



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:20 PM UTC

PDB ID : 2D1L / pdb_00002d1l
Title : Structure of F-actin binding domain IMD of MIM (Missing In Metastasis)
Authors : Lee, S.H.; Kerff, F.; Chereau, D.; Ferron, F.; Dominguez, R.
Deposited on : 2005-08-27
Resolution : 1.85 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

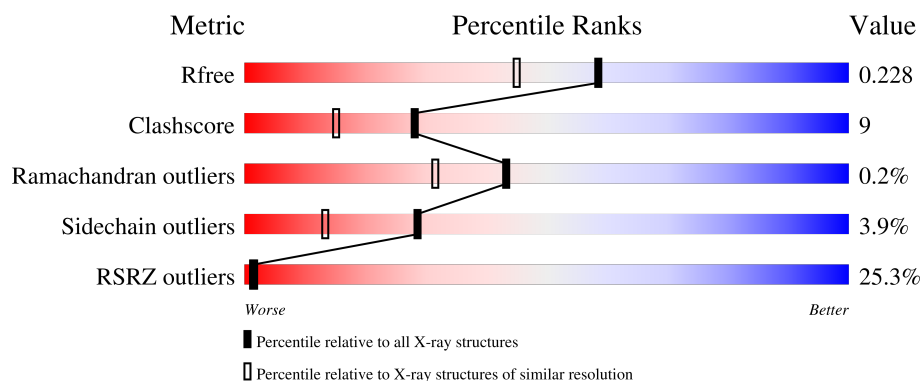
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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}	180053	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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 $\leq 5\%$. 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	253	21% 84% 13% ..
1	B	253	26% 72% 17% • 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4390 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 Metastasis suppressor protein 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	249	Total	C	N	O	S	Se	0	19	0
			2058	1290	358	394	4	12			
1	B	231	Total	C	N	O	S	Se	0	20	0
			1940	1224	339	362	4	11			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	ALA	-	cloning artifact	UNP Q8R1S4
A	-1	GLY	-	cloning artifact	UNP Q8R1S4
A	0	HIS	-	cloning artifact	UNP Q8R1S4
A	1	MSE	MET	modified residue	UNP Q8R1S4
A	23	MSE	MET	modified residue	UNP Q8R1S4
A	64	MSE	MET	modified residue	UNP Q8R1S4
A	82	MSE	MET	modified residue	UNP Q8R1S4
A	84	MSE	MET	modified residue	UNP Q8R1S4
A	112	MSE	MET	modified residue	UNP Q8R1S4
A	139	LYS	ASN	modified residue	UNP Q8R1S4
A	205	MSE	MET	modified residue	UNP Q8R1S4
A	216	MSE	MET	modified residue	UNP Q8R1S4
A	235	MSE	MET	modified residue	UNP Q8R1S4
B	-2	ALA	-	cloning artifact	UNP Q8R1S4
B	-1	GLY	-	cloning artifact	UNP Q8R1S4
B	0	HIS	-	cloning artifact	UNP Q8R1S4
B	1	MSE	MET	modified residue	UNP Q8R1S4
B	23	MSE	MET	modified residue	UNP Q8R1S4
B	64	MSE	MET	modified residue	UNP Q8R1S4
B	82	MSE	MET	modified residue	UNP Q8R1S4
B	84	MSE	MET	modified residue	UNP Q8R1S4
B	112	MSE	MET	modified residue	UNP Q8R1S4
B	139	LYS	ASN	modified residue	UNP Q8R1S4
B	205	MSE	MET	modified residue	UNP Q8R1S4
B	216	MSE	MET	modified residue	UNP Q8R1S4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	235	MSE	MET	modified residue	UNP Q8R1S4

