



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 9, 2025 – 12:18 PM JST

PDB ID : 9KUR / pdb_00009kur
Title : Crystal structure of mAb nCoV400Fab with SARS-CoV-2 N-CTD Complex
Authors : Xue, S.J.; Chen, S.D.
Deposited on : 2024-12-04
Resolution : 2.06 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	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
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)	:	2.46

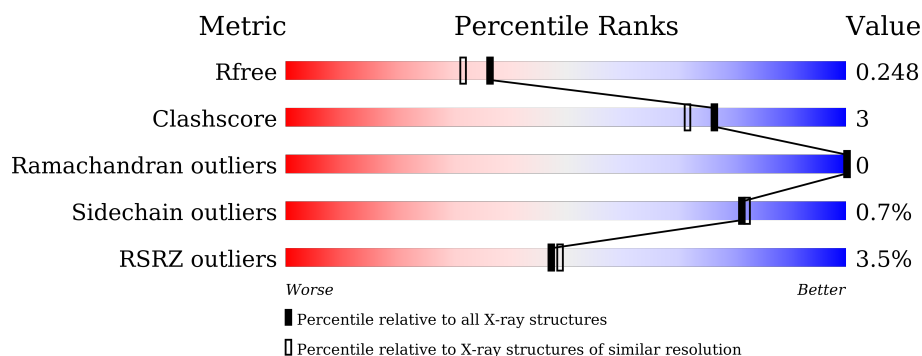
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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}	164625	3436 (2.08-2.04)
Clashscore	180529	3661 (2.08-2.04)
Ramachandran outliers	177936	3649 (2.08-2.04)
Sidechain outliers	177891	3649 (2.08-2.04)
RSRZ outliers	164620	3436 (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	<div> <div>4%</div> <div> <div></div> <div>87%</div> <div>12%</div> <div>.</div> </div> </div>
1	B	117	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>10%</div> <div>.</div> </div> </div>
2	G	235	<div> <div>%</div> <div> <div></div> <div>85%</div> <div>9%</div> <div>6%</div> <div></div> </div> </div>
2	H	235	<div> <div>3%</div> <div> <div></div> <div>85%</div> <div>10%</div> <div>5%</div> <div></div> </div> </div>
3	D	215	<div> <div></div> <div> <div></div> <div>97%</div> <div></div> <div>..</div> </div> </div>
3	L	215	<div> <div>10%</div> <div> <div></div> <div>94%</div> <div></div> <div>..</div> </div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9097 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 Nucleoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	116	Total	C	N	O	S	0	0	0
			908	575	162	169	2			
1	B	116	Total	C	N	O	S	0	0	0
			916	579	163	172	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	249	SER	-	expression tag	UNP P0DTC9
B	249	SER	-	expression tag	UNP P0DTC9

- Molecule 2 is a protein called 400Fab Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	223	Total	C	N	O	S	0	1	0
			1670	1056	276	331	7			
2	G	220	Total	C	N	O	S	0	1	0
			1651	1046	272	326	7			

- Molecule 3 is a protein called 400Fab Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	211	Total	C	N	O	S	0	0	0
			1576	989	259	324	4			
3	D	213	Total	C	N	O	S	0	0	0
			1596	1001	263	328	4			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	64	Total	O	0	0
			64	64		

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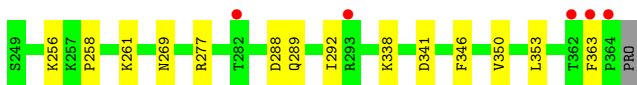
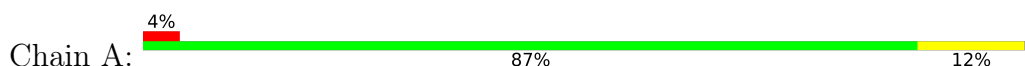
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	90	Total 90	O 90	0	0
4	H	157	Total 157	O 157	0	0
4	L	159	Total 159	O 159	0	0
4	D	149	Total 149	O 149	0	0
4	G	161	Total 161	O 161	0	0

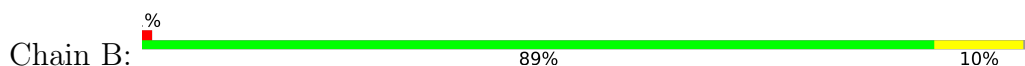
3 Residue-property plots [i](#)

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.

