



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:43 PM UTC

PDB ID : 8HN6 / pdb_00008hn6
Title : Crystal structure of monoclonal antibody complexed with SARS-CoV-2 RBD
Authors : Qi, J.; Chen, Y.
Deposited on : 2022-12-07
Resolution : 2.07 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

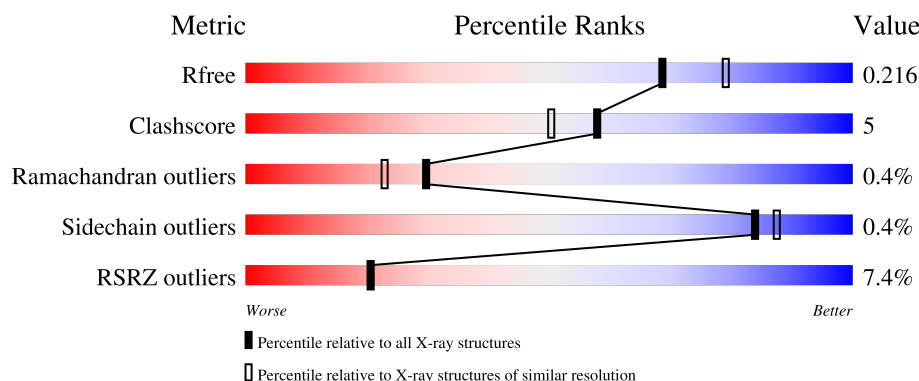
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 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	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

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	117	3% 86% 13% .
1	C	117	3% 93% 7% .
2	B	108	5% 90% 9% .
2	D	108	6% 88% 11% .
3	E	195	12% 89% 11% .

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Mol	Chain	Length	Quality of chain
3	F	195	11% 87% 13%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7012 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 Heavy chain of monoclonal antibody 3G10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	116	Total	C	N	O	S	0	0	0
			882	553	149	174	6			
1	C	117	Total	C	N	O	S	0	0	0
			887	556	150	175	6			

- Molecule 2 is a protein called Light chain of monoclonal antibody 3G10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	108	Total	C	N	O	S	0	0	0
			833	533	137	160	3			
2	D	108	Total	C	N	O	S	0	0	0
			827	527	137	160	3			

- Molecule 3 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	195	Total	C	N	O	S	0	1	0
			1533	979	257	289	8			
3	F	195	Total	C	N	O	S	0	1	0
			1545	990	257	290	8			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	57	Total	O	0	0
			57	57		
4	B	71	Total	O	0	0
			71	71		
4	E	107	Total	O	0	0
			107	107		
4	C	87	Total	O	0	0
			87	87		

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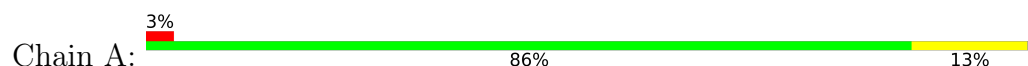
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	64	Total 64	O 64	0	0
4	F	119	Total 119	O 119	0	0

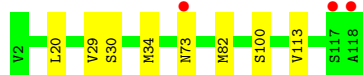
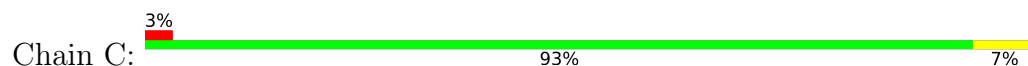
3 Residue-property plots [i](#)

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: Heavy chain of monoclonal antibody 3G10



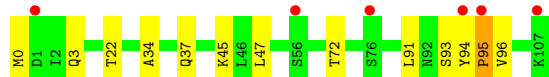
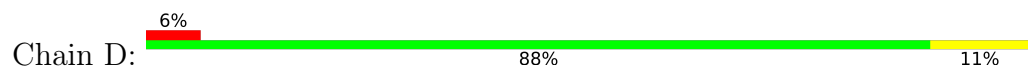
- Molecule 1: Heavy chain of monoclonal antibody 3G10



