



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:22 PM UTC

PDB ID : 7PQ6 / pdb_00007pq6
Title : Crystal Structure of the Ring Nuclease 0811 mutant-S12A from *Sulfolobus islandicus* (Sis0811)
Authors : Molina, R.; Jensen, A.L.G.; Marchena-Hurtado, J.; Lopez-Mendez, B.; Stella, S.; Montoya, G.
Deposited on : 2021-09-16
Resolution : 2.67 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
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

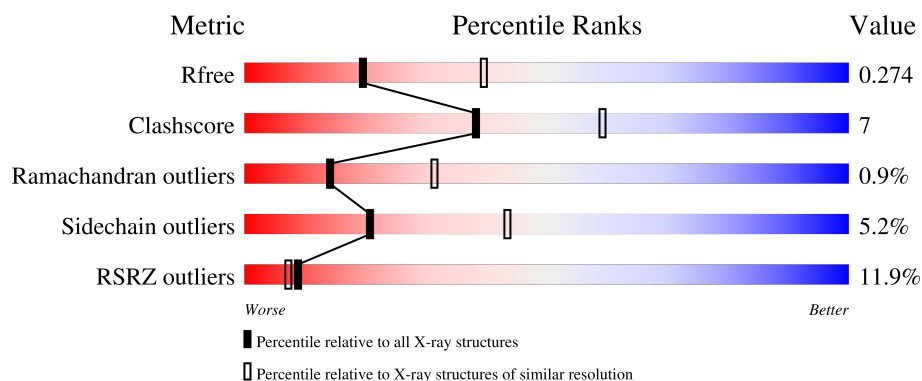
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.67 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	5070 (2.70-2.66)
Clashscore	190562	5409 (2.70-2.66)
Ramachandran outliers	187476	5324 (2.70-2.66)
Sidechain outliers	187428	5324 (2.70-2.66)
RSRZ outliers	180081	5070 (2.70-2.66)

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	AAA	275	
1	BBB	275	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4443 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 CRISPR-associated protein, APE2256 family.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	275	Total	C	N	O	S	0	0	0
			2233	1443	358	430	2			
1	BBB	272	Total	C	N	O	S	0	0	0
			2207	1427	355	423	2			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	12	ALA	SER	engineered mutation	UNP F0NH89
AAA	269	GLY	-	expression tag	UNP F0NH89
AAA	270	SER	-	expression tag	UNP F0NH89
AAA	271	GLU	-	expression tag	UNP F0NH89
AAA	272	PHE	-	expression tag	UNP F0NH89
AAA	273	GLU	-	expression tag	UNP F0NH89
AAA	274	LEU	-	expression tag	UNP F0NH89
AAA	275	GLU	-	expression tag	UNP F0NH89
BBB	12	ALA	SER	engineered mutation	UNP F0NH89
BBB	269	GLY	-	expression tag	UNP F0NH89
BBB	270	SER	-	expression tag	UNP F0NH89
BBB	271	GLU	-	expression tag	UNP F0NH89
BBB	272	PHE	-	expression tag	UNP F0NH89
BBB	273	GLU	-	expression tag	UNP F0NH89
BBB	274	LEU	-	expression tag	UNP F0NH89
BBB	275	GLU	-	expression tag	UNP F0NH89

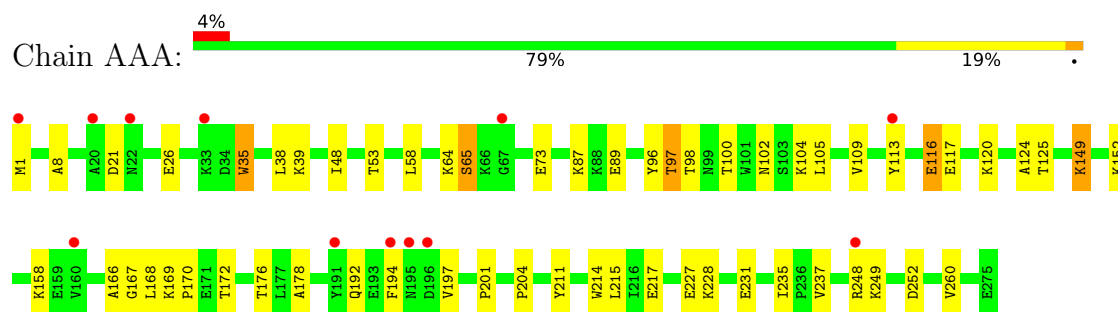
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AAA	2	Total	O	0	0
			2	2		
2	BBB	1	Total	O	0	0
			1	1		

