

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
2	Т	0	1
2	Y	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
2	Y	76	ARG	CB-CG	18.73	2.03	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	В	122	ARG	NE-CZ-NH1	-7.60	116.50	120.30
2	Y	76	ARG	CA-CB-CG	-7.53	96.83	113.40
2	Y	76	ARG	CB-CG-CD	7.01	129.82	111.60
2	Y	74	LEU	CA-CB-CG	-6.58	100.18	115.30



2F8V

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	Т	84	PRO	N-CD-CG	-5.97	94.25	103.20
1	А	149	ASP	CB-CG-OD2	5.73	123.46	118.30
2	Y	84	PRO	N-CD-CG	-5.70	94.66	103.20
2	Y	75	GLY	N-CA-C	-5.37	99.67	113.10
2	Т	22[A]	TRP	CB-CA-C	-5.35	99.70	110.40
2	Т	22[B]	TRP	CB-CA-C	-5.35	99.70	110.40
2	Y	22	TRP	CB-CA-C	-5.33	99.74	110.40
1	С	122	ARG	NE-CZ-NH2	5.29	122.94	120.30
1	A	122	ARG	NE-CZ-NH2	5.03	122.81	120.30
1	A	170	ASP	CB-CG-OD2	5.01	122.81	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	Т	83	LEU	Peptide
2	Y	83	LEU	Peptide

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	А	1455	0	1446	57	0
1	В	1479	0	1471	72	0
1	С	1437	0	1429	49	0
1	D	1462	0	1455	67	0
2	Т	743	0	697	54	0
2	Y	729	0	688	45	0
3	А	5	0	0	2	0
3	В	10	0	0	2	0
3	С	5	0	0	1	0
3	D	5	0	0	0	0
4	А	33	0	0	11	0
4	В	24	0	0	4	0
4	С	10	0	0	2	0
4	D	3	0	0	0	0
4	Т	8	0	0	1	0



Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	Y	1	0	0	0	0
All	All	7409	0	7186	310	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 21.

All (310) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom_1	Atom_2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:T:47:ARG:HG2	2:T:47:ARG:HH11	1.05	1.12
1:D:100:GLU:HG2	2:Y:83:LEU:CD1	1.79	1.11
2:T:76:ARG:HH11	2:T:76:ARG:CG	1.66	1.06
2:Y:47:ARG:HG2	2:Y:47:ARG:HH11	1.17	1.06
1:A:2:THR:HG23	4:A:603:HOH:O	1.55	1.05
2:T:70:ARG:HD3	2:T:80:GLU:HG2	1.06	1.05
2:Y:69:MET:HG3	2:Y:83:LEU:HD21	1.36	1.05
2:Y:70:ARG:HD3	2:Y:80:GLU:HG2	1.07	1.03
1:B:100:GLU:HG2	2:T:83:LEU:HD11	1.38	1.02
2:T:70:ARG:CD	2:T:80:GLU:HG2	1.91	0.99
2:Y:70:ARG:HD3	2:Y:80:GLU:CG	1.94	0.98
1:B:155:GLU:OE1	1:B:155:GLU:HA	1.59	0.97
2:T:70:ARG:HD3	2:T:80:GLU:CG	1.96	0.96
2:T:76:ARG:HH11	2:T:76:ARG:HG3	1.30	0.95
2:Y:70:ARG:CD	2:Y:80:GLU:HG2	1.97	0.93
1:B:100:GLU:HG2	2:T:83:LEU:CD1	1.98	0.93
2:T:83:LEU:HB3	2:T:84:PRO:HD2	1.52	0.92
1:D:100:GLU:HG2	2:Y:83:LEU:HD11	1.52	0.91
1:B:196:GLU:CD	1:B:196:GLU:H	1.68	0.90
1:D:155:GLU:OE1	1:D:155:GLU:HA	1.70	0.89
2:T:47:ARG:HG2	2:T:47:ARG:NH1	1.84	0.88
1:D:100:GLU:CG	2:Y:83:LEU:CD1	2.53	0.85
2:Y:47:ARG:HH11	2:Y:47:ARG:CG	1.90	0.84
2:T:76:ARG:HH11	2:T:76:ARG:HG2	1.44	0.82
1:C:126:ARG:HG3	1:C:126:ARG:HH11	1.44	0.81
2:Y:17:ARG:HG3	2:Y:17:ARG:HH11	1.45	0.81
1:B:155:GLU:OE1	1:B:155:GLU:CA	2.28	0.80
1:B:150:PHE:HB3	1:B:161:LEU:HD11	1.62	0.80
2:T:47:ARG:HH11	2:T:47:ARG:CG	1.89	0.79
1:C:126:ARG:HH12	1:C:158:LEU:HB2	1.45	0.79
1:B:124:GLN:HB3	1:B:160:SER:HB3	1.64	0.79
1:B:145:GLN:OE1	1:B:145:GLN:HA	1.81	0.79



