



Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 04:13 PM GMT

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 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/ValidationPDFNotes.html>

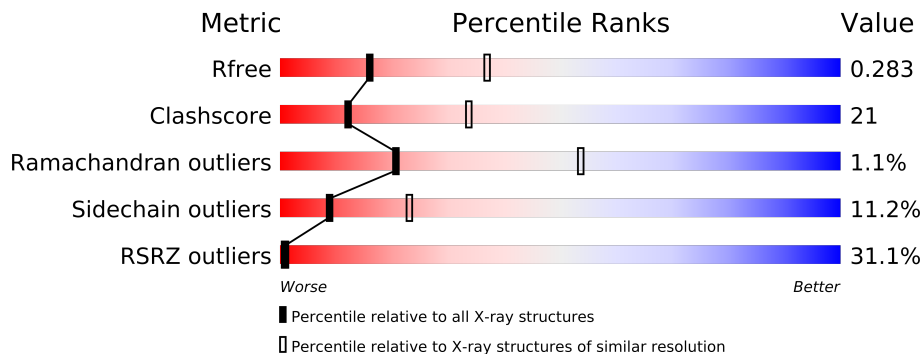
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	2406 (2.80-2.72)
Clashscore	79885	2995 (2.80-2.72)
Ramachandran outliers	78287	2941 (2.80-2.72)
Sidechain outliers	78261	2944 (2.80-2.72)
RSRZ outliers	66119	2409 (2.80-2.72)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	201	
1	B	201	
1	C	201	
1	D	201	
2	T	167	
2	Y	167	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	SO4	B	602	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7409 atoms, of which 0 are hydrogen and 0 are deuterium.

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 N2B-Titin Isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	194	Total	C	N	O	S	0	0	0
			1455	911	249	294	1			
1	B	197	Total	C	N	O	S	0	0	0
			1479	925	252	300	2			
1	C	191	Total	C	N	O	S	0	0	0
			1437	901	246	289	1			
1	D	193	Total	C	N	O	S	0	1	0
			1462	915	252	294	1			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	197	THR	-	CLONING ARTIFACT	UNP Q8WZ42
A	198	ARG	-	CLONING ARTIFACT	UNP Q8WZ42
A	199	GLU	-	CLONING ARTIFACT	UNP Q8WZ42
A	200	GLU	-	CLONING ARTIFACT	UNP Q8WZ42
A	201	PHE	-	CLONING ARTIFACT	UNP Q8WZ42
B	197	THR	-	CLONING ARTIFACT	UNP Q8WZ42
B	198	ARG	-	CLONING ARTIFACT	UNP Q8WZ42
B	199	GLU	-	CLONING ARTIFACT	UNP Q8WZ42
B	200	GLU	-	CLONING ARTIFACT	UNP Q8WZ42
B	201	PHE	-	CLONING ARTIFACT	UNP Q8WZ42
C	197	THR	-	CLONING ARTIFACT	UNP Q8WZ42
C	198	ARG	-	CLONING ARTIFACT	UNP Q8WZ42
C	199	GLU	-	CLONING ARTIFACT	UNP Q8WZ42
C	200	GLU	-	CLONING ARTIFACT	UNP Q8WZ42
C	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

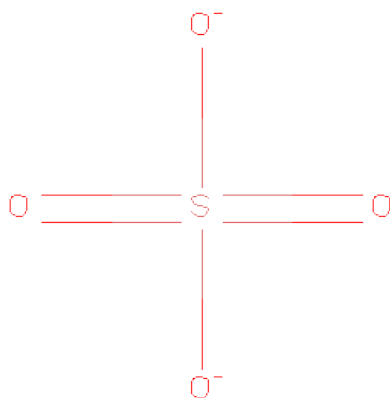
- Molecule 2 is a protein called Telethonin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	88	Total	C	N	O	S	0	1	0
			743	458	134	147	4			
2	Y	88	Total	C	N	O	S	6	0	0
			729	447	132	146	4			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	8	SER	CYS	ENGINEERED	UNP O15273
T	15	SER	CYS	ENGINEERED	UNP O15273
T	38	SER	CYS	ENGINEERED	UNP O15273
T	57	SER	CYS	ENGINEERED	UNP O15273
T	127	SER	CYS	ENGINEERED	UNP O15273
Y	8	SER	CYS	ENGINEERED	UNP O15273
Y	15	SER	CYS	ENGINEERED	UNP O15273
Y	38	SER	CYS	ENGINEERED	UNP O15273
Y	57	SER	CYS	ENGINEERED	UNP O15273
Y	127	SER	CYS	ENGINEERED	UNP O15273