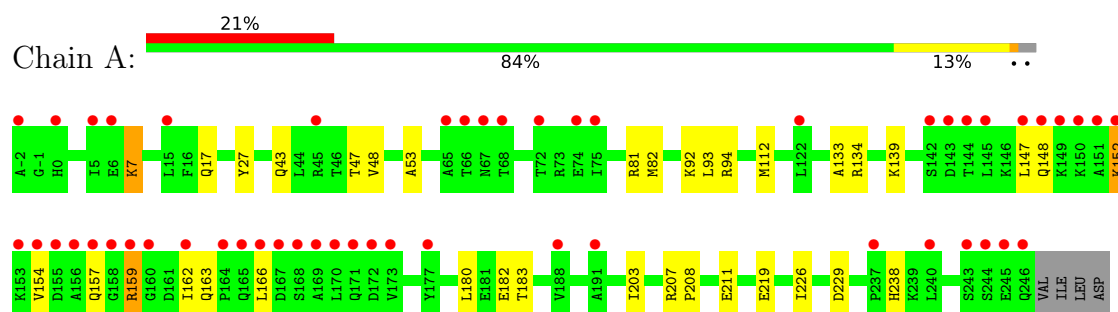
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	208	Total 208	O 208	0	0
2	B	184	Total 184	O 184	0	0

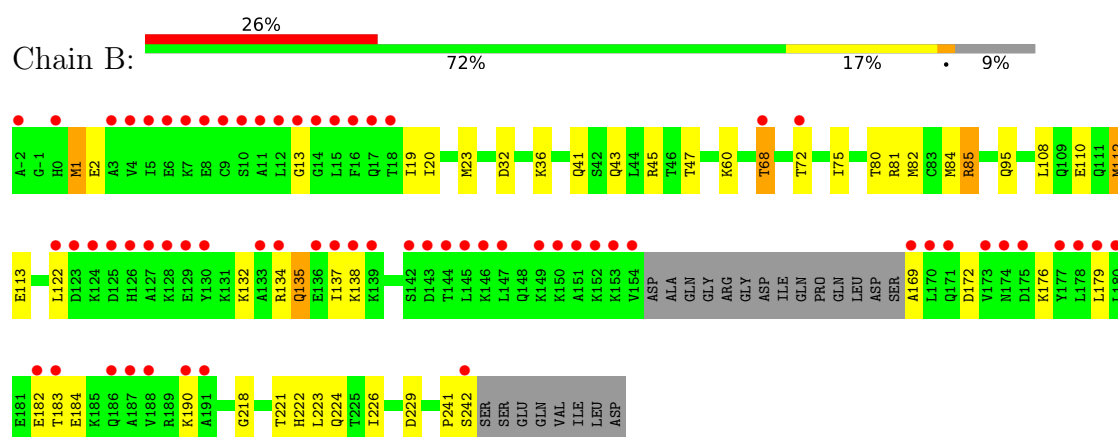
3 Residue-property plots [i](#)

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: Metastasis suppressor protein 1



• Molecule 1: Metastasis suppressor protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.50Å 37.32Å 129.02Å 90.00° 94.07° 90.00°	Depositor
Resolution (Å)	48.10 – 1.85 48.10 – 1.85	Depositor EDS
% Data completeness (in resolution range)	98.7 (48.10-1.85) 98.7 (48.10-1.85)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.183 , 0.228 0.184 , 0.228	Depositor DCC
R_{free} test set	2197 reflections (4.59%)	wwPDB-VP
Wilson B-factor (Å ²)	24.9	Xtriage
Anisotropy	0.295	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 60.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4390	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.41% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.64	0/2127	0.77	0/2825
1	B	0.77	2/2012 (0.1%)	0.77	0/2670
All	All	0.71	2/4139 (0.0%)	0.77	0/5495

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1	MSE	SE-CE	17.13	2.46	1.95
1	B	112	MSE	SE-CE	-6.95	1.74	1.95