		Interatomic Clash	
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:B:154:GLN:O	1:B:155:GLU:OE1	2.02	0.78
1:A:126:ARG:HH12	1:A:158:LEU:HB2	1.47	0.77
1:B:26:GLU:OE2	1:B:28:HIS:HE1	1.68	0.76
1:A:67:ILE:HG21	1:A:70:VAL:HG12	1.67	0.75
1:B:72:LYS:HE2	3:B:602:SO4:O1	1.85	0.75
1:B:51:LEU:O	1:B:54:VAL:HG22	1.87	0.74
1:A:77:ARG:HG3	1:A:77:ARG:HH11	1.51	0.74
2:Y:83:LEU:HB3	2:Y:84:PRO:HD2	1.68	0.74
1:A:126:ARG:NH1	1:A:158:LEU:HD13	2.03	0.73
1:C:51:LEU:O	1:C:54:VAL:HG22	1.89	0.73
1:D:145:GLN:OE1	1:D:145:GLN:HA	1.88	0.73
1:B:47:SER:H	1:B:50:THR:HG23	1.53	0.73
1:A:126:ARG:NH1	1:A:158:LEU:HB2	2.04	0.72
1:B:100:GLU:OE1	2:T:83:LEU:HD12	1.90	0.72
2:T:76:ARG:HG3	2:T:76:ARG:NH1	2.02	0.72
2:Y:47:ARG:HG2	2:Y:47:ARG:NH1	1.91	0.72
2:T:76:ARG:CG	2:T:76:ARG:NH1	2.37	0.72
1:B:136:LYS:HD3	1:B:143:GLU:OE2	1.90	0.72
1:A:67:ILE:CG2	1:A:70:VAL:HG12	2.20	0.71
2:T:83:LEU:HB3	2:T:84:PRO:CD	2.19	0.71
1:A:77:ARG:HH11	1:A:77:ARG:CG	2.05	0.70
2:T:69:MET:HG3	2:T:83:LEU:CD2	2.21	0.70
1:B:196:GLU:CD	1:B:196:GLU:N	2.44	0.69
1:C:126:ARG:NH1	1:C:158:LEU:HB2	2.08	0.69
2:T:69:MET:HG3	2:T:83:LEU:HD21	1.74	0.69
1:D:47:SER:H	1:D:50:THR:HG23	1.58	0.69
1:D:125:VAL:O	1:D:158:LEU:HD12	1.93	0.68
1:D:51:LEU:O	1:D:54:VAL:HG22	1.93	0.68
2:T:70:ARG:CD	2:T:80:GLU:CG	2.66	0.68
1:D:16:VAL:HG21	2:Y:59:VAL:HB	1.76	0.68
2:T:17:ARG:HG3	2:T:17:ARG:HH11	1.60	0.67
1:B:77:ARG:NH2	2:T:36:GLU:O	2.28	0.67
1:A:139:ARG:NH1	1:A:171:SER:O	2.28	0.67
1:B:177:ASN:HD21	1:B:179:THR:CG2	2.08	0.67
1:C:39:TRP:O	1:C:46:ILE:HB	1.95	0.66
1:A:4:GLN:HB2	4:A:602:HOH:O	1.95	0.66
1:B:3:THR:HG23	1:B:3:THR:O	1.96	0.66
1:C:168:PRO:HG3	4:C:606:HOH:O	1.96	0.65
1:A:126:ARG:HG3	1:A:126:ARG:HH11	1.60	0.65
1:A:72:LYS:NZ	3:A:601:SO4:S	2.66	0.65
1:B:84:ASN:OD1	1:B:84:ASN:C	2.34	0.64