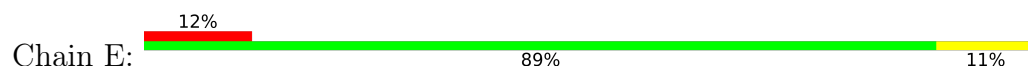
- Molecule 2: Light chain of monoclonal antibody 3G10



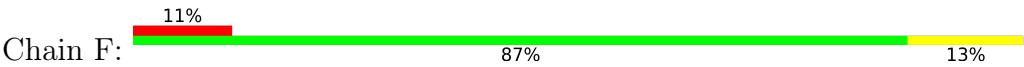
- Molecule 2: Light chain of monoclonal antibody 3G10



- Molecule 3: Spike protein S1



- Molecule 3: Spike protein S1



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	98.68Å 105.73Å 209.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.43 – 2.07 26.43 – 2.07	Depositor EDS
% Data completeness (in resolution range)	99.6 (26.43-2.07) 99.9 (26.43-2.07)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.06Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.192 , 0.214 0.193 , 0.216	Depositor DCC
R_{free} test set	3120 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å ²)	35.5	Xtriage
Anisotropy	0.269	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.0	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	0.95	EDS
Total number of atoms	7012	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.02% of the height of the origin peak. No significant pseudotranslation is detected.*

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	0.34	0/899	0.67	1/1218 (0.1%)
1	C	0.39	0/904	0.61	0/1225
2	B	0.45	0/853	0.72	1/1158 (0.1%)
2	D	0.47	0/846	0.77	1/1149 (0.1%)
3	E	0.36	0/1578	0.55	0/2149
3	F	0.36	0/1592	0.59	0/2169
All	All	0.39	0/6672	0.64	3/9068 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	101	TYR	N-CA-C	-8.26	103.80	114.04
2	D	95	PRO	N-CA-C	-7.78	96.45	112.47
2	B	95	PRO	N-CA-C	-7.44	97.15	112.47

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	882	0	852	10	0
1	C	887	0	857	5	0
2	B	833	0	823	10	0
2	D	827	0	816	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	1533	0	1451	14	0
3	F	1545	0	1457	18	0
4	A	57	0	0	0	0
4	B	71	0	0	1	0
4	C	87	0	0	0	0
4	D	64	0	0	1	0
4	E	107	0	0	0	0
4	F	119	0	0	2	0
All	All	7012	0	6256	58	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 5.