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	A	2058	0	2157	32	0
1	B	1940	0	2058	46	0
2	A	208	0	0	1	0
2	B	184	0	0	9	0
All	All	4390	0	4215	73	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 (73) 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:224[B]:GLN:HG3	2:B:340:HOH:O	1.47	1.14
1:B:1:MSE:CE	1:B:1:MSE:SE	2.46	1.13
1:A:48:VAL:HG11	1:A:94:ARG:HG2	1.46	0.98
1:B:85[A]:ARG:HD3	1:B:222:HIS:HB3	1.45	0.95
1:B:85[A]:ARG:HD3	1:B:222:HIS:CB	1.98	0.93
1:B:84[A]:MSE:SE	2:B:420:HOH:O	2.40	0.89
1:A:152:LYS:HE3	1:A:152:LYS:HA	1.57	0.84
1:A:148:GLN:HG3	1:A:166:LEU:HD11	1.62	0.82
1:A:48:VAL:HG22	1:A:93:LEU:HD23	1.62	0.81
1:B:134:ARG:HD2	1:B:138:LYS:HE2	1.62	0.80
1:A:207[B]:ARG:HG3	1:A:208:PRO:HD3	1.65	0.77
1:B:81[A]:ARG:HA	1:B:84[A]:MSE:HE3	1.67	0.77
1:B:113[B]:GLU:HB2	2:B:316:HOH:O	1.86	0.75
1:A:154:VAL:HG13	1:A:159:ARG:HG3	1.72	0.72
1:B:95:GLN:NE2	2:B:432:HOH:O	2.23	0.72
1:A:48:VAL:HG11	1:A:94:ARG:CG	2.20	0.72
1:A:27:TYR:HD1	1:A:112[A]:MSE:HE1	1.57	0.70
1:B:80:THR:HG22	1:B:84[A]:MSE:HE2	1.74	0.69
1:B:81[A]:ARG:NH2	1:B:229[A]:ASP:OD2	2.20	0.68
1:A:27:TYR:HD1	1:A:112[A]:MSE:CE	2.08	0.66
1:B:122:LEU:HD13	1:B:190:LYS:HE2	1.76	0.66
1:A:112[B]:MSE:HA	1:A:112[B]:MSE:HE2	1.77	0.66
1:B:41:GLN:HE22	1:B:45[A]:ARG:HH11	1.45	0.63
1:B:68:THR:OG1	1:B:72:THR:HB	2.01	0.61
1:A:112[B]:MSE:HA	1:A:112[B]:MSE:CE	2.31	0.61
1:A:7:LYS:N	1:A:7:LYS:HD3	2.17	0.60
1:A:207[B]:ARG:HG3	1:A:208:PRO:CD	2.33	0.59
1:B:110[B]:GLU:OE2	2:B:292:HOH:O	2.17	0.59
1:A:133:ALA:HB3	1:A:180:LEU:HD13	1.83	0.59
1:B:19:ILE:HG22	1:B:23:MSE:HE2	1.85	0.58
1:B:80:THR:O	1:B:84[A]:MSE:HG3	2.04	0.58
1:A:43[B]:GLN:HG3	1:B:47:THR:OG1	2.03	0.58
1:B:85[A]:ARG:HD3	1:B:222:HIS:HB2	1.81	0.58
1:B:241:PRO:O	1:B:242:SER:C	2.47	0.57
1:A:238:HIS:H	1:A:238:HIS:CD2	2.24	0.55
1:B:113[A]:GLU:HB2	2:B:316:HOH:O	2.07	0.55