		Interatomic Clash		
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:D:84:ASN:OD1	1:D:84:ASN:C	2.35	0.64	
1:C:126:ARG:HG3	1:C:126:ARG:NH1	2.10	0.64	
1:D:100:GLU:CG	2:Y:83:LEU:HD12	2.28	0.64	
1:D:62:ARG:NH1	1:D:64:LYS:NZ	2.45	0.63	
1:B:117:GLN:NE2	4:B:615:HOH:O	2.31	0.63	
1:D:122[B]:ARG:HD2	1:D:124:GLN:NE2	2.13	0.63	
1:B:65:LEU:C	1:B:65:LEU:HD23	2.19	0.63	
2:Y:83:LEU:HB3	2:Y:84:PRO:CD	2.28	0.63	
1:B:32:PHE:HA	1:B:33:PRO:C	2.18	0.62	
1:B:130:ILE:HD11	2:T:84:PRO:HD3	1.82	0.62	
1:D:135:VAL:HG21	1:D:159:TYR:CD2	2.35	0.62	
1:A:36:GLU:HB2	4:A:619:HOH:O	1.99	0.62	
1:A:34:VAL:HG23	1:A:34:VAL:O	1.99	0.62	
1:D:32:PHE:HA	1:D:33:PRO:C	2.20	0.61	
1:D:150:PHE:HB3	1:D:161:LEU:HD11	1.80	0.61	
1:A:35:PRO:HA	1:A:83:THR:O	2.00	0.61	
1:D:100:GLU:CD	2:Y:83:LEU:HD12	2.21	0.61	
1:D:100:GLU:HG2	2:Y:83:LEU:HD13	1.77	0.61	
1:D:92:THR:O	2:Y:38:SER:HA	2.01	0.60	
1:D:71:THR:H	1:D:74:ASN:HD22	1.48	0.60	
2:Y:70:ARG:CD	2:Y:80:GLU:CG	2.71	0.60	
1:D:100:GLU:OE1	2:Y:83:LEU:CD1	2.50	0.59	
2:T:9:GLU:HG3	2:T:24:GLU:HG3	1.83	0.59	
2:T:1:MET:N	2:T:32:THR:HB	2.17	0.59	
1:A:77:ARG:NH1	1:A:94:GLU:OE1	2.35	0.59	
1:A:51:LEU:HB3	1:A:54:VAL:HG13	1.85	0.59	
1:B:167:TYR:HD2	4:B:615:HOH:O	1.86	0.58	
2:T:76:ARG:HG2	2:T:76:ARG:NH1	2.10	0.58	
2:T:79:GLN:OE1	1:D:116:ARG:NH2	2.36	0.58	
1:D:100:GLU:OE1	2:Y:83:LEU:HD12	2.03	0.58	
1:C:53:GLY:O	1:C:54:VAL:O	2.22	0.58	
1:D:71:THR:H	1:D:74:ASN:ND2	2.00	0.58	
1:B:167:TYR:CD2	4:B:615:HOH:O	2.52	0.58	
1:C:8:PHE:HE2	1:C:80:LEU:HD13	1.68	0.58	
1:D:65:LEU:HD23	1:D:65:LEU:C	2.24	0.58	
1:B:125:VAL:O	1:B:158:LEU:HD12	2.04	0.57	
2:T:75:GLY:O	1:D:120:GLN:N	2.38	0.57	
1:C:126:ARG:NH1	1:C:158:LEU:HD13	2.20	0.56	
2:T:1:MET:H3	2:T:32:THR:HB	1.70	0.56	
1:B:62:ARG:NH1	1:B:64:LYS:NZ	2.53	0.56	
1:C:10:GLN:CG	1:C:10:GLN:O	2.53	0.56	



A 4 1		Interatomic	Clash	
Atom-1	Atom-2	distance (\AA)	overlap (Å)	
2:T:63:ARG:HG2	2:T:63:ARG:HH11	1.70	0.56	
1:A:167:TYR:HB3	1:A:168:PRO:HD2	1.87	0.56	
1:A:167:TYR:HB3	1:A:168:PRO:CD	2.35	0.56	
1:C:175:SER:CB	1:C:188:THR:HG22	2.36	0.56	
1:D:12:LEU:HD23	1:D:27:ALA:HB2	1.88	0.55	
2:Y:41:HIS:C	2:Y:41:HIS:CD2	2.79	0.55	
2:Y:9:GLU:HG3	2:Y:24:GLU:HG3	1.89	0.55	
1:D:62:ARG:HH11	1:D:64:LYS:NZ	2.04	0.55	
2:T:35:GLU:OE1	2:T:54:GLN:NE2	2.40	0.55	
1:B:52:PRO:HD2	4:B:626:HOH:O	2.07	0.55	
2:T:67:LEU:HD22	2:T:84:PRO:HD2	1.88	0.55	
1:A:2:THR:N	4:A:603:HOH:O	2.40	0.54	
1:B:107:VAL:HG12	1:B:107:VAL:O	2.06	0.54	
1:B:146:SER:HB2	1:B:152:ILE:HB	1.89	0.54	
1:A:126:ARG:NH1	1:A:126:ARG:HG3	2.22	0.54	
2:Y:1:MET:H3	2:Y:32:THR:HB	1.73	0.54	
1:A:67:ILE:CG2	1:A:70:VAL:CG1	2.86	0.54	
1:C:139:ARG:NH1	1:C:171:SER:O	2.41	0.54	
1:D:169:GLU:CD	1:D:169:GLU:H	2.11	0.54	
1:C:16:VAL:HG12	2:Y:74:LEU:CD2	2.38	0.54	
1:D:41:ARG:HB2	1:D:46:ILE:HD11	1.90	0.54	
1:D:146:SER:HB2	1:D:152:ILE:HB	1.91	0.53	
2:Y:17:ARG:HH11	2:Y:17:ARG:CG	2.18	0.53	
1:B:196:GLU:N	1:B:196:GLU:OE1	2.28	0.53	
1:D:139:ARG:HH11	1:D:139:ARG:HG2	1.73	0.53	
1:A:122:ARG:HD3	1:A:162:LEU:HD13	1.91	0.53	
1:D:62:ARG:HH11	1:D:64:LYS:HZ3	1.57	0.53	
1:D:41:ARG:NH1	1:D:75:SER:O	2.43	0.52	
1:A:2:THR:HB	4:A:602:HOH:O	2.09	0.52	
1:B:18:LEU:O	1:B:19:GLU:C	2.48	0.52	
1:D:155:GLU:OE1	1:D:155:GLU:CA	2.47	0.52	
1:A:71:THR:O	1:A:71:THR:OG1	2.26	0.52	
1:C:7:THR:HG23	1:C:30:SER:OG	2.10	0.52	
1:B:84:ASN:OD1	1:B:85:GLY:N	2.42	0.52	
1:C:180:ASN:C	1:C:180:ASN:OD1	2.48	0.52	
2:T:86:GLN:O	2:T:87:ARG:HG2	2.10	0.52	
1:C:81:LYS:HB2	1:C:81:LYS:NZ	2.25	0.52	
2:Y:17:ARG:HG3	2:Y:17:ARG:NH1	2.22	0.51	
1:C:175:SER:HB2	1:C:188:THR:HG22	1.92	0.51	
2:Y:1:MET:N	2:Y:32:THR:HB	2.25	0.51	
1:A:77:ARG:CZ	4:A:608:HOH:O	2.58	0.51	