All (58) 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)
3:E:503:VAL:HG12	2:D:0:MET:HE1	1.68	0.74
1:A:12:VAL:HG22	1:A:16:GLU:HB2	1.73	0.71
3:E:362:VAL:HG13	3:E:527:PRO:HD2	1.73	0.69
2:D:22:THR:HG22	2:D:72:THR:HG22	1.75	0.68
3:F:377:PHE:CD1	3:F:434:ILE:HG12	2.30	0.66
2:B:24:ARG:NH1	3:F:374:PHE:O	2.29	0.66
3:F:372:ALA:C	3:F:374:PHE:H	2.05	0.65
1:C:30:SER:HB3	1:C:73:ASN:ND2	2.14	0.62
3:E:386:LYS:HE3	3:E:390:LEU:HD21	1.80	0.62
3:F:362:VAL:HG13	3:F:527:PRO:HD2	1.81	0.62
3:E:362:VAL:HG13	3:E:526:GLY:HA2	1.83	0.60
2:D:94:TYR:O	2:D:96:VAL:N	2.36	0.58
3:E:443:SER:O	3:E:444:LYS:HE2	2.04	0.57
1:A:50:VAL:HG21	2:B:94:TYR:CZ	2.39	0.57
2:B:94:TYR:O	2:B:96:VAL:N	2.37	0.57
3:F:364:ASP:O	3:F:367:VAL:HG22	2.05	0.56
2:D:45:LYS:HD2	4:D:227:HOH:O	2.06	0.56
3:F:377:PHE:HD1	3:F:434:ILE:HG12	1.72	0.55
3:E:364:ASP:O	3:E:367:VAL:HG22	2.07	0.54
1:A:12:VAL:HG11	1:A:85:LEU:HD13	1.88	0.54
2:D:94:TYR:C	2:D:96:VAL:N	2.65	0.54
3:F:376:THR:HG22	4:F:669:HOH:O	2.08	0.53
2:D:34:ALA:HB2	2:D:91:LEU:HD21	1.91	0.53
3:E:368:LEU:HD22	3:E:377:PHE:HE2	1.73	0.52
3:F:371:SER:O	3:F:372:ALA:HB3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:LEU:HG	1:A:82:MET:HE2	1.94	0.50
1:A:82:MET:HE1	1:A:113:VAL:HG21	1.94	0.49
3:F:372:ALA:C	3:F:374:PHE:N	2.70	0.48
2:B:7:PHE:HA	2:B:8:PRO:C	2.39	0.48
1:C:20:LEU:HG	1:C:82:MET:HE2	1.96	0.48
3:E:368:LEU:HD22	3:E:377:PHE:CE2	2.49	0.47
3:E:374:PHE:O	3:E:375:SER:C	2.57	0.47
2:B:37:GLN:HB2	2:B:47:LEU:HD11	1.96	0.47
3:F:357:ARG:NH1	3:F:359:SER:OG	2.44	0.47
3:F:391:CYS:HB3	3:F:522:ALA:HB1	1.97	0.46
3:F:354:ASN:O	3:F:398:ASP:HA	2.15	0.46
2:B:2:ILE:CD1	2:B:27:GLN:HB2	2.46	0.46
2:D:95:PRO:HG2	4:F:718:HOH:O	2.16	0.46
3:E:376:THR:HG23	2:D:3:GLN:OE1	2.17	0.44
1:A:47:TRP:CG	2:B:96:VAL:HB	2.54	0.43
1:C:29:VAL:HG13	1:C:34:MET:HG3	2.00	0.43
1:A:42:GLY:C	1:A:43:LYS:HD2	2.43	0.43
2:D:37:GLN:HB2	2:D:47:LEU:HD11	2.00	0.43
3:F:368:LEU:O	3:F:371:SER:HB3	2.18	0.43
1:C:82:MET:HE1	1:C:113:VAL:HG21	2.01	0.43
3:F:369:TYR:HA	3:F:374:PHE:CD2	2.53	0.43
1:A:33:TYR:HB3	2:B:94:TYR:OH	2.19	0.43
1:C:100:SER:HB3	3:F:455:LEU:HD11	2.01	0.42
1:A:50:VAL:HG21	2:B:94:TYR:CE1	2.54	0.42
3:E:412:PRO:HG3	3:E:429:PHE:HB3	2.02	0.42
2:B:27:GLN:NE2	4:B:205:HOH:O	2.52	0.41
1:A:66:ARG:HG2	1:A:83:ASN:O	2.19	0.41
3:F:387:LEU:C	3:F:389:ASP:H	2.28	0.41
3:E:342:PHE:CZ	3:E:368:LEU:HD11	2.55	0.41
3:E:354:ASN:O	3:E:398:ASP:HA	2.21	0.40
3:F:412:PRO:HG3	3:F:429:PHE:HB3	2.02	0.40
3:E:376:THR:O	3:E:434:ILE:HA	2.22	0.40
3:F:379:CYS:HA	3:F:432:CYS:HA	2.04	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	114/117 (97%)	113 (99%)	1 (1%)	0	100	100
1	C	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
2	B	106/108 (98%)	101 (95%)	4 (4%)	1 (1%)	14	7
2	D	106/108 (98%)	100 (94%)	6 (6%)	0	100	100
3	E	194/195 (100%)	183 (94%)	9 (5%)	2 (1%)	12	5
3	F	194/195 (100%)	185 (95%)	9 (5%)	0	100	100
All	All	829/840 (99%)	795 (96%)	31 (4%)	3 (0%)	30	23