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

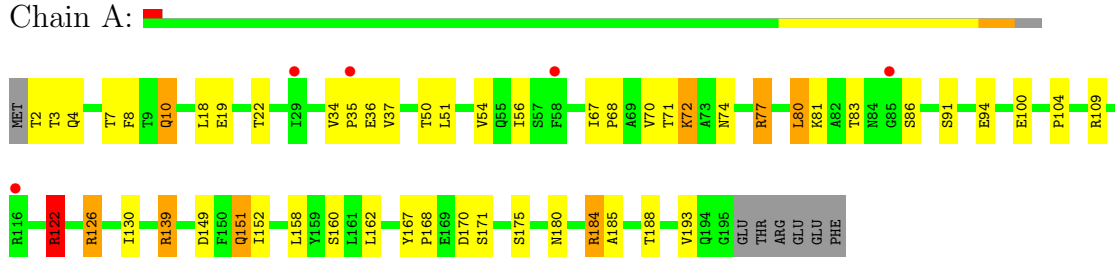
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	33	Total	O	0	0
			33	33		
4	B	24	Total	O	0	0
			24	24		
4	C	10	Total	O	0	0
			10	10		
4	D	3	Total	O	0	0
			3	3		
4	T	8	Total	O	0	0
			8	8		
4	Y	1	Total	O	0	0
			1	1		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

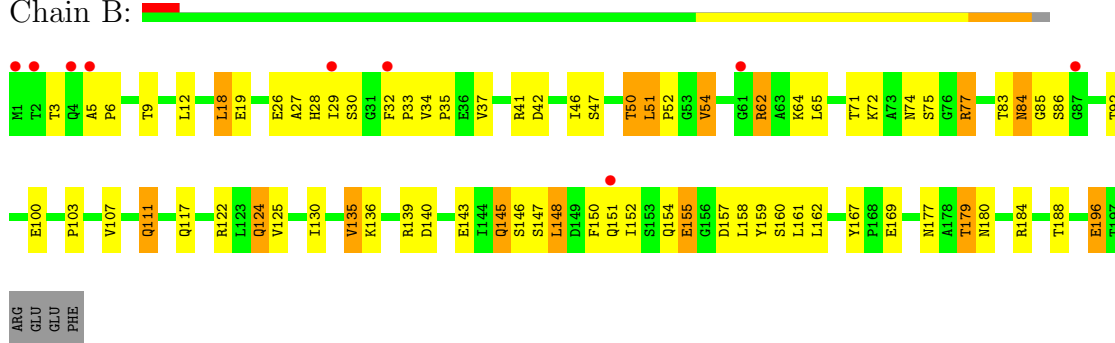
• Molecule 1: N2B-Titin Isoform

Chain A:



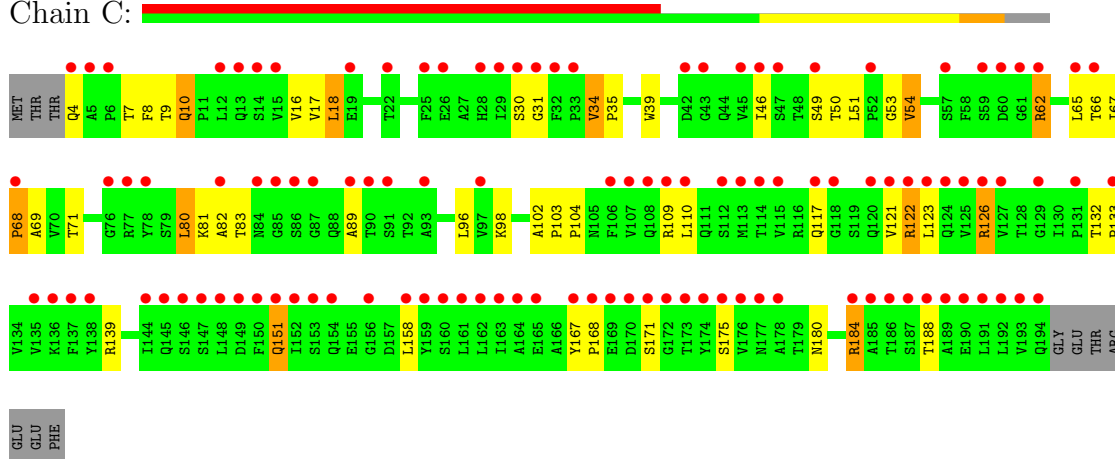
• Molecule 1: N2B-Titin Isoform

Chain B:

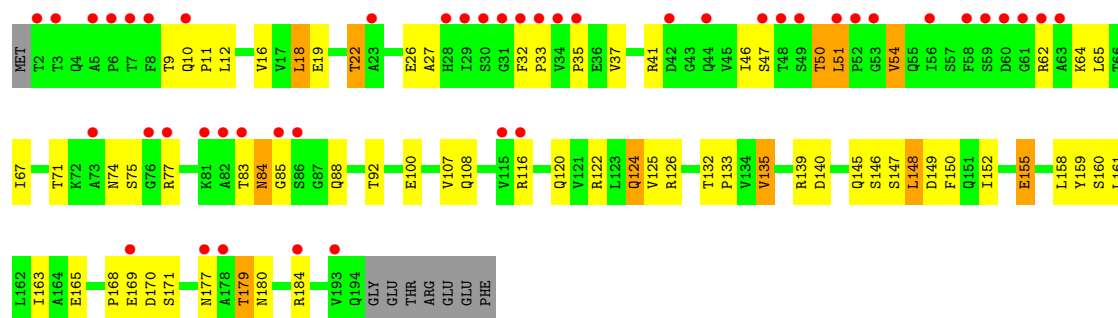


• Molecule 1: N2B-Titin Isoform

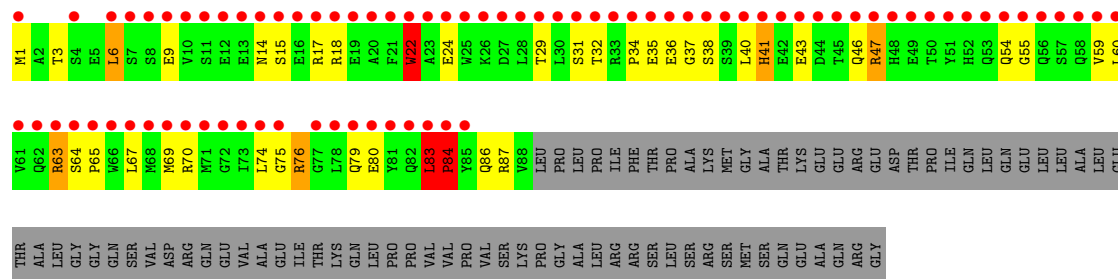
Chain C:



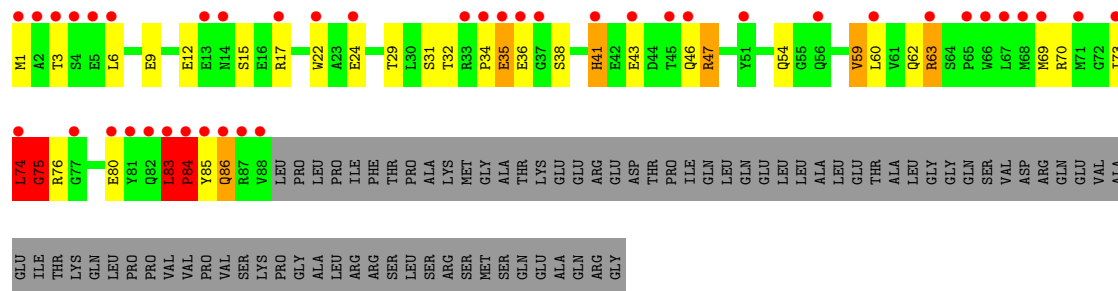
- Molecule 1: N2B-Titin Isoform

Chain D: 

- Molecule 2: Telethonin

Chain T: 

- Molecule 2: Telethonin

Chain Y: 

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	112.51Å 46.88Å 128.03Å 90.00° 98.30° 90.00°	Depositor
Resolution (Å)	23.90 – 2.75 23.93 – 2.75	Depositor EDS
% Data completeness (in resolution range)	100.0 (23.90-2.75) 95.9 (23.93-2.75)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.73 (at 2.76Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.267 , 0.287 0.266 , 0.283	Depositor DCC
R_{free} test set	1063 reflections (3.26%)	DCC
Wilson B-factor (Å ²)	47.6	Xtriage
Anisotropy	0.938	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 38.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 33627 reflections	Xtriage
F_o, F_c correlation	0.81	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.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.57	0/1481	0.78	3/2020 (0.1%)
1	B	0.64	0/1505	0.83	1/2052 (0.0%)
1	C	0.41	0/1463	0.66	1/1995 (0.1%)
1	D	0.45	0/1488	0.70	0/2029
2	T	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	T	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)	Ideal(Å)
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	Observed(°)	Ideal(°)
1	B	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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	84	PRO	N-CD-CG	-5.97	94.25	103.20
1	A	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	T	22[A]	TRP	CB-CA-C	-5.35	99.70	110.40
2	T	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	C	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	T	83	LEU	Peptide
2	Y	83	LEU	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1455	0	1446	57	0
1	B	1479	0	1471	72	0
1	C	1437	0	1429	49	0
1	D	1462	0	1455	67	0
2	T	743	0	697	54	0
2	Y	729	0	688	45	0
3	A	5	0	0	2	0
3	B	10	0	0	2	0
3	C	5	0	0	1	0
3	D	5	0	0	0	0
4	A	33	0	0	11	0
4	B	24	0	0	4	0
4	C	10	0	0	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	3	0	0	0	0
4	T	8	0	0	1	0
4	Y	1	0	0	0	0
All	All	7409	0	7186	310	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 21.