		Interatomic Clash	
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:B:26:GLU:OE2	1:B:28:HIS:CE1	2.56	0.51
1:C:167:TYR:HB3	1:C:168:PRO:HD2	1.92	0.51
1:D:147:SER:O	1:D:149:ASP:N	2.44	0.51
1:B:139:ARG:O	1:B:140:ASP:C	2.49	0.51
1:C:104:PRO:HG2	1:C:184:ARG:HA	1.92	0.51
1:A:77:ARG:CG	1:A:77:ARG:NH1	2.68	0.51
1:B:72:LYS:CE	3:B:602:SO4:O1	2.59	0.51
2:Y:35:GLU:OE1	2:Y:54:GLN:NE2	2.44	0.50
1:C:89:ALA:HB1	2:Y:12:GLU:HG2	1.92	0.50
1:D:84:ASN:OD1	1:D:85:GLY:N	2.44	0.50
1:A:86:SER:N	4:A:625:HOH:O	2.44	0.50
1:B:177:ASN:HD21	1:B:179:THR:HG22	1.76	0.50
1:D:150:PHE:CE2	1:D:163:ILE:HG12	2.46	0.50
1:D:83:THR:HG22	1:D:84:ASN:N	2.27	0.50
1:A:94:GLU:HG2	2:T:6:LEU:HG	1.94	0.50
2:Y:63:ARG:HG2	2:Y:63:ARG:HH11	1.75	0.50
2:T:63:ARG:HG2	2:T:63:ARG:NH1	2.26	0.49
1:B:12:LEU:HD23	1:B:27:ALA:HB2	1.94	0.49
1:D:62:ARG:NH1	1:D:64:LYS:HZ2	2.08	0.49
1:C:65:LEU:HD23	1:C:66:THR:N	2.27	0.49
1:A:18:LEU:HG	1:D:165:GLU:OE2	2.12	0.49
1:B:150:PHE:HB3	1:B:161:LEU:CD1	2.39	0.49
1:A:72:LYS:NZ	3:A:601:SO4:O2	2.44	0.49
1:A:80:LEU:HD23	1:A:81:LYS:N	2.28	0.49
2:Y:73:ILE:O	2:Y:75:GLY:N	2.41	0.49
1:B:71:THR:H	1:B:74:ASN:HD22	1.61	0.48
1:A:71:THR:O	1:A:72:LYS:C	2.51	0.48
1:C:4:GLN:OE1	1:C:31:GLY:HA2	2.14	0.48
1:D:100:GLU:CD	2:Y:83:LEU:CD1	2.81	0.48
1:A:104:PRO:HG2	1:A:184:ARG:HA	1.96	0.48
1:D:124:GLN:HB3	1:D:160:SER:HB3	1.95	0.48
2:Y:63:ARG:HG2	2:Y:63:ARG:NH1	2.27	0.48
1:A:56:ILE:CG2	4:A:631:HOH:O	2.62	0.48
1:C:53:GLY:O	1:C:54:VAL:C	2.52	0.48
1:D:18:LEU:HD22	1:D:19:GLU:O	2.14	0.48
1:B:5:ALA:HB1	1:B:6:PRO:HD2	1.96	0.48
1:B:47:SER:H	1:B:50:THR:CG2	2.24	0.47
1:B:135:VAL:HG21	1:B:159:TYR:CD2	2.49	0.47
1:B:169:GLU:CD	1:B:169:GLU:H	2.18	0.47
1:B:71:THR:H	1:B:74:ASN:ND2	2.11	0.47
1:B:100:GLU:HG2	2:T:83:LEU:HD12	1.90	0.47