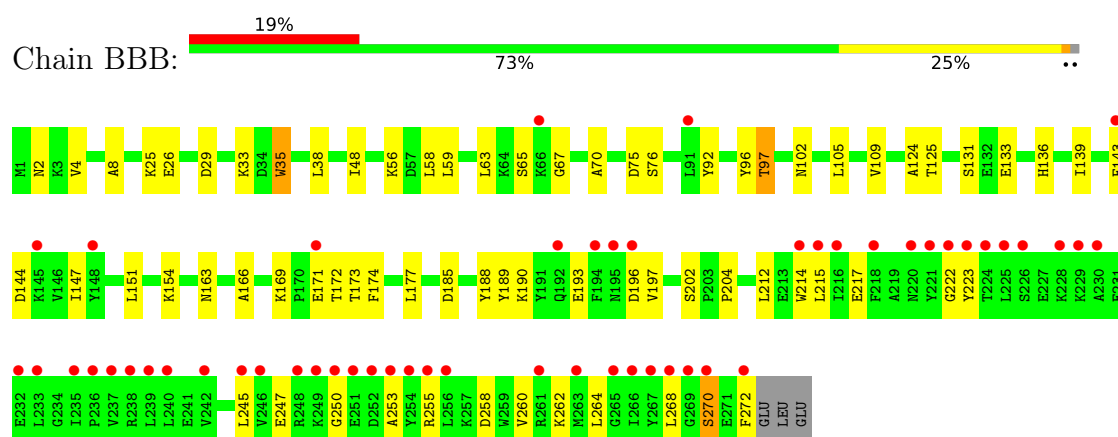
3 Residue-property plots [i](#)

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: CRISPR-associated protein, APE2256 family



- Molecule 1: CRISPR-associated protein, APE2256 family



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	77.05Å 103.73Å 77.68Å 90.00° 102.99° 90.00°	Depositor
Resolution (Å)	60.82 – 2.67 60.82 – 2.67	Depositor EDS
% Data completeness (in resolution range)	95.5 (60.82-2.67) 95.5 (60.82-2.67)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.30 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.220 , 0.280 0.220 , 0.274	Depositor DCC
R_{free} test set	839 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	34.0	Xtriage
Anisotropy	0.363	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 25.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	4443	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.30% 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

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	AAA	1.05	0/2274	1.52	7/3066 (0.2%)
1	BBB	1.05	0/2248	1.46	4/3031 (0.1%)
All	All	1.05	0/4522	1.49	11/6097 (0.2%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	97	THR	CA-CB-OG1	-6.81	99.38	109.60
1	BBB	136	HIS	CA-CB-CG	-5.82	107.98	113.80
1	BBB	97	THR	CA-CB-OG1	-5.76	100.97	109.60
1	AAA	178	ALA	CA-C-N	5.47	126.17	119.99
1	AAA	178	ALA	C-N-CA	5.47	126.17	119.99
1	BBB	67	GLY	CA-C-N	5.36	129.27	120.63
1	BBB	67	GLY	C-N-CA	5.36	129.27	120.63
1	AAA	53	THR	CA-C-N	5.17	127.47	120.65
1	AAA	53	THR	C-N-CA	5.17	127.47	120.65
1	AAA	98	THR	CA-CB-OG1	-5.11	101.93	109.60
1	AAA	237	VAL	CA-C-O	-5.09	115.76	121.05

