



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 24, 2026 – 11:15 AM UTC

PDB ID : 3GI8 / pdb_00003gi8
Title : Crystal Structure of ApcT K158A Transporter Bound to 7F11 Monoclonal Fab Fragment
Authors : Shaffer, P.L.; Goehring, A.S.; Shankaranarayanan, A.; Gouaux, E.; New York Consortium on Membrane Protein Structure (NYCOMPS)
Deposited on : 2009-03-05
Resolution : 2.59 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

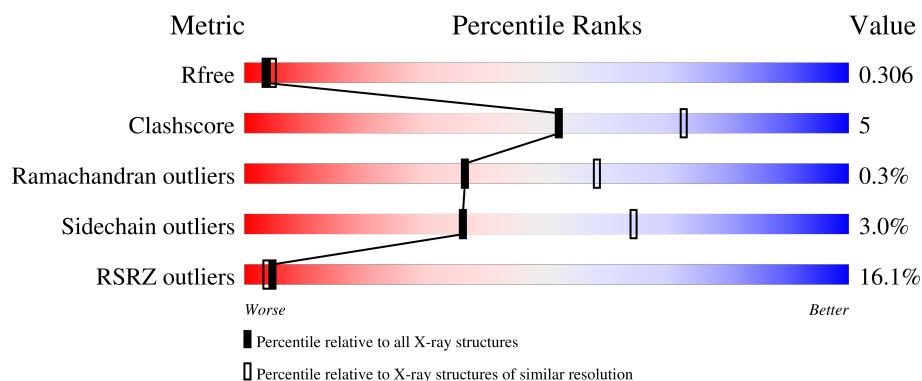
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.59 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	C	444	
2	L	220	
3	H	223	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6924 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 Uncharacterized protein MJ0609.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	435	Total	C	N	O	S	0	0	0
			3351	2261	512	567	11			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	158	ALA	LYS	engineered mutation	UNP Q58026
C	436	LEU	-	expression tag	UNP Q58026
C	437	GLU	-	expression tag	UNP Q58026
C	438	SER	-	expression tag	UNP Q58026
C	439	SER	-	expression tag	UNP Q58026
C	440	GLY	-	expression tag	UNP Q58026
C	441	LEU	-	expression tag	UNP Q58026
C	442	VAL	-	expression tag	UNP Q58026
C	443	PRO	-	expression tag	UNP Q58026
C	444	ARG	-	expression tag	UNP Q58026

- Molecule 2 is a protein called 7F11 Anti-ApcT Monoclonal Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	220	Total	C	N	O	S	0	0	0
			1705	1061	285	351	8			

- Molecule 3 is a protein called 7F11 Anti-ApcT Monoclonal Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	220	Total	C	N	O	S	0	0	0
			1664	1057	264	334	9			

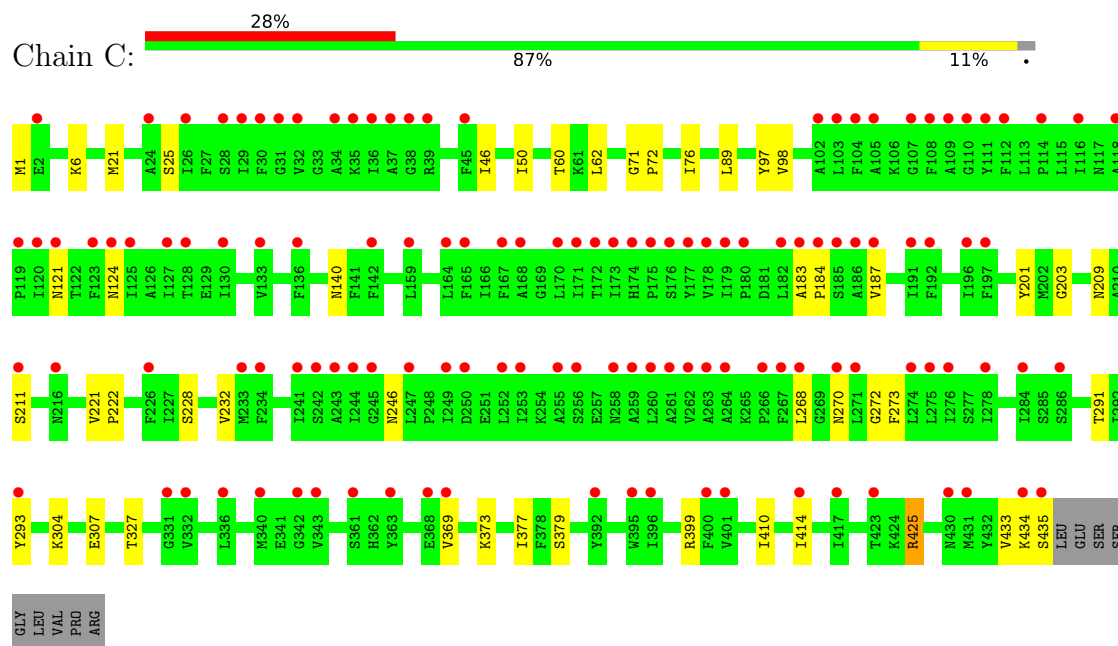
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	57	Total 57	O 57	0	0
4	L	76	Total 76	O 76	0	0
4	H	71	Total 71	O 71	0	0