All (310) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(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:Y:69:MET:HG3	2:Y:83:LEU:HD21	1.36	1.05
2:T:70:ARG:HD3	2:T:80:GLU:HG2	1.06	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:HA	1:D:155:GLU:OE1	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:CG	2:Y:47:ARG:HH11	1.90	0.84
2:T:76:ARG:HH11	2:T:76:ARG:HG2	1.44	0.82
1:C:126:ARG:HH11	1:C:126:ARG:HG3	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

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(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:NH1	2:T:76:ARG:HG3	2.02	0.72
2:Y:47:ARG:HG2	2:Y:47:ARG:NH1	1.91	0.72
2:T:76:ARG:NH1	2:T:76:ARG:CG	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:HH11	2:T:17:ARG:HG3	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:HH11	1:A:126:ARG:HG3	1.60	0.65
1:A:72:LYS:NZ	3:A:601:SO4:S	2.66	0.65
1:B:84:ASN:C	1:B:84:ASN:OD1	2.34	0.64
1:D:84:ASN:OD1	1:D:84:ASN:C	2.35	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:100:GLU:CG	2:Y:83:LEU:HD12	2.28	0.64
1:C:126:ARG:NH1	1:C:126:ARG:HG3	2.10	0.64
1:D:62:ARG:NH1	1:D:64:LYS:NZ	2.45	0.63
1:D:122[B]:ARG:HD2	1:D:124:GLN:NE2	2.13	0.63
1:B:117:GLN:NE2	4:B:615:HOH:O	2.31	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:O	1:A:34:VAL:HG23	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
2:Y:70:ARG:CD	2:Y:80:GLU:CG	2.71	0.60
1:D:71:THR:H	1:D:74:ASN:HD22	1.48	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
1:D:100:GLU:OE1	2:Y:83:LEU:HD12	2.03	0.58
2:T:76:ARG:NH1	2:T:76:ARG:HG2	2.10	0.58
2:T:79:GLN:OE1	1:D:116:ARG:NH2	2.36	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:D:65:LEU:HD23	1:D:65:LEU:C	2.24	0.58
1:C:8:PHE:HE2	1:C:80:LEU:HD13	1.68	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:O	1:C:10:GLN:CG	2.53	0.56
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

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
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:CD2	2:Y:41:HIS:C	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:OE1	1:B:196:GLU:N	2.28	0.53
1:D:139:ARG:HG2	1:D:139:ARG:HH11	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:D:155:GLU:OE1	1:D:155:GLU:CA	2.47	0.52
1:B:18:LEU:O	1:B:19:GLU:C	2.48	0.52
1:A:71:THR:OG1	1:A:71:THR:O	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
1:C:81:LYS:HB2	1:C:81:LYS:NZ	2.25	0.52
2:T:86:GLN:O	2:T:87:ARG:HG2	2.10	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:B:26:GLU:OE2	1:B:28:HIS:CE1	2.56	0.51
1:A:77:ARG:CZ	4:A:608:HOH:O	2.58	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

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:104:PRO:HG2	1:C:184:ARG:HA	1.92	0.51
1:B:139:ARG:O	1:B:140:ASP:C	2.49	0.51
1:B:72:LYS:CE	3:B:602:SO4:O1	2.59	0.51
1:A:77:ARG:NH1	1:A:77:ARG:CG	2.68	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:B:177:ASN:HD21	1:B:179:THR:HG22	1.76	0.50
1:A:86:SER:N	4:A:625:HOH:O	2.44	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:HH11	2:Y:63:ARG:HG2	1.75	0.50
2:T:63:ARG:HG2	2:T:63:ARG:NH1	2.26	0.49
1:D:62:ARG:NH1	1:D:64:LYS:HZ2	2.08	0.49
1:B:12:LEU:HD23	1:B:27:ALA:HB2	1.94	0.49
1:C:65:LEU:HD23	1:C:66:THR:N	2.27	0.49
1:B:150:PHE:HB3	1:B:161:LEU:CD1	2.39	0.49
1:A:18:LEU:HG	1:D:165:GLU:OE2	2.12	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:D:100:GLU:CD	2:Y:83:LEU:CD1	2.81	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: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:104:PRO:HG2	1:A:184:ARG:HA	1.96	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:A:56:ILE:CG2	4:A:631:HOH:O	2.62	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:100:GLU:HG2	2:T:83:LEU:HD12	1.90	0.47
1:B:71:THR:H	1:B:74:ASN:ND2	2.11	0.47
2:Y:34:PRO:HB2	2:Y:36:GLU:OE1	2.15	0.47
2:T:40:LEU:HG	2:T:41:HIS:N	2.27	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