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AAA	2233	0	2263	32	0
1	BBB	2207	0	2240	41	0
2	AAA	2	0	0	0	0
2	BBB	1	0	0	0	0
All	All	4443	0	4503	62	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (62) 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:AAA:211:TYR:CD2	1:BBB:204:PRO:HG2	2.25	0.70
1:AAA:89:GLU:H	1:AAA:89:GLU:CD	2.05	0.65
1:BBB:131:SER:HB2	1:BBB:133:GLU:OE2	1.98	0.63
1:AAA:176:THR:HG21	1:BBB:173:THR:CG2	2.33	0.59
1:AAA:149:LYS:HE2	1:AAA:152:LYS:HE2	1.85	0.59
1:AAA:214:TRP:CD1	1:AAA:235:ILE:HG12	2.39	0.57
1:BBB:26:GLU:HA	1:BBB:26:GLU:OE1	2.05	0.57
1:AAA:73:GLU:HG3	1:AAA:166:ALA:HB2	1.89	0.55
1:AAA:169:LYS:NZ	1:BBB:166:ALA:O	2.41	0.54
1:BBB:247:GLU:OE1	1:BBB:255:ARG:NH1	2.35	0.54
1:BBB:215:LEU:HB3	1:BBB:264:LEU:HD11	1.89	0.53
1:BBB:212:LEU:HD11	1:BBB:268:LEU:HD13	1.91	0.52
1:BBB:97:THR:O	1:BBB:125:THR:HA	2.08	0.52
1:BBB:96:TYR:HA	1:BBB:124:ALA:O	2.11	0.51
1:AAA:96:TYR:HA	1:AAA:124:ALA:O	2.11	0.51
1:BBB:25:LYS:NZ	1:BBB:29:ASP:OD2	2.42	0.51
1:AAA:97:THR:O	1:AAA:125:THR:HA	2.12	0.50
1:AAA:204:PRO:HD3	1:BBB:245:LEU:HD11	1.94	0.49
1:AAA:201:PRO:HG2	1:BBB:139:ILE:HG21	1.95	0.49
1:AAA:100:THR:O	1:AAA:104:LYS:HG3	2.13	0.48
1:BBB:250:GLY:HA3	1:BBB:253:ALA:HB3	1.94	0.48
1:AAA:167:GLY:O	1:BBB:169:LYS:NZ	2.43	0.47
1:AAA:211:TYR:CG	1:BBB:204:PRO:HG2	2.50	0.47
1:BBB:35:TRP:HA	1:BBB:38:LEU:HG	1.97	0.46
1:AAA:149:LYS:HE2	1:AAA:152:LYS:CE	2.46	0.46
1:BBB:163:ASN:HB2	1:BBB:188:TYR:CZ	2.50	0.46
1:AAA:64:LYS:NZ	1:AAA:116:GLU:OE1	2.44	0.46
1:AAA:48:ILE:CD1	1:AAA:102:ASN:HB3	2.46	0.46
1:AAA:1:MET:O	1:AAA:158:LYS:HD3	2.17	0.45
1:BBB:4:VAL:HA	1:BBB:92:TYR:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:214:TRP:O	1:AAA:217:GLU:HB2	2.17	0.45
1:AAA:26:GLU:HG2	1:AAA:58:LEU:HD22	1.99	0.45
1:BBB:8:ALA:HB2	1:BBB:96:TYR:CZ	2.52	0.45
1:AAA:176:THR:HG21	1:BBB:173:THR:HG21	1.99	0.44
1:BBB:59:LEU:O	1:BBB:63:LEU:HB2	2.17	0.44
1:AAA:227:GLU:O	1:AAA:231:GLU:HG3	2.17	0.44
1:BBB:222:GLY:O	1:BBB:223:TYR:CG	2.71	0.44
1:BBB:143:PHE:HA	1:BBB:147:ILE:HB	2.00	0.44
1:AAA:166:ALA:O	1:AAA:172:THR:HG21	2.17	0.43
1:AAA:215:LEU:HD22	1:AAA:260:VAL:HG11	2.01	0.43
1:BBB:144:ASP:OD2	1:BBB:262:LYS:HD2	2.17	0.43
1:AAA:8:ALA:HB2	1:AAA:96:TYR:CZ	2.53	0.43
1:AAA:169:LYS:HE2	1:BBB:172:THR:HG21	2.01	0.43
1:BBB:222:GLY:O	1:BBB:223:TYR:CD2	2.72	0.43
1:AAA:105:LEU:O	1:AAA:109:VAL:HG23	2.19	0.43
1:BBB:143:PHE:CE2	1:BBB:174:PHE:HZ	2.37	0.43
1:AAA:113:TYR:O	1:AAA:117:GLU:HG2	2.19	0.43
1:BBB:105:LEU:O	1:BBB:109:VAL:HG23	2.19	0.43
1:BBB:48:ILE:CD1	1:BBB:102:ASN:HB3	2.49	0.42
1:BBB:76:SER:HB3	1:BBB:190:LYS:HB3	2.01	0.42
1:AAA:194:PHE:CZ	1:BBB:131:SER:N	2.88	0.42
1:BBB:63:LEU:HD12	1:BBB:63:LEU:HA	1.79	0.42
1:BBB:215:LEU:HD22	1:BBB:260:VAL:HG11	2.02	0.41
1:BBB:75:ASP:CG	1:BBB:190:LYS:NZ	2.78	0.41
1:BBB:58:LEU:HD12	1:BBB:58:LEU:HA	1.87	0.41
1:BBB:154:LYS:NZ	1:BBB:185:ASP:OD2	2.51	0.41
1:AAA:35:TRP:HA	1:AAA:38:LEU:HG	2.03	0.41
1:BBB:63:LEU:CD1	1:BBB:70:ALA:HB3	2.51	0.41
1:BBB:214:TRP:O	1:BBB:217:GLU:HB2	2.21	0.41
1:AAA:87:LYS:HB3	1:AAA:89:GLU:OE2	2.21	0.40
1:AAA:170:PRO:HD3	1:BBB:189:TYR:CZ	2.56	0.40
1:BBB:151:LEU:HD12	1:BBB:151:LEU:HA	1.94	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	AAA	273/275 (99%)	265 (97%)	7 (3%)	1 (0%)	30	51
1	BBB	270/275 (98%)	251 (93%)	15 (6%)	4 (2%)	8	19
All	All	543/550 (99%)	516 (95%)	22 (4%)	5 (1%)	14	31