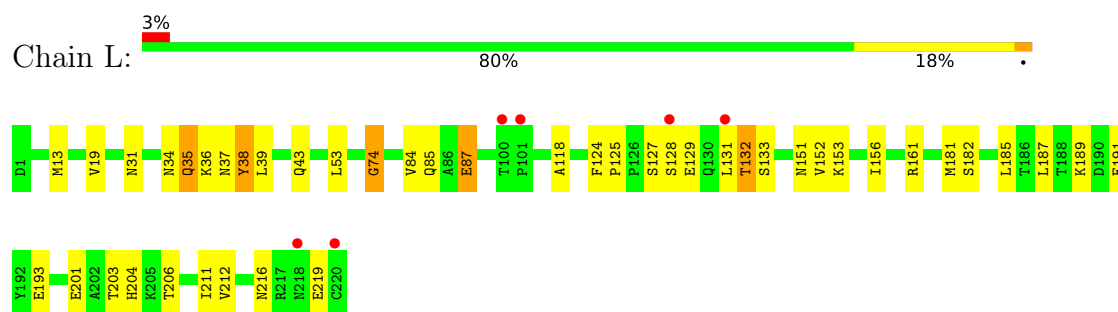
3 Residue-property plots [i](#)

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.

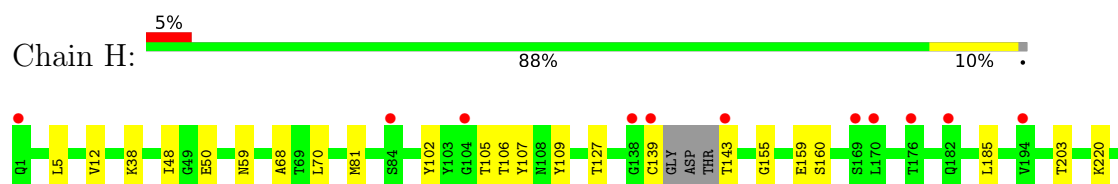
• Molecule 1: Uncharacterized protein MJ0609



• Molecule 2: 7F11 Anti-ApcT Monoclonal Fab Light Chain



• Molecule 3: 7F11 Anti-ApcT Monoclonal Fab Heavy Chain



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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	46.04Å 111.19Å 115.67Å 90.00° 90.92° 90.00°	Depositor
Resolution (Å)	50.00 – 2.59 50.00 – 2.59	Depositor EDS
% Data completeness (in resolution range)	99.6 (50.00-2.59) 99.5 (50.00-2.59)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 2.58Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.254 , 0.307 0.252 , 0.306	Depositor DCC
R_{free} test set	1805 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	47.9	Xtriage
Anisotropy	0.549	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 35.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k 0.013 for -h,-l,-k 0.029 for h,-k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6924	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.60% 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	C	0.46	0/3432	0.85	0/4660
2	L	0.44	0/1742	0.75	1/2361 (0.0%)
3	H	0.43	0/1713	0.71	0/2345
All	All	0.45	0/6887	0.79	1/9366 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	35	GLN	N-CA-C	5.42	117.95	108.52