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
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:D:100:GLU:OE1	2:Y:83:LEU:HD13	2.16	0.46
1:D:62:ARG:NH1	1:D:64:LYS:HZ3	2.11	0.46
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
2:T:41:HIS:CD2	2:T:41:HIS:C	2.88	0.46
1:C:35:PRO:HA	1:C:83:THR:O	2.16	0.46
1:D:18:LEU:CD2	1:D:19:GLU:N	2.79	0.46
2:T:60:LEU:C	2:T:60:LEU:HD23	2.36	0.46
1:D:125:VAL:O	1:D:158:LEU:CD1	2.63	0.46
2:T:35:GLU:HA	2:T:55:GLY:O	2.16	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:HA	1:C:51:LEU:HD23	1.73	0.45
2:Y:85:TYR:CG	2:Y:86:GLN:N	2.84	0.45
1:D:47:SER:H	1:D:50:THR:CG2	2.26	0.45
1:C:16:VAL:HG22	1:C:96:LEU:HB3	1.97	0.45
1:A:10:GLN:HB2	1:A:10:GLN:HE21	1.55	0.45
2:T:69:MET:HG3	2:T:83:LEU:HD22	1.97	0.45
1:B:177:ASN:ND2	1:B:179:THR:CG2	2.78	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:C:54:VAL:HG12	1:C:67:ILE:HG12	1.99	0.45
1:A:71:THR:O	1:A:74:ASN:N	2.32	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:HD23	2:Y:60:LEU:C	2.38	0.44
2:Y:46:GLN:HG2	2:Y:47:ARG:HG3	1.99	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
1:A:34:VAL:CG2	1:A:34:VAL:O	2.65	0.44
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:C:18:LEU:HG	1:C:18:LEU:H	1.51	0.43
1:B:29:ILE:CG2	1:B:30:SER:N	2.81	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
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:126:ARG:HH11	1:C:126:ARG:CG	2.21	0.43
1:C:117:GLN:HB2	4:C:606:HOH:O	2.18	0.43
1:C:10:GLN:O	1:C:10:GLN:HG2	2.18	0.43
1:B:107:VAL:O	1:B:107:VAL:CG1	2.67	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:3:THR:CG2	1:B:3:THR:O	2.63	0.43
1:D:18:LEU:C	1:D:18:LEU:CD2	2.87	0.43
1:C:62:ARG:HE	1:C:62:ARG:C	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
2:Y:62:GLN:HB3	2:Y:70:ARG:HB3	2.01	0.42
1:C:126:ARG:HH12	1:C:158:LEU:CB	2.24	0.42
1:A:126:ARG:HH11	1:A:126:ARG:CG	2.28	0.42
2:Y:41:HIS:HD2	2:Y:41:HIS:O	2.02	0.42
1:D:18:LEU:O	1:D:19:GLU:C	2.56	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:170:ASP:O	1:D:171:SER:C	2.55	0.42
1:C:151:GLN:HE21	1:C:151:GLN:HB2	1.61	0.42
1:B:35:PRO:HA	1:B:83:THR:O	2.20	0.42
1:B:18:LEU:HD22	1:B:19:GLU:O	2.19	0.42
2:T:14:ASN:C	2:T:14:ASN:OD1	2.58	0.42
1:A:100:GLU:HB3	4:A:618:HOH:O	2.20	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:D:180:ASN:C	1:D:180:ASN:OD1	2.59	0.41
1:A:151:GLN:HE21	1:A:151:GLN:HB2	1.65	0.41
1:C:16:VAL:HG12	2:Y:74:LEU:HD21	2.02	0.41
1:D:107:VAL:HG12	1:D:107:VAL:O	2.21	0.41
1:B:103:PRO:HG2	2:T:65:PRO:HA	2.02	0.41
2:T:35:GLU:C	2:T:37:GLY:N	2.73	0.41
1:C:46:ILE:HD13	1:C:65:LEU:HD11	2.02	0.41
1:A:130:ILE:HD13	4:A:618:HOH:O	2.19	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
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:34:VAL:HA	1:B:35:PRO:HD3	1.86	0.41
1:A:152:ILE:HA	1:A:160:SER:O	2.20	0.41
1:B:92:THR:O	2:T:38:SER:HA	2.20	0.41
1:C:175:SER:HB3	1:C:188:THR:HG22	2.02	0.41
1:C:16:VAL:CG1	2:Y:74:LEU:CD2	2.99	0.41
1:D:18:LEU:C	1:D:18:LEU:HD22	2.41	0.41
1:C:34:VAL:HA	1:C:35:PRO:HD3	1.82	0.41
1:B:103:PRO:HG2	2:T:65:PRO:CA	2.51	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:A:34:VAL:HA	1:A:35:PRO:HD3	1.84	0.41
1:A:8:PHE:CE1	1:A:91:SER:HB2	2.56	0.41
1:D:51:LEU:HB3	1:D:54:VAL:HG13	2.01	0.41
1:D:168:PRO:C	1:D:170:ASP:N	2.73	0.41
1:D:22:THR:HA	1:D:67:ILE:O	2.21	0.41
1:D:132:THR:HA	1:D:133:PRO:HD3	1.86	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
2:Y:41:HIS:CD2	2:Y:41:HIS:O	2.74	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
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

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	192/201 (96%)	180 (94%)	10 (5%)	2 (1%)	22	56
1	B	195/201 (97%)	186 (95%)	9 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	189/201 (94%)	179 (95%)	8 (4%)	2 (1%)	21	53
1	D	192/201 (96%)	181 (94%)	10 (5%)	1 (0%)	38	74
2	T	87/167 (52%)	82 (94%)	4 (5%)	1 (1%)	21	53
2	Y	86/167 (52%)	79 (92%)	3 (4%)	4 (5%)	4	9
All	All	941/1138 (83%)	887 (94%)	44 (5%)	10 (1%)	21	53

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	T	84	PRO
1	C	54	VAL
2	Y	74	LEU
2	Y	84	PRO
1	C	68	PRO
1	D	148	LEU
2	Y	83	LEU
2	Y	75	GLY
1	A	68	PRO
1	A	72	LYS