1:B:134:ARG:O	1:B:137:ILE:HG12	2.07	0.54
1:B:218:GLY:O	1:B:221:THR:HG22	2.08	0.54
1:A:203:ILE:HD11	1:B:75:ILE:HG23	1.89	0.53
1:B:32:ASP:OD2	2:B:408:HOH:O	2.18	0.53
1:A:152:LYS:HA	1:A:152:LYS:CE	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:LEU:O	1:B:112:MSE:HG2	2.09	0.52
1:A:43[B]:GLN:OE1	1:B:43[B]:GLN:NE2	2.40	0.52
1:B:13:GLY:HA3	1:B:184:GLU:OE2	2.10	0.50
1:A:207[B]:ARG:NH1	1:A:211:GLU:HB2	2.27	0.50
1:B:85[A]:ARG:HG3	1:B:226:ILE:CD1	2.41	0.50
1:B:113[A]:GLU:HG2	2:B:369:HOH:O	2.11	0.50
1:A:47:THR:HA	1:B:43[A]:GLN:HG2	1.94	0.50
1:A:133:ALA:CB	1:A:180:LEU:HD13	2.41	0.50
1:B:85[A]:ARG:HG3	1:B:226:ILE:HD12	1.95	0.48
1:B:137:ILE:HG22	1:B:176:LYS:CB	2.43	0.48
1:B:82[A]:MSE:SE	1:B:223:LEU:HD22	2.64	0.47
1:A:147:LEU:HB3	1:A:166:LEU:HD13	1.96	0.47
1:A:27:TYR:CD1	1:A:112[A]:MSE:CE	2.94	0.46
1:B:122:LEU:CD1	1:B:190:LYS:HE2	2.44	0.46
1:B:137:ILE:CG2	1:B:176:LYS:HB3	2.46	0.46
1:B:137:ILE:HG22	1:B:176:LYS:HB2	1.99	0.45
1:A:81[B]:ARG:NH1	1:A:229[B]:ASP:OD2	2.49	0.45
1:B:224[B]:GLN:CG	2:B:340:HOH:O	2.30	0.45
1:B:169:ALA:HA	1:B:172:ASP:OD2	2.17	0.44
1:B:20:ILE:HD13	1:B:23:MSE:HE3	1.99	0.44
1:B:135:GLN:O	1:B:135:GLN:HG3	2.19	0.43
1:A:82[B]:MSE:HE2	1:A:226:ILE:HG22	2.00	0.43
1:A:207[B]:ARG:NE	2:A:368:HOH:O	2.52	0.43
1:B:134:ARG:HD2	1:B:138:LYS:CE	2.38	0.42
1:A:159:ARG:HH11	1:A:163:GLN:HG2	1.83	0.42
1:A:154:VAL:HG12	1:A:154:VAL:O	2.20	0.42
1:A:92:LYS:NZ	1:A:219:GLU:OE2	2.37	0.42
1:B:2:GLU:HG3	1:B:138:LYS:HD3	2.01	0.42
1:B:60:LYS:HE2	1:B:60:LYS:HB3	1.76	0.42
1:A:27:TYR:CD1	1:A:112[A]:MSE:HE3	2.55	0.41
1:A:53:ALA:HB1	1:B:36[B]:LYS:HD2	2.03	0.41
1:B:41:GLN:HE22	1:B:45[A]:ARG:NH1	2.14	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	266/253 (105%)	258 (97%)	8 (3%)	0	100	100
1	B	247/253 (98%)	242 (98%)	4 (2%)	1 (0%)	30	17
All	All	513/506 (101%)	500 (98%)	12 (2%)	1 (0%)	43	31