		Interatomic	Clash	
Atom-1	Atom-2	distance (\AA)	overlap (Å)	
2:T:40:LEU:HG	2:T:41:HIS:N	2.27	0.47	
2:Y:34:PRO:HB2	2:Y:36:GLU:OE1	2.15	0.47	
1:B:111:GLN:HG3	2:T:17:ARG:HH22	1.78	0.47	
1:B:62:ARG:O	1:B:62:ARG:HG3	2.14	0.47	
1:C:98:LYS:HD3	3:C:603:SO4:O1	2.13	0.47	
1:D:177:ASN:HD21	1:D:179:THR:CG2	2.28	0.47	
2:T:47:ARG:NE	4:T:168:HOH:O	2.47	0.47	
1:A:67:ILE:HG22	1:A:70:VAL:CG1	2.45	0.47	
1:A:51:LEU:HB3	1:A:54:VAL:CG1	2.44	0.46	
1:B:184:ARG:HG3	2:T:22[B]:TRP:HZ3	1.80	0.46	
1:D:62:ARG:NH1	1:D:64:LYS:HZ3	2.11	0.46	
1:D:100:GLU:OE1	2:Y:83:LEU:HD13	2.16	0.46	
2:T:41:HIS:C	2:T:41:HIS:CD2	2.88	0.46	
1:C:35:PRO:HA	1:C:83:THR:O	2.16	0.46	
2:T:60:LEU:C	2:T:60:LEU:HD23	2.36	0.46	
1:D:18:LEU:CD2	1:D:19:GLU:N	2.79	0.46	
2:T:35:GLU:HA	2:T:55:GLY:O	2.16	0.46	
1:D:125:VAL:O	1:D:158:LEU:CD1	2.63	0.46	
1:C:117:GLN:HE21	1:C:168:PRO:HD3	1.81	0.45	
1:D:108:GLN:HB3	1:D:126:ARG:HB2	1.97	0.45	
1:C:51:LEU:HD23	1:C:51:LEU:HA	1.73	0.45	
2:Y:85:TYR:CG	2:Y:86:GLN:N	2.84	0.45	
1:A:10:GLN:HE21	1:A:10:GLN:HB2	1.55	0.45	
1:C:16:VAL:HG22	1:C:96:LEU:HB3	1.97	0.45	
1:D:47:SER:H	1:D:50:THR:CG2	2.26	0.45	
1:B:177:ASN:ND2	1:B:179:THR:CG2	2.78	0.45	
2:T:69:MET:HG3	2:T:83:LEU:HD22	1.97	0.45	
1:B:148:LEU:HD13	1:B:148:LEU:HA	1.73	0.45	
1:B:86:SER:HB3	2:T:46:GLN:HE21	1.81	0.45	
1:A:71:THR:O	1:A:74:ASN:N	2.32	0.45	
1:C:54:VAL:HG12	1:C:67:ILE:HG12	1.99	0.45	
1:C:68:PRO:HB2	1:C:69:ALA:H	1.66	0.45	
1:B:180:ASN:OD1	1:B:180:ASN:C	2.56	0.44	
1:D:135:VAL:O	1:D:135:VAL:CG2	2.63	0.44	
1:B:151:GLN:HE21	1:B:162:LEU:HD23	1.83	0.44	
2:Y:60:LEU:C	2:Y:60:LEU:HD23	2.38	0.44	
1:A:126:ARG:HH11	1:A:158:LEU:HD13	1.82	0.44	
2:T:34:PRO:HB2	2:T:36:GLU:OE1	2.17	0.44	
1:C:110:LEU:HD11	1:C:123:LEU:HB3	2.00	0.44	
2:Y:46:GLN:HG2	2:Y:47:ARG:HG3	1.99	0.44	
1:A:34:VAL:O	1:A:34:VAL:CG2	2.65	0.44	



		Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:A:175:SER:CB	1:A:188:THR:HG22	2.47	0.44
1:C:167:TYR:HB3	1:C:168:PRO:CD	2.47	0.44
1:A:184:ARG:HG2	1:A:185:ALA:N	2.31	0.43
1:B:29:ILE:CG2	1:B:30:SER:N	2.81	0.43
1:C:18:LEU:H	1:C:18:LEU:HG	1.51	0.43
1:A:3:THR:C	4:A:602:HOH:O	2.56	0.43
1:D:18:LEU:HD22	1:D:19:GLU:N	2.32	0.43
1:A:67:ILE:HG22	1:A:70:VAL:HG12	2.00	0.43
1:A:167:TYR:C	1:A:193:VAL:HG11	2.38	0.43
1:D:147:SER:C	1:D:149:ASP:N	2.72	0.43
2:T:74:LEU:HD12	2:T:74:LEU:HA	1.61	0.43
1:C:117:GLN:HB2	4:C:606:HOH:O	2.18	0.43
1:C:126:ARG:HH11	1:C:126:ARG:CG	2.21	0.43
1:C:10:GLN:O	1:C:10:GLN:HG2	2.18	0.43
1:B:41:ARG:O	1:B:42:ASP:C	2.57	0.43
1:B:41:ARG:NH1	1:B:75:SER:O	2.51	0.43
1:B:107:VAL:O	1:B:107:VAL:CG1	2.67	0.43
1:B:3:THR:O	1:B:3:THR:CG2	2.63	0.43
1:D:18:LEU:CD2	1:D:18:LEU:C	2.87	0.43
1:C:62:ARG:C	1:C:62:ARG:HE	2.23	0.43
1:D:177:ASN:HD21	1:D:179:THR:HG22	1.84	0.42
1:D:10:GLN:HA	1:D:11:PRO:HD3	1.91	0.42
1:A:126:ARG:HH11	1:A:126:ARG:CG	2.28	0.42
1:C:126:ARG:HH12	1:C:158:LEU:CB	2.24	0.42
2:Y:41:HIS:HD2	2:Y:41:HIS:O	2.02	0.42
2:Y:62:GLN:HB3	2:Y:70:ARG:HB3	2.01	0.42
1:A:180:ASN:C	1:A:180:ASN:OD1	2.56	0.42
1:C:121:VAL:HG12	1:C:122:ARG:N	2.35	0.42
1:C:132:THR:HA	1:C:133:PRO:HD3	1.88	0.42
1:D:18:LEU:O	1:D:19:GLU:C	2.56	0.42
1:D:170:ASP:O	1:D:171:SER:C	2.55	0.42
1:B:35:PRO:HA	1:B:83:THR:O	2.20	0.42
1:C:151:GLN:HE21	1:C:151:GLN:HB2	1.61	0.42
1:A:100:GLU:HB3	4:A:618:HOH:O	2.20	0.42
1:B:18:LEU:HD22	1:B:19:GLU:O	2.19	0.42
2:T:14:ASN:OD1	2:T:14:ASN:C	2.58	0.42
1:B:51:LEU:HB3	1:B:54:VAL:HG13	2.01	0.42
1:B:77:ARG:HE	1:B:77:ARG:HB3	1.60	0.42
1:A:8:PHE:CZ	1:A:91:SER:CB	3.03	0.42
1:A:151:GLN:HE21	1:A:151:GLN:HB2	1.65	0.41
1:D:180:ASN:OD1	1:D:180:ASN:C	2.59	0.41