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	162/169 (96%)	150 (93%)	12 (7%)	20	45
1	B	165/169 (98%)	145 (88%)	20 (12%)	7	19
1	C	160/169 (95%)	146 (91%)	14 (9%)	14	36
1	D	163/169 (96%)	145 (89%)	18 (11%)	9	24
2	T	81/147 (55%)	65 (80%)	16 (20%)	2	5
2	Y	80/147 (54%)	68 (85%)	12 (15%)	4	11
All	All	811/970 (84%)	719 (89%)	92 (11%)	9	22

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

Mol	Chain	Res	Type
1	A	7	THR
1	A	10	GLN
1	A	22	THR
1	A	50	THR
1	A	77	ARG
1	A	80	LEU
1	A	109	ARG
1	A	122	ARG
1	A	126	ARG
1	A	139	ARG
1	A	151	GLN
1	A	184	ARG
1	B	9	THR
1	B	18	LEU
1	B	37	VAL
1	B	46	ILE
1	B	50	THR
1	B	51	LEU
1	B	54	VAL
1	B	62	ARG
1	B	77	ARG
1	B	84	ASN
1	B	111	GLN
1	B	124	GLN
1	B	135	VAL
1	B	145	GLN
1	B	147	SER
1	B	148	LEU
1	B	155	GLU
1	B	179	THR
1	B	188	THR
1	B	196	GLU
2	T	3	THR
2	T	6	LEU
2	T	15	SER
2	T	18	ARG
2	T	22[A]	TRP
2	T	22[B]	TRP
2	T	29	THR
2	T	31	SER
2	T	41	HIS
2	T	43	GLU
2	T	47	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	T	59	VAL
2	T	63	ARG
2	T	64	SER
2	T	76	ARG
2	T	83	LEU
1	C	9	THR
1	C	10	GLN
1	C	17	VAL
1	C	18	LEU
1	C	34	VAL
1	C	49	SER
1	C	50	THR
1	C	62	ARG
1	C	71	THR
1	C	80	LEU
1	C	109	ARG
1	C	126	ARG
1	C	151	GLN
1	C	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
1	D	135	VAL
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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

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

Mol	Chain	Res	Type
1	A	10	GLN
1	A	74	ASN
1	A	117	GLN
1	A	124	GLN
1	A	151	GLN
1	A	194	GLN
1	B	28	HIS
1	B	74	ASN
1	B	88	GLN
1	B	105	ASN
1	B	117	GLN
1	B	124	GLN
1	B	151	GLN
1	B	177	ASN
2	T	41	HIS
2	T	46	GLN
2	T	48	HIS
2	T	52	HIS
2	T	53	GLN
2	T	62	GLN
1	C	10	GLN
1	C	117	GLN
1	C	151	GLN
1	C	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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	Y	41	HIS
2	Y	52	HIS
2	Y	53	GLN
2	Y	62	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	A	601	-	4,4,4	0.35	0	6,6,6	0.07	0
3	SO4	B	602	-	4,4,4	0.39	0	6,6,6	0.51	0
3	SO4	B	605	-	4,4,4	0.21	0	6,6,6	0.15	0
3	SO4	C	603	-	4,4,4	0.12	0	6,6,6	0.24	0
3	SO4	D	604	-	4,4,4	0.09	0	6,6,6	0.13	0

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	SO4	A	601	-	-	0/0/0/0	0/0/0/0
3	SO4	B	602	-	-	0/0/0/0	0/0/0/0
3	SO4	B	605	-	-	0/0/0/0	0/0/0/0
3	SO4	C	603	-	-	0/0/0/0	0/0/0/0
3	SO4	D	604	-	-	0/0/0/0	0/0/0/0

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.

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	194/201 (96%)	0.13	5 (2%)	53	57	19, 22, 25, 27	0
1	B	197/201 (98%)	0.24	9 (4%)	31	33	19, 22, 25, 31	0
1	C	191/201 (95%)	2.59	114 (59%)	0	0	17, 23, 26, 30	0
1	D	193/201 (96%)	1.21	46 (23%)	1	1	16, 23, 27, 30	0
2	T	88/167 (52%)	5.10	81 (92%)	0	0	19, 22, 26, 38	0
2	Y	88/167 (52%)	2.11	42 (47%)	1	0	19, 23, 27, 36	2 (2%)
All	All	951/1138 (83%)	1.51	297 (31%)	1	1	16, 23, 26, 38	2 (0%)