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	68	THR

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	234/210 (111%)	224 (96%)	10 (4%)	26	11
1	B	220/210 (105%)	213 (97%)	7 (3%)	34	19
All	All	454/420 (108%)	437 (96%)	17 (4%)	28	15

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LYS
1	A	17	GLN
1	A	134	ARG
1	A	139	LYS
1	A	152	LYS
1	A	157	GLN
1	A	159	ARG
1	A	162	ILE
1	A	182	GLU
1	A	183	THR
1	B	85[A]	ARG

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Mol	Chain	Res	Type
1	B	85[B]	ARG
1	B	132	LYS
1	B	135	GLN
1	B	179	LEU
1	B	182	GLU
1	B	183	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	GLN
1	A	135	GLN
1	A	238	HIS
1	B	41	GLN
1	B	59	GLN
1	B	95	GLN
1	B	106	ASN
1	B	121	GLN
1	B	135	GLN
1	B	186	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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, 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	240/253 (94%)	1.06	52 (21%)	2 2	10, 26, 70, 84	16 (6%)
1	B	222/253 (87%)	1.24	65 (29%)	1 1	10, 26, 64, 83	18 (8%)
All	All	462/506 (91%)	1.15	117 (25%)	1 1	10, 26, 69, 84	34 (7%)

All (117) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	158	GLY	6.9
1	B	191	ALA	6.6
1	B	154	VAL	6.2
1	B	122	LEU	5.4
1	B	147	LEU	5.3
1	A	170	LEU	5.1
1	B	173	VAL	5.0
1	B	16	PHE	4.8
1	A	154	VAL	4.5
1	A	145	LEU	4.5
1	A	65	ALA	4.4
1	A	-2	ALA	4.4
1	B	-2	ALA	4.2
1	A	144	THR	4.2
1	A	75	ILE	4.2
1	B	130	TYR	4.2
1	B	151	ALA	4.1
1	A	244	SER	4.0
1	A	67	ASN	4.0
1	A	147	LEU	3.9
1	B	124	LYS	3.9
1	B	150	LYS	3.9
1	B	18	THR	3.7
1	A	169	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	133	ALA	3.7
1	B	123	ASP	3.6
1	A	166	LEU	3.6
1	A	68	THR	3.5
1	A	155	ASP	3.5
1	B	153	LYS	3.5
1	B	170	LEU	3.5
1	B	125	ASP	3.5
1	B	127	ALA	3.5
1	B	14	GLY	3.5
1	A	142	SER	3.4
1	B	146	LYS	3.3
1	A	191	ALA	3.3
1	B	9	CYS	3.3
1	A	5	ILE	3.3
1	B	5	ILE	3.3
1	A	177	TYR	3.2
1	A	0	HIS	3.2
1	B	126	HIS	3.2
1	A	151	ALA	3.2
1	A	66	THR	3.2
1	B	188	VAL	3.2
1	B	15	LEU	3.2
1	A	150	LYS	3.2
1	B	0	HIS	3.2
1	B	171	GLN	3.1
1	A	153	LYS	3.1
1	B	169	ALA	3.1
1	B	177	TYR	3.1
1	A	171	GLN	3.1
1	B	143	ASP	3.0
1	B	4	VAL	3.0
1	B	8	GLU	3.0
1	B	134	ARG	3.0
1	B	139	LYS	2.9
1	B	149	LYS	2.9
1	B	3	ALA	2.9
1	A	122	LEU	2.9
1	B	145	LEU	2.9
1	A	156	ALA	2.8
1	A	172	ASP	2.8
1	B	187	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	182	GLU	2.8
1	B	144	THR	2.7
1	B	12	LEU	2.7
1	A	72	THR	2.6
1	A	152	LYS	2.6
1	A	237	PRO	2.6
1	B	128	LYS	2.6
1	A	240	LEU	2.6
1	A	160	GLY	2.6
1	B	178	LEU	2.6
1	B	11	ALA	2.6
1	B	7	LYS	2.6
1	B	142	SER	2.6
1	B	137	ILE	2.6
1	B	152	LYS	2.6
1	A	246	GLN	2.5
1	B	129	GLU	2.5
1	B	17	GLN	2.5
1	B	13	GLY	2.4
1	B	186	GLN	2.4
1	A	243	SER	2.4
1	B	72	THR	2.4
1	B	180	LEU	2.4
1	B	190	LYS	2.4
1	B	10	SER	2.4
1	A	159	ARG	2.4
1	A	162	ILE	2.4
1	A	245	GLU	2.3
1	B	136	GLU	2.3
1	A	173	VAL	2.3
1	A	165	GLN	2.3
1	B	183	THR	2.3
1	A	148	GLN	2.2
1	A	188	VAL	2.2
1	B	6	GLU	2.2
1	A	164	PRO	2.2
1	B	138	LYS	2.2
1	B	179	LEU	2.2
1	A	149	LYS	2.2
1	A	74	GLU	2.2
1	B	242	SER	2.2
1	A	15	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	45	ARG	2.1
1	A	157	GLN	2.1
1	A	168	SER	2.1
1	A	6	GLU	2.1
1	B	174	ASN	2.1
1	A	143	ASP	2.1
1	A	167	ASP	2.1
1	B	175	ASP	2.0
1	B	68	THR	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 oligosaccharides 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.