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	E	375	SER
3	E	373	SER
2	B	95	PRO

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	95/95 (100%)	94 (99%)	1 (1%)	65	68
1	C	95/95 (100%)	95 (100%)	0	100	100
2	B	92/92 (100%)	91 (99%)	1 (1%)	65	68
2	D	91/92 (99%)	90 (99%)	1 (1%)	65	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	E	167/168 (99%)	167 (100%)	0	100	100
3	F	168/168 (100%)	168 (100%)	0	100	100
All	All	708/710 (100%)	705 (100%)	3 (0%)	84	87

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	VAL
2	B	93	SER
2	D	93	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	39	GLN
1	A	81	GLN
2	B	3	GLN
2	B	27	GLN
2	B	38	GLN
3	E	370	ASN
3	E	414	GLN
1	C	73	ASN
2	D	97	HIS
3	F	343	ASN
3	F	360	ASN
3	F	439	ASN
3	F	498	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [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	A	116/117 (99%)	0.12	3 (2%) 57 59	29, 40, 62, 90	0
1	C	117/117 (100%)	-0.09	3 (2%) 57 59	26, 33, 50, 78	0
2	B	108/108 (100%)	0.03	5 (4%) 37 37	25, 33, 50, 69	0
2	D	108/108 (100%)	0.23	6 (5%) 30 30	27, 37, 58, 78	0
3	E	195/195 (100%)	0.59	24 (12%) 8 8	28, 40, 90, 121	1 (0%)
3	F	195/195 (100%)	0.40	21 (10%) 11 11	24, 36, 79, 100	1 (0%)
All	All	839/840 (99%)	0.27	62 (7%) 20 20	24, 37, 73, 121	2 (0%)

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	374	PHE	10.7
2	D	94	TYR	8.6
2	B	94	TYR	8.5
3	E	369	TYR	6.3
3	F	527	PRO	5.9
3	E	527	PRO	5.3
2	B	95	PRO	5.3
2	D	95	PRO	5.3
3	F	374	PHE	5.2
1	C	118	ALA	5.1
3	E	368	LEU	5.1
1	C	117	SER	4.8
3	E	376	THR	4.2
3	E	372	ALA	4.1
3	E	367	VAL	4.0
1	A	100	SER	3.4
3	F	367	VAL	3.4
3	E	373	SER	3.4
3	F	372	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
3	E	377	PHE	3.2
3	F	373	SER	3.1
3	E	333	THR	3.1
3	F	368	LEU	3.0
1	C	73	ASN	2.9
3	F	526	GLY	2.9
3	E	449	TYR	2.9
3	F	377	PHE	2.9
3	F	369	TYR	2.9
3	F	517	LEU	2.9
2	D	76	SER	2.9
3	F	388	ASN	2.9
3	E	389	ASP	2.8
3	E	443	SER	2.8
3	F	338	PHE	2.8
3	E	371	SER	2.7
3	F	522	ALA	2.7
1	A	117	SER	2.7
3	E	365	TYR	2.6
3	E	346	ARG	2.6
3	E	366	SER	2.6
3	F	341	VAL	2.6
3	E	445	VAL	2.6
3	F	333	THR	2.6
3	F	371	SER	2.5
3	F	334	ASN	2.5
3	F	343	ASN	2.4
3	E	364	ASP	2.4
3	E	370	ASN	2.3
3	E	517	LEU	2.3
3	E	519	HIS	2.3
3	F	444	LYS	2.3
3	F	339	GLY	2.3
3	E	375	SER	2.2
2	D	56	SER	2.2
2	B	42	ARG	2.2
2	B	107	LYS	2.2
2	D	1	ASP	2.2
1	A	88	GLU	2.1
2	D	107	LYS	2.1
3	E	335	LEU	2.1
3	F	364	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	106	ILE	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 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.