All (297) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	T	20	ALA	12.9
2	T	40	LEU	9.1
2	T	22[A]	TRP	8.9
2	T	39	SER	8.8
2	T	21	PHE	8.7
2	T	41	HIS	8.6
2	T	52	HIS	8.5
1	C	85	GLY	8.1
2	T	18	ARG	8.1
2	T	50	THR	8.0
2	Y	85	TYR	7.9
2	T	53	GLN	7.7
2	T	12	GLU	7.6
2	T	42	GLU	7.6
2	T	10	VAL	7.5
2	T	71	MET	7.4
2	T	69	MET	7.3
2	T	15	SER	7.3
2	T	25	TRP	7.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	T	38	SER	7.2
2	T	11	SER	7.2
1	D	2	THR	7.1
2	T	51	TYR	7.1
1	C	32	PHE	7.1
2	T	27	ASP	7.0
2	T	65	PRO	7.0
1	C	148	LEU	7.0
1	C	5	ALA	6.8
2	T	14	ASN	6.8
2	T	43	GLU	6.8
2	Y	1	MET	6.7
2	T	23	ALA	6.7
1	C	4	GLN	6.7
2	T	19	GLU	6.7
1	C	12	LEU	6.4
2	T	49	GLU	6.4
1	C	30	SER	6.4
2	T	8	SER	6.3
2	T	13	GLU	6.3
2	T	61	VAL	6.1
1	D	58	PHE	6.0
1	C	174	TYR	6.0
1	C	123	LEU	5.9
2	T	54	GLN	5.9
2	T	72	GLY	5.9
2	T	60	LEU	5.7
1	C	46	ILE	5.7
2	Y	86	GLN	5.7
1	D	33	PRO	5.7
2	T	68	MET	5.6
2	Y	4	SER	5.6
2	Y	88	VAL	5.5
2	T	67	LEU	5.5
2	T	74	LEU	5.3
2	T	83	LEU	5.3
1	C	147	SER	5.2
2	Y	84	PRO	5.2
2	T	62	GLN	5.2
2	T	78	LEU	5.1
1	C	122	ARG	5.1
1	D	32	PHE	5.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	T	28	LEU	5.1
2	Y	36	GLU	5.1
1	C	161	LEU	5.1
2	T	63	ARG	5.1
2	T	26	LYS	5.0
1	D	85	GLY	5.0
2	T	44	ASP	5.0
1	C	162	LEU	4.9
2	T	29	THR	4.9
2	T	30	LEU	4.9
1	C	124	GLN	4.9
1	D	3	THR	4.8
1	C	146	SER	4.8
1	C	93	ALA	4.8
2	T	37	GLY	4.7
1	C	176	VAL	4.7
1	C	60	ASP	4.7
1	C	125	VAL	4.7
1	C	189	ALA	4.7
1	C	175	SER	4.7
2	T	58	GLN	4.6
2	T	73	ILE	4.6
2	T	64	SER	4.6
1	C	165	GLU	4.6
1	C	117	GLN	4.5
1	C	151	GLN	4.5
1	C	149	ASP	4.5
1	C	167	TYR	4.5
2	T	57	SER	4.5
2	T	17	ARG	4.4
2	T	9	GLU	4.4
2	T	56	GLN	4.4
1	C	160	SER	4.4
1	C	87	GLY	4.4
1	D	31	GLY	4.4
1	C	78	TYR	4.4
1	C	187	SER	4.4
2	T	81	TYR	4.4
1	C	31	GLY	4.4
2	Y	66	TRP	4.4
1	C	113	MET	4.3
1	C	152	ILE	4.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	172	GLY	4.3
1	C	121	VAL	4.2
2	T	7	SER	4.2
1	C	188	THR	4.2
1	C	59	SER	4.2
2	T	75	GLY	4.2
1	D	60	ASP	4.2
2	Y	35	GLU	4.1
1	C	29	ILE	4.1
2	T	85	TYR	4.1
2	T	84	PRO	4.0
2	T	45	THR	4.0
1	C	153	SER	4.0
1	B	61	GLY	4.0
1	C	150	PHE	3.9
1	D	51	LEU	3.9
2	T	66	TRP	3.9
2	T	16	GLU	3.8
2	T	32	THR	3.8
1	C	62	ARG	3.8
2	T	70	ARG	3.8
1	D	47	SER	3.8
2	T	31	SER	3.8
2	T	24	GLU	3.7
2	T	55	GLY	3.7
2	Y	34	PRO	3.7
1	C	47	SER	3.7
1	D	73	ALA	3.7
1	C	194	GLN	3.7
1	C	110	LEU	3.7
2	Y	45	THR	3.7
1	C	159	TYR	3.7
2	T	6	LEU	3.7
1	D	34	VAL	3.7
2	T	59	VAL	3.7
1	C	164	ALA	3.6
2	Y	77	GLY	3.6
1	C	171	SER	3.6
1	C	191	LEU	3.6
1	B	4	GLN	3.5
1	C	163	ILE	3.5
2	T	46	GLN	3.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	118	GLY	3.5
1	D	35	PRO	3.5
1	D	29	ILE	3.5
2	Y	71	MET	3.5
1	D	8	PHE	3.5
1	C	45	VAL	3.5
2	Y	22	TRP	3.5
2	Y	3	THR	3.5
2	Y	68	MET	3.4
2	Y	83	LEU	3.4
1	D	116	ARG	3.4
1	C	19	GLU	3.4
1	C	115	VAL	3.3
1	C	86	SER	3.3