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	BBB	270	SER
1	BBB	196	ASP
1	AAA	65	SER
1	BBB	65	SER
1	BBB	193	GLU

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	AAA	244/244 (100%)	230 (94%)	14 (6%)	18	40
1	BBB	241/244 (99%)	230 (95%)	11 (5%)	24	48
All	All	485/488 (99%)	460 (95%)	25 (5%)	21	43

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	21	ASP
1	AAA	35	TRP
1	AAA	39	LYS
1	AAA	65	SER
1	AAA	116	GLU
1	AAA	120	LYS
1	AAA	149	LYS

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Mol	Chain	Res	Type
1	AAA	168	LEU
1	AAA	192	GLN
1	AAA	197	VAL
1	AAA	228	LYS
1	AAA	248	ARG
1	AAA	249	LYS
1	AAA	252	ASP
1	BBB	2	ASN
1	BBB	33	LYS
1	BBB	35	TRP
1	BBB	56	LYS
1	BBB	171	GLU
1	BBB	177	LEU
1	BBB	197	VAL
1	BBB	202	SER
1	BBB	258	ASP
1	BBB	270	SER
1	BBB	272	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 [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

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	AAA	275/275 (100%)	0.46	12 (4%) 39 34	20, 32, 64, 85	0
1	BBB	272/275 (98%)	0.96	53 (19%) 3 2	17, 32, 117, 135	0
All	All	547/550 (99%)	0.71	65 (11%) 9 7	17, 32, 97, 135	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	218	PHE	10.3
1	BBB	266	ILE	7.2
1	BBB	253	ALA	6.9
1	BBB	267	TYR	6.5
1	BBB	239	LEU	5.6
1	BBB	233	LEU	5.3
1	BBB	242	VAL	5.1
1	BBB	225	LEU	4.8
1	BBB	226	SER	4.8
1	BBB	272	PHE	4.8
1	BBB	268	LEU	4.5
1	BBB	215	LEU	4.4
1	BBB	236	PRO	4.3
1	BBB	235	ILE	4.0
1	BBB	256	LEU	4.0
1	BBB	228	LYS	3.9
1	AAA	33	LYS	3.7
1	AAA	195	ASN	3.5
1	BBB	220	ASN	3.4
1	BBB	252	ASP	3.4
1	BBB	221	TYR	3.3
1	BBB	240	LEU	3.3
1	BBB	254	TYR	3.3
1	BBB	148	TYR	3.3

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Mol	Chain	Res	Type	RSRZ
1	BBB	196	ASP	3.2
1	BBB	249	LYS	3.2
1	BBB	66	LYS	3.2
1	BBB	245	LEU	3.2
1	BBB	222	GLY	3.2
1	BBB	230	ALA	3.1
1	BBB	265	GLY	3.0
1	BBB	229	LYS	2.9
1	BBB	143	PHE	2.9
1	BBB	250	GLY	2.9
1	AAA	196	ASP	2.9
1	BBB	171	GLU	2.8
1	BBB	246	VAL	2.7
1	BBB	223	TYR	2.6
1	BBB	91	LEU	2.6
1	BBB	255	ARG	2.6
1	BBB	237	VAL	2.6
1	BBB	263	MET	2.5
1	AAA	248	ARG	2.5
1	BBB	238	ARG	2.5
1	BBB	194	PHE	2.5
1	BBB	270	SER	2.4
1	AAA	1	MET	2.4
1	BBB	269	GLY	2.4
1	BBB	261	ARG	2.4
1	AAA	191	TYR	2.3
1	BBB	145	LYS	2.3
1	BBB	216	ILE	2.2
1	BBB	248	ARG	2.2
1	AAA	22	ASN	2.2
1	BBB	232	GLU	2.2
1	AAA	20	ALA	2.1
1	BBB	224	THR	2.1
1	AAA	113	TYR	2.1
1	BBB	251	GLU	2.1
1	BBB	214	TRP	2.0
1	BBB	192	GLN	2.0
1	AAA	67	GLY	2.0
1	AAA	160	VAL	2.0
1	AAA	194	PHE	2.0
1	BBB	195	ASN	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.