Atom 1	Atom 2	Interatomic	Clash	
Atom-1	Atom-2	distance (\AA)	overlap (Å)	
1:B:103:PRO:HG2	2:T:65:PRO:HA	2.02	0.41	
1:C:16:VAL:HG12	2:Y:74:LEU:HD21	2.02	0.41	
1:D:107:VAL:O	1:D:107:VAL:HG12	2.21	0.41	
2:T:35:GLU:C	2:T:37:GLY:N	2.73	0.41	
1:A:130:ILE:HD13	4:A:618:HOH:O	2.19	0.41	
1:C:46:ILE:HD13	1:C:65:LEU:HD11	2.02	0.41	
1:A:152:ILE:HA	1:A:160:SER:O	2.20	0.41	
1:B:34:VAL:HA	1:B:35:PRO:HD3	1.86	0.41	
1:B:92:THR:O	2:T:38:SER:HA	2.20	0.41	
1:B:100:GLU:CG	2:T:83:LEU:CD1	2.86	0.41	
1:B:130:ILE:CD1	2:T:84:PRO:HD3	2.48	0.41	
2:Y:17:ARG:CG	2:Y:17:ARG:NH1	2.79	0.41	
1:B:103:PRO:HG2	2:T:65:PRO:CA	2.51	0.41	
1:C:16:VAL:CG1	2:Y:74:LEU:CD2	2.99	0.41	
1:C:34:VAL:HA	1:C:35:PRO:HD3	1.82	0.41	
1:C:175:SER:HB3	1:C:188:THR:HG22	2.02	0.41	
1:D:18:LEU:HD22	1:D:18:LEU:C	2.41	0.41	
1:A:8:PHE:CE1	1:A:91:SER:HB2	2.56	0.41	
1:A:34:VAL:HA	1:A:35:PRO:HD3	1.84	0.41	
2:T:17:ARG:HH11	2:T:17:ARG:CG	2.32	0.41	
1:D:35:PRO:HA	1:D:83:THR:O	2.21	0.41	
1:D:22:THR:HA	1:D:67:ILE:O	2.21	0.41	
1:D:51:LEU:HB3	1:D:54:VAL:HG13	2.01	0.41	
1:D:132:THR:HA	1:D:133:PRO:HD3	1.86	0.41	
1:D:168:PRO:C	1:D:170:ASP:N	2.73	0.41	
1:B:124:GLN:HE21	1:B:160:SER:HB3	1.86	0.40	
1:C:35:PRO:HB3	1:C:82:ALA:HB1	2.03	0.40	
1:B:157:ASP:OD1	1:B:157:ASP:C	2.60	0.40	
1:C:102:ALA:HA	1:C:103:PRO:HD3	1.97	0.40	
2:Y:41:HIS:CD2	2:Y:41:HIS:O	2.74	0.40	
1:A:18:LEU:O	1:A:19:GLU:C	2.59	0.40	
1:A:37:VAL:HA	1:A:81:LYS:O	2.22	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.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	P	erce	entiles
1	А	192/201~(96%)	180 (94%)	10~(5%)	2(1%)		15	27
1	В	195/201~(97%)	186 (95%)	9~(5%)	0	1	100	100
1	С	189/201~(94%)	179 (95%)	8 (4%)	2(1%)		14	25
1	D	192/201~(96%)	181 (94%)	10 (5%)	1 (0%)		29	47
2	Т	87/167~(52%)	82 (94%)	4 (5%)	1 (1%)		14	25
2	Y	86/167~(52%)	79~(92%)	3 (4%)	4 (5%)		2	2
All	All	941/1138 (83%)	887 (94%)	44 (5%)	10 (1%)		14	25