1	C	82	ALA	3.3
1	D	63	ALA	3.3
2	Y	65	PRO	3.3
1	D	10	GLN	3.3
1	C	126	ARG	3.3
1	C	61	GLY	3.2
2	T	47	ARG	3.2
1	B	1	MET	3.2
2	T	36	GLU	3.2
1	C	89	ALA	3.2
1	C	170	ASP	3.2
1	C	84	ASN	3.2
1	C	43	GLY	3.2
2	T	1	MET	3.2
2	T	77	GLY	3.2
1	D	193	VAL	3.1
1	C	49	SER	3.1
1	C	42	ASP	3.1
1	C	193	VAL	3.1
1	C	178	ALA	3.1
1	D	169	GLU	3.1
2	Y	41	HIS	3.0
2	Y	60	LEU	3.0
1	C	14	SER	3.0
2	T	34	PRO	3.0
1	D	62	ARG	3.0
2	Y	46	GLN	3.0
2	Y	33	ARG	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	T	80	GLU	2.9
2	T	4	SER	2.9
2	Y	24	GLU	2.9
1	B	32	PHE	2.9
1	C	129	GLY	2.9
1	C	144	ILE	2.9
2	Y	67	LEU	2.9
2	Y	6	LEU	2.8
2	Y	81	TYR	2.8
1	C	33	PRO	2.8
1	C	186	THR	2.8
1	C	109	ARG	2.8
2	T	35	GLU	2.8
1	D	52	PRO	2.8
1	C	91	SER	2.8
1	C	76	GLY	2.8
1	C	192	LEU	2.8
1	D	42	ASP	2.8
1	C	133	PRO	2.7
1	C	90	THR	2.7
1	C	106	PHE	2.7
2	Y	87	ARG	2.7
1	D	59	SER	2.7
1	C	6	PRO	2.7
1	C	154	GLN	2.7
1	C	177	ASN	2.7
2	T	33	ARG	2.7
1	C	145	GLN	2.7
1	D	5	ALA	2.7
1	D	44	GLN	2.7
1	D	6	PRO	2.6
1	D	30	SER	2.6
1	C	185	ALA	2.6
2	Y	63	ARG	2.6
2	Y	14	ASN	2.6
1	C	173	THR	2.6
1	C	137	PHE	2.6
1	C	127	VAL	2.6
2	Y	74	LEU	2.6
1	C	138	TYR	2.6
2	Y	51	TYR	2.6
1	C	184	ARG	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	53	GLY	2.5
1	C	66	THR	2.5
1	C	168	PRO	2.5
1	D	48	THR	2.5
1	C	131	PRO	2.5
1	A	116	ARG	2.5
1	C	120	GLN	2.5
1	D	178	ALA	2.5
1	C	156	GLY	2.4
1	C	13	GLN	2.4
1	C	108	GLN	2.4
1	A	58	PHE	2.4
2	Y	43	GLU	2.4
2	T	79	GLN	2.4
1	D	49	SER	2.4
1	C	107	VAL	2.4
2	Y	73	ILE	2.4
1	D	83	THR	2.4
1	D	23	ALA	2.3
1	D	56	ILE	2.3
1	D	76	GLY	2.3
1	C	190	GLU	2.3
2	Y	13	GLU	2.3
2	Y	17	ARG	2.3
1	C	112	SER	2.3
1	C	28	HIS	2.3
1	D	77	ARG	2.3
2	Y	56	GLN	2.3
1	D	61	GLY	2.3
1	B	29	ILE	2.3
1	D	115	VAL	2.3
1	C	136	LYS	2.3
1	A	85	GLY	2.3
2	Y	37	GLY	2.3
2	T	48	HIS	2.3
2	Y	5	GLU	2.3
1	D	86	SER	2.3
1	C	22	THR	2.2
2	Y	2	ALA	2.2
1	B	5	ALA	2.2
1	C	135	VAL	2.2
1	D	28	HIS	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	7	THR	2.2
1	B	2	THR	2.2
1	D	177	ASN	2.2
1	C	25	PHE	2.2
1	D	184	ARG	2.2
1	C	158	LEU	2.1
1	D	82	ALA	2.1
2	Y	69	MET	2.1
1	A	35	PRO	2.1
1	C	26	GLU	2.1
1	C	68	PRO	2.1
2	T	82	GLN	2.1
1	D	81	LYS	2.1
1	C	169	GLU	2.1
1	C	65	LEU	2.1
1	C	114	THR	2.1
1	C	15	VAL	2.1
1	C	52	PRO	2.1
1	C	57	SER	2.1
2	Y	82	GLN	2.1
1	A	29	ILE	2.1
1	C	77	ARG	2.1
1	C	97	VAL	2.0
1	B	151	GLN	2.0
1	B	87	GLY	2.0
2	Y	80	GLU	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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, 95th 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	SO4	B	602	5/5	0.27	5.70	16,17,19,20	5
3	SO4	A	601	5/5	0.27	1.97	13,13,15,16	5
3	SO4	D	604	5/5	0.31	1.26	21,25,26,26	5
3	SO4	B	605	5/5	0.31	0.24	18,20,21,22	5
3	SO4	C	603	5/5	0.23	-0.62	22,23,26,26	5

6.5 Other polymers ⓘ

There are no such residues in this entry.