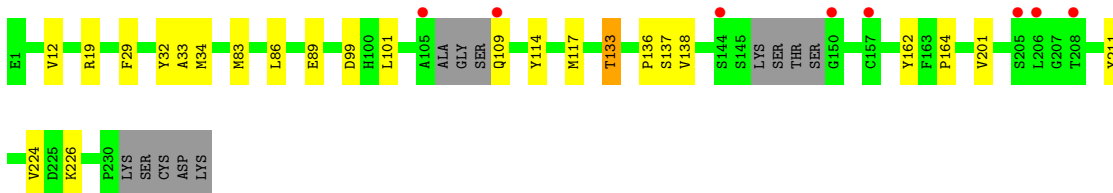
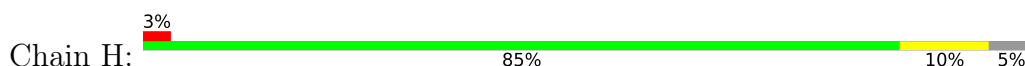
- Molecule 1: Nucleoprotein



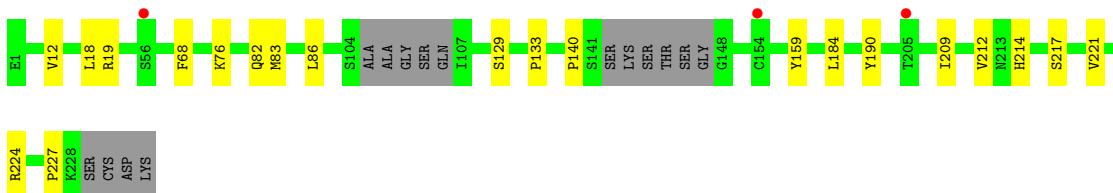
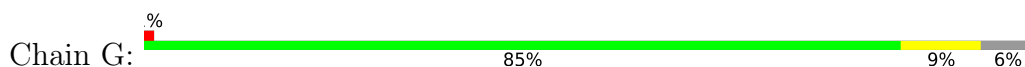
- Molecule 1: Nucleoprotein



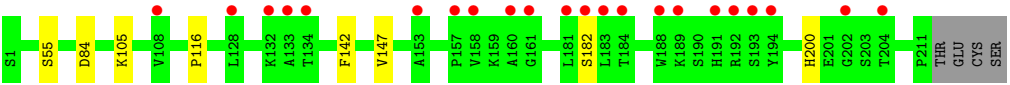
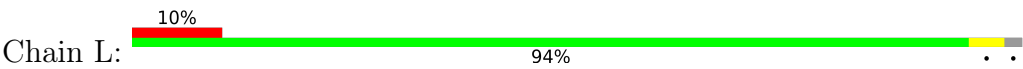
- Molecule 2: 400Fab Heavy chain



- Molecule 2: 400Fab Heavy chain



- Molecule 3: 400Fab Light chain



● Molecule 3: 400Fab Light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	48.41Å 74.22Å 96.51Å 106.63° 103.63° 96.07°	Depositor
Resolution (Å)	24.98 – 2.06 24.98 – 2.06	Depositor EDS
% Data completeness (in resolution range)	97.6 (24.98-2.06) 97.6 (24.98-2.06)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 2.06Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.199 , 0.249 0.199 , 0.248	Depositor DCC
R_{free} test set	3526 reflections (4.64%)	wwPDB-VP
Wilson B-factor (Å ²)	26.8	Xtriage
Anisotropy	0.400	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 41.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9097	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.48% 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	0.10	0/931	0.29	0/1258
1	B	0.09	0/939	0.27	0/1268
2	G	0.14	0/1693	0.35	0/2306
2	H	0.12	0/1712	0.35	0/2331
3	D	0.11	0/1638	0.33	0/2241
3	L	0.12	0/1618	0.33	0/2215
All	All	0.12	0/8531	0.33	0/11619

There are no bond length outliers.

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	908	0	885	11	0
1	B	916	0	895	9	0
2	G	1651	0	1601	10	0
2	H	1670	0	1620	14	0
3	D	1596	0	1536	2	0
3	L	1576	0	1510	3	0
4	A	64	0	0	1	0
4	B	90	0	0	1	0
4	D	149	0	0	0	0
4	G	161	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	157	0	0	2	0
4	L	159	0	0	0	0
All	All	9097	0	8047	45	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 3.