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	C	3351	0	3510	33	0
2	L	1705	0	1635	24	0
3	H	1664	0	1592	13	0
4	C	57	0	0	2	0
4	H	71	0	0	0	0
4	L	76	0	0	1	0
All	All	6924	0	6737	68	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 (68) 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:C:425:ARG:HH11	1:C:425:ARG:HG2	1.38	0.87
2:L:216:ASN:HB2	2:L:219:GLU:HG3	1.59	0.81
3:H:70:LEU:HD21	3:H:81:MET:HE3	1.71	0.71
2:L:216:ASN:HB2	2:L:219:GLU:CG	2.21	0.70
2:L:13:MET:HG3	2:L:19:VAL:HG22	1.72	0.70
1:C:121:ASN:HB2	1:C:124:ASN:H	1.57	0.68
1:C:1:MET:HE1	3:H:109:TYR:CD1	2.30	0.67
1:C:434:LYS:HB3	1:C:435:SER:HA	1.77	0.66
3:H:102:TYR:O	3:H:105:THR:HG22	1.96	0.66
1:C:1:MET:HE1	3:H:109:TYR:HD1	1.61	0.64
2:L:43:GLN:HB2	2:L:53:LEU:HD11	1.82	0.61
2:L:31:ASN:O	2:L:35:GLN:HA	2.00	0.60
2:L:131:LEU:O	2:L:189:LYS:HE3	2.02	0.60
1:C:433:VAL:HG12	1:C:434:LYS:O	2.02	0.59
1:C:425:ARG:HH11	1:C:425:ARG:CG	2.14	0.58
1:C:268:LEU:HB3	1:C:272:GLY:HA3	1.84	0.58
2:L:131:LEU:C	2:L:133:SER:H	2.11	0.58
2:L:152:VAL:HG21	2:L:181:MET:HE1	1.85	0.58
1:C:433:VAL:O	1:C:434:LYS:HB2	2.08	0.53
3:H:105:THR:HG23	3:H:107:TYR:H	1.74	0.52
1:C:270:ASN:HA	1:C:273:PHE:HB3	1.91	0.51
1:C:97:TYR:HD1	1:C:291:THR:HG23	1.77	0.50
1:C:21:MET:HE3	1:C:203:GLY:H	1.76	0.49
2:L:151:ASN:HB3	2:L:203:THR:HB	1.95	0.49
2:L:127:SER:C	2:L:129:GLU:H	2.20	0.49
1:C:97:TYR:OH	1:C:209:ASN:ND2	2.40	0.49
3:H:203:THR:HG23	3:H:220:LYS:HE3	1.96	0.48
1:C:98:VAL:HG22	1:C:327:THR:HG23	1.96	0.47
3:H:48:ILE:HG21	3:H:81:MET:HE1	1.97	0.47
1:C:304:LYS:O	1:C:425:ARG:HD3	2.16	0.46
1:C:140:ASN:HB2	1:C:293:TYR:OH	2.15	0.46
1:C:183:ALA:HA	1:C:184:PRO:HD3	1.87	0.45
2:L:37:ASN:HD21	2:L:74:GLY:H	1.63	0.45
3:H:68:ALA:HB1	3:H:81:MET:HE2	1.99	0.45
3:H:159:GLU:HA	3:H:160:SER:HA	1.75	0.45
2:L:118:ALA:HA	2:L:206:THR:HG21	1.99	0.44
1:C:414:ILE:HA	4:C:488:HOH:O	2.17	0.44
1:C:71:GLY:HA3	1:C:72:PRO:HD2	1.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:161:ARG:HH22	2:L:191:GLU:CD	2.25	0.43
2:L:131:LEU:C	2:L:133:SER:N	2.76	0.43
1:C:76:ILE:HD13	1:C:89:LEU:HD13	1.99	0.43
2:L:153:LYS:HB2	2:L:201:GLU:HB2	2.01	0.43
2:L:156:ILE:HD11	2:L:185:LEU:HD21	2.01	0.43
3:H:155:GLY:HA2	3:H:185:LEU:HB3	1.99	0.43
2:L:124:PHE:HA	2:L:125:PRO:HD3	1.92	0.42
3:H:38:LYS:HB2	3:H:48:ILE:HD11	2.00	0.42
2:L:87:GLU:H	2:L:87:GLU:HG3	1.71	0.42
1:C:379:SER:HB2	4:C:490:HOH:O	2.19	0.42
3:H:50:GLU:HG2	3:H:59:ASN:HB3	2.02	0.42
1:C:46:ILE:O	1:C:50:ILE:HG12	2.19	0.42
1:C:221:VAL:HB	1:C:222:PRO:HD3	2.02	0.42
2:L:201:GLU:HG2	2:L:212:VAL:HG22	2.00	0.42
1:C:60:THR:HG22	1:C:222:PRO:HA	2.01	0.41
1:C:373:LYS:O	1:C:377:ILE:HG13	2.20	0.41
2:L:34:ASN:HB2	4:L:288:HOH:O	2.20	0.41
2:L:38:TYR:CD2	2:L:38:TYR:N	2.88	0.41
1:C:211:SER:HB2	1:C:221:VAL:HG21	2.02	0.41
1:C:434:LYS:CB	1:C:435:SER:HA	2.46	0.41
1:C:62:LEU:HD23	1:C:369:VAL:HG11	2.03	0.41
2:L:37:ASN:ND2	2:L:74:GLY:H	2.19	0.41
1:C:410:ILE:O	1:C:414:ILE:HG12	2.20	0.41
1:C:425:ARG:HG2	1:C:425:ARG:NH1	2.18	0.41
2:L:181:MET:HE3	2:L:182:SER:C	2.46	0.41
2:L:204:HIS:HB3	2:L:206:THR:HG22	2.02	0.41
3:H:48:ILE:HG21	3:H:81:MET:CE	2.51	0.41
1:C:21:MET:HE2	1:C:201:TYR:HA	2.02	0.40
1:C:228:SER:O	1:C:232:VAL:HG22	2.21	0.40
1:C:184:PRO:HA	1:C:187:VAL:HB	2.02	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	C	433/444 (98%)	414 (96%)	19 (4%)	0	100	100
2	L	218/220 (99%)	204 (94%)	11 (5%)	3 (1%)	9	19
3	H	216/223 (97%)	210 (97%)	6 (3%)	0	100	100
All	All	867/887 (98%)	828 (96%)	36 (4%)	3 (0%)	36	58