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	Т	84	PRO
1	С	54	VAL
2	Y	74	LEU
2	Y	84	PRO
1	С	68	PRO
1	D	148	LEU
2	Y	83	LEU
2	Y	75	GLY
1	А	68	PRO
1	А	72	LYS

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	А	162/169~(96%)	150~(93%)	12 (7%)	13 24
1	В	165/169~(98%)	145 (88%)	20 (12%)	5 8
1	С	160/169~(95%)	146 (91%)	14 (9%)	10 17



Mol	Chain	Analysed	Rotameric	Outliers	Per	ce	\mathbf{ntile}	es
1	D	163/169~(96%)	145~(89%)	18 (11%)	6		10	
2	Т	81/147~(55%)	65~(80%)	16 (20%)]	L	1	
2	Y	80/147~(54%)	68~(85%)	12 (15%)	ę	3	4	
All	All	811/970 (84%)	719~(89%)	92 (11%)	6	5	9	

Continued from previous page...

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	THR
1	А	10	GLN
1	А	22	THR
1	А	50	THR
1	А	77	ARG
1	А	80	LEU
1	А	109	ARG
1	А	122	ARG
1	А	126	ARG
1	А	139	ARG
1	А	151	GLN
1	А	184	ARG
1	В	9	THR
1	В	18	LEU
1	В	37	VAL
1	В	46	ILE
1	В	50	THR
1	В	51	LEU
1	В	54	VAL
1	В	62	ARG
1	В	77	ARG
1	В	84	ASN
1	В	111	GLN
1	В	124	GLN
1	В	135	VAL
1	В	145	GLN
1	В	147	SER
1	В	148	LEU
1	В	155	GLU
1	В	179	THR
1	В	188	THR
1	В	196	GLU
2	Т	3	THR



Mol	Chain	Res	Type
2	Т	6	LEU
2	Т	15	SER
2	Т	18	ARG
2	Т	22[A]	TRP
2	T	22[B]	TRP
2	Т	29	THR
2	Т	31	SER
2	Т	41	HIS
2	Т	43	GLU
2	Т	47	ARG
2	Т	59	VAL
2	Т	63	ARG
2	Т	64	SER
2	Т	76	ARG
2	Т	83	LEU
1	С	9	THR
1	С	10	GLN
1	С	17	VAL
1	С	18	LEU
1	С	34	VAL
1	С	49	SER
1	С	50	THR
1	С	62	ARG
1	С	71	THR
1	С	80	LEU
1	С	109	ARG
1	С	126	ARG
1	С	151	GLN
1	С	184	ARG
1	D	9	THR
1	D	18	LEU
1	D	22	THR
1	D	26	GLU
1	D	37	VAL
1	D	50	THR
1	D	51	LEU
1	D	54	VAL
1	D	77	ARG
1	D	84	ASN
1	D	88	GLN
1	D	124	GLN

Continued from previous page...



N/L_1	Chain	Dec	T
IVIOI	Chain	Res	Type
1	D	140	ASP
1	D	148	LEU
1	D	155	GLU
1	D	179	THR
1	D	184	ARG
2	Y	3	THR
2	Y	6	LEU
2	Y	15	SER
2	Y	29	THR
2	Y	31	SER
2	Y	35	GLU
2	Y	41	HIS
2	Y	43	GLU
2	Y	47	ARG
2	Y	59	VAL
2	Y	63	ARG
2	Y	86	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	10	GLN
1	А	74	ASN
1	А	117	GLN
1	А	124	GLN
1	А	151	GLN
1	А	194	GLN
1	В	28	HIS
1	В	74	ASN
1	В	88	GLN
1	В	105	ASN
1	В	117	GLN
1	В	124	GLN
1	В	151	GLN
1	В	177	ASN
2	Т	41	HIS
2	Т	46	GLN
2	Т	48	HIS
2	Т	52	HIS
2	Т	53	GLN
2	Т	62	GLN
1	С	10	GLN



Mol	Chain	Res	Type
1	С	117	GLN
1	С	151	GLN
1	С	194	GLN
1	D	10	GLN
1	D	74	ASN
1	D	105	ASN
1	D	111	GLN
1	D	124	GLN
1	D	151	GLN
1	D	177	ASN
2	Y	41	HIS
2	Y	52	HIS
2	Y	53	GLN
2	Y	62	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

5 ligands 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).



Mal	Iol Turno Choin Dog Li		T in le	Bond lengths			Bond angles			
	Moi Type Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2	
3	SO4	С	603	-	4,4,4	0.14	0	6,6,6	0.32	0
3	SO4	D	604	-	4,4,4	0.17	0	6,6,6	0.12	0
3	SO4	В	605	-	4,4,4	0.14	0	6,6,6	0.20	0
3	SO4	А	601	-	4,4,4	0.17	0	6,6,6	0.07	0
3	SO4	В	602	-	4,4,4	0.16	0	6,6,6	0.30	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	С	603	SO4	1	0
3	А	601	SO4	2	0
3	В	602	SO4	2	0