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	132	THR
2	L	128	SER
2	L	74	GLY

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	C	352/360 (98%)	346 (98%)	6 (2%)	53	78
2	L	198/198 (100%)	188 (95%)	10 (5%)	21	45
3	H	191/194 (98%)	185 (97%)	6 (3%)	35	63
All	All	741/752 (98%)	719 (97%)	22 (3%)	36	64

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	6	LYS
1	C	25	SER
1	C	246	ASN
1	C	307	GLU
1	C	399	ARG
1	C	425	ARG
2	L	36	LYS

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Mol	Chain	Res	Type
2	L	38	TYR
2	L	39	LEU
2	L	84	VAL
2	L	85	GLN
2	L	87	GLU
2	L	132	THR
2	L	187	LEU
2	L	193	GLU
2	L	211	ILE
3	H	5	LEU
3	H	12	VAL
3	H	106	THR
3	H	127	THR
3	H	139	CYS
3	H	143	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	5	ASN
1	C	220	ASN
1	C	246	ASN
1	C	289	ASN
1	C	394	GLN
1	C	430	ASN
2	L	27	GLN
2	L	37	ASN
2	L	44	GLN
2	L	130	GLN
2	L	162	GLN
2	L	163	ASN
2	L	167	ASN
3	H	39	GLN
3	H	62	GLN

5.3.3 RNA ⓘ

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	C	435/444 (97%)	1.52	124 (28%) 1 1	36, 71, 101, 104	0
2	L	220/220 (100%)	0.36	6 (2%) 56 50	28, 41, 54, 68	0
3	H	220/223 (98%)	0.52	11 (5%) 34 28	29, 43, 64, 67	0
All	All	875/887 (98%)	0.98	141 (16%) 4 3	28, 53, 96, 104	0

All (141) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	168	ALA	6.3
2	L	220	CYS	6.3
1	C	31	GLY	6.1
1	C	127	ILE	5.6
2	L	100	THR	5.3
1	C	125	ILE	4.8
1	C	38	GLY	4.6
1	C	178	VAL	4.4
1	C	278	ILE	4.3
3	H	139	CYS	4.3
1	C	186	ALA	4.2
1	C	179	ILE	4.2
1	C	259	ALA	4.0
1	C	177	TYR	3.9
1	C	111	TYR	3.8
1	C	258	ASN	3.8
1	C	112	PHE	3.8
1	C	103	LEU	3.8
1	C	263	ALA	3.7
1	C	120	ILE	3.7
1	C	260	LEU	3.7
1	C	435	SER	3.6
1	C	182	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	C	340	MET	3.5
1	C	26	ILE	3.5
1	C	172	THR	3.4
1	C	167	PHE	3.4
1	C	400	PHE	3.4
3	H	1	GLN	3.4
1	C	274	LEU	3.4
1	C	250	ASP	3.3
1	C	133	VAL	3.3
1	C	262	VAL	3.3
1	C	392	TYR	3.3
1	C	34	ALA	3.3
1	C	124	ASN	3.2
1	C	107	GLY	3.2
1	C	128	THR	3.2
1	C	244	ILE	3.2
1	C	105	ALA	3.2
1	C	256	SER	3.2
1	C	261	ALA	3.2
1	C	175	PRO	3.2
1	C	36	ILE	3.2
1	C	116	ILE	3.2
1	C	249	ILE	3.2
1	C	171	ILE	3.1
1	C	123	PHE	3.1
1	C	164	LEU	3.1
1	C	252	LEU	3.1
1	C	183	ALA	3.1
1	C	234	PHE	3.1
1	C	331	GLY	3.1
1	C	241	ILE	3.1
1	C	253	ILE	3.1
1	C	142	PHE	3.0
1	C	32	VAL	3.0
2	L	218	ASN	3.0
1	C	276	ILE	2.9
1	C	396	ILE	2.9
1	C	284	ILE	2.9
1	C	108	PHE	2.9
1	C	196	ILE	2.9
1	C	2	GLU	2.9
1	C	267	PHE	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	226	PHE	2.8
1	C	414	ILE	2.8
3	H	138	GLY	2.8
1	C	185	SER	2.8
3	H	170	LEU	2.8
1	C	165	PHE	2.8
1	C	271	LEU	2.7
2	L	101	PRO	2.7
1	C	268	LEU	2.7
1	C	245	GLY	2.7
1	C	192	PHE	2.6
3	H	143	THR	2.6
1	C	395	TRP	2.6
1	C	336	LEU	2.6
1	C	37	ALA	2.6
1	C	170	LEU	2.6
1	C	332	VAL	2.6
1	C	24	ALA	2.6
3	H	84	SER	2.6
1	C	184	PRO	2.5
1	C	430	ASN	2.5
1	C	266	PRO	2.5
1	C	187	VAL	2.5
1	C	401	VAL	2.5
1	C	110	GLY	2.5
1	C	29	ILE	2.5
1	C	28	SER	2.5
1	C	173	ILE	2.4
1	C	363	TYR	2.4
1	C	30	PHE	2.4
1	C	369	VAL	2.4
1	C	109	ALA	2.4
1	C	211	SER	2.4
1	C	368	GLU	2.4
1	C	434	LYS	2.4
1	C	275	LEU	2.4
2	L	131	LEU	2.4
1	C	247	LEU	2.3
3	H	194	VAL	2.3
1	C	130	ILE	2.3
1	C	39	ARG	2.3
1	C	45	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	197	PHE	2.3
1	C	174	HIS	2.2
1	C	255	ALA	2.2
1	C	417	ILE	2.2
1	C	176	SER	2.2
3	H	169	SER	2.2
1	C	104	PHE	2.2
1	C	136	PHE	2.2
1	C	121	ASN	2.1
1	C	216	ASN	2.1
1	C	270	ASN	2.1
1	C	342	GLY	2.1
1	C	431	MET	2.1
1	C	191	ILE	2.1
1	C	286	SER	2.1
1	C	119	PRO	2.1
1	C	243	ALA	2.1
1	C	361	SER	2.1
1	C	180	PRO	2.1
1	C	264	ALA	2.1
1	C	35	LYS	2.1
1	C	242	SER	2.1
3	H	104	GLY	2.0
1	C	423	THR	2.0
3	H	176	THR	2.0
1	C	114	PRO	2.0
1	C	233	MET	2.0
2	L	128	SER	2.0
3	H	182	GLN	2.0
1	C	343	VAL	2.0
1	C	102	ALA	2.0
1	C	118	ALA	2.0
1	C	159	LEU	2.0
1	C	293	TYR	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 [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.