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, 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	А	194/201~(96%)	-0.03	3 (1%) 73 81	19, 22, 25, 27	0
1	В	197/201~(98%)	0.10	3 (1%) 73 81	19, 22, 25, 31	0
1	С	191/201~(95%)	1.07	40 (20%) 1 0	17, 23, 26, 30	0
1	D	193/201~(96%)	0.92	31 (16%) 1 1	16, 23, 27, 30	0
2	Т	88/167~(52%)	0.30	2 (2%) 60 69	19, 22, 26, 38	0
2	Y	88/167~(52%)	1.81	30 (34%) 0 0	19, 23, 27, 36	2(2%)
All	All	951/1138 (83%)	0.61	109 (11%) 4 5	16, 23, 26, 38	2 (0%)

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	Y	88	VAL	10.4
2	Y	85	TYR	9.5
1	D	2	THR	8.7
2	Y	1	MET	7.7
2	Y	86	GLN	7.1
1	D	58	PHE	6.9
1	С	32	PHE	6.3
1	С	60	ASP	6.2
1	С	5	ALA	5.7
1	С	4	GLN	5.3
1	D	32	PHE	5.2
2	Y	87	ARG	5.1
1	С	12	LEU	4.9
1	С	117	GLN	4.8
2	Y	36	GLU	4.8
1	D	85	GLY	4.5
1	С	62	ARG	4.4
1	С	61	GLY	4.4
1	С	82	ALA	4.3



Mol	Chain	Res	Type	RSRZ
2	Y	66	TRP	4.3
2	Y	34	PRO	4.3
1	С	31	GLY	4.2
1	С	30	SER	4.2
2	Y	22	TRP	4.2
1	С	43	GLY	4.2
1	D	31	GLY	4.2
1	С	85	GLY	4.2
2	Т	1	MET	3.9
1	С	59	SER	3.9
1	С	28	HIS	3.8
2	Y	46	GLN	3.8
1	С	87	GLY	3.6
1	В	4	GLN	3.6
1	С	46	ILE	3.6
1	С	49	SER	3.5
1	В	61	GLY	3.5
1	D	47	SER	3.4
1	D	86	SER	3.4
1	D	62	ARG	3.4
1	D	33	PRO	3.3
1	С	42	ASP	3.3
2	Y	45	THR	3.3
1	D	60	ASP	3.3
2	Y	4	SER	3.2
1	С	50	THR	3.2
1	D	43	GLY	3.2
1	D	116	ARG	3.2
1	С	165	GLU	3.1
2	Y	84	PRO	3.1
1	В	1	MET	3.1
1	С	45	VAL	3.1
2	Y	13	GLU	3.1
1	С	47	SER	3.0
1	D	51	LEU	3.0
1	D	29	ILE	3.0
1	D	42	ASP	3.0
2	Y	3	THR	3.0
1	D	89	ALA	2.9
2	Y	35	GLU	2.9
1	С	167	TYR	2.9
1	С	91	SER	2.8



2F8V	
------	--

Mol	Chain	Res	Type	RSRZ
2	Y	80	GLU	2.8
1	D	184	ARG	2.8
1	С	10	GLN	2.7
1	С	118	GLY	2.7
1	С	78	TYR	2.7
1	С	51	LEU	2.7
1	С	68	PRO	2.7
1	D	169	GLU	2.7
1	D	61	GLY	2.6
1	С	86	SER	2.6
2	Y	81	TYR	2.6
2	Y	73	ILE	2.6
2	Y	33	ARG	2.6
1	С	44	GLN	2.6
1	D	76	GLY	2.6
1	С	33	PRO	2.5
1	С	52	PRO	2.5
1	D	3	THR	2.5
1	D	87	GLY	2.5
1	D	80	LEU	2.5
2	Y	9	GLU	2.5
2	Y	74	LEU	2.4
2	Y	68	MET	2.4
1	С	64	LYS	2.4
2	Y	14	ASN	2.4
2	Y	67	LEU	2.4
2	Y	43	GLU	2.4
1	С	168	PRO	2.3
1	С	93	ALA	2.3
2	Y	41	HIS	2.3
1	А	195	GLY	2.3
1	D	5	ALA	2.3
1	А	58	PHE	2.3
1	D	36	GLU	2.3
1	С	38	SER	2.3
2	Y	83	LEU	2.3
1	С	48	THR	2.2
1	С	77	ARG	2.2
1	D	77	ARG	2.2
2	Y	17	ARG	2.2
1	D	44	GLN	2.2
1	D	81	LYS	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 monosaccharides 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. 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	$B-factors(Å^2)$	Q < 0.9
3	SO4	С	603	5/5	0.87	0.29	22,23,26,26	5
3	SO4	В	605	5/5	0.91	0.28	18,20,21,22	5
3	SO4	D	604	5/5	0.91	0.32	21,25,26,26	5
3	SO4	В	602	5/5	0.97	0.12	16,17,19,20	5
3	SO4	А	601	5/5	0.98	0.15	13,13,15,16	5

6.5 Other polymers (i)

There are no such residues in this entry.



Chain RSRZ Mol \mathbf{Res} Type $\mathbf{2}$ TRP Т 662.11 D 34VAL 2.1THR D 71 2.12 Y 10 VAL 2.11 А 116 ARG 2.11 D 50THR 2.1

Continued from previous page...