All (45) 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:A:353:LEU:HD13	1:B:331:LEU:HD13	1.74	0.69
2:H:136:PRO:HB3	2:H:162:TYR:HB3	1.75	0.69
2:G:209:ILE:HG12	2:G:224:ARG:HG2	1.79	0.65
2:G:76:LYS:NZ	4:G:303:HOH:O	2.31	0.64
2:G:133:PRO:HB3	2:G:159:TYR:HB3	1.79	0.62
1:A:269:ASN:HB2	1:A:292:ILE:O	2.02	0.58
2:G:12:VAL:HG11	2:G:18:LEU:HG	1.84	0.58
1:A:350:VAL:HG13	1:B:322:MET:HE1	1.87	0.57
1:B:358:ASP:HB3	1:B:361:LYS:HD2	1.85	0.56
2:H:138:VAL:HG21	2:H:224:VAL:HG11	1.88	0.54
1:B:269:ASN:HB2	1:B:292:ILE:O	2.09	0.53
2:H:114:TYR:OH	2:H:117:MET:HG3	2.09	0.52
3:L:116:PRO:HB3	3:L:142:PHE:HB3	1.91	0.52
2:H:109:GLN:N	4:H:307:HOH:O	2.43	0.52
1:B:289:GLN:O	1:B:293:ARG:HG3	2.10	0.52
1:A:258:PRO:HD2	1:A:261:LYS:HB2	1.93	0.50
1:B:262:ARG:NH2	4:B:404:HOH:O	2.39	0.50
1:A:256:LYS:NZ	4:A:404:HOH:O	2.44	0.49
1:A:288:ASP:O	1:A:292:ILE:HG12	2.13	0.49
2:H:19:ARG:NE	4:H:309:HOH:O	2.45	0.48
1:B:341:ASP:HA	1:B:346:PHE:CG	2.48	0.47
1:A:341:ASP:HA	1:A:346:PHE:CG	2.50	0.47
3:L:84:ASP:OD1	3:L:105:LYS:HD2	2.15	0.47
2:H:12:VAL:HG21	2:H:86:LEU:HD13	1.97	0.46
2:H:89:GLU:H	2:H:89:GLU:CD	2.23	0.46
2:G:68:PHE:CZ	2:G:83:MET:HG2	2.51	0.46
1:A:289:GLN:HG2	1:A:363:PHE:CZ	2.51	0.45
3:L:147:VAL:HG12	3:L:200:HIS:HB2	1.98	0.45
1:A:277:ARG:HD2	1:A:292:ILE:CD1	2.47	0.45
2:G:214:HIS:ND1	2:G:217:SER:OG	2.35	0.45
2:H:133:THR:HG22	2:H:164:PRO:HD3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:34:TRP:HB2	3:D:47:ILE:HB	1.98	0.44
2:G:212:VAL:HB	2:G:221:VAL:HG13	2.00	0.44
1:A:338:LYS:HD2	1:B:330:TRP:CZ2	2.53	0.43
2:G:140:PRO:HD2	2:G:227:PRO:HA	2.00	0.43
2:H:201:VAL:HG11	2:H:211:TYR:CE1	2.53	0.42
2:H:33:ALA:HB3	2:H:99:ASP:HB3	2.01	0.42
2:H:138:VAL:HG23	2:H:226:LYS:HD3	2.01	0.42
2:G:19:ARG:HD2	2:G:82:GLN:OE1	2.20	0.41
2:H:32:TYR:CE2	2:H:101:LEU:HB2	2.56	0.41
2:H:83:MET:HE2	2:H:86:LEU:HD21	2.02	0.41
2:G:184:LEU:HD23	2:G:190:TYR:CZ	2.56	0.41
1:A:338:LYS:HB2	1:B:330:TRP:CZ3	2.56	0.41
3:D:135:LEU:HB2	3:D:181:LEU:HB3	2.03	0.40
2:H:29:PHE:CE1	2:H:34:MET:HG3	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	B	114/117 (97%)	113 (99%)	1 (1%)	0	100	100
2	G	215/235 (92%)	211 (98%)	4 (2%)	0	100	100
2	H	218/235 (93%)	215 (99%)	3 (1%)	0	100	100
3	D	211/215 (98%)	205 (97%)	6 (3%)	0	100	100
3	L	209/215 (97%)	201 (96%)	8 (4%)	0	100	100
All	All	1081/1134 (95%)	1058 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	93/96 (97%)	93 (100%)	0	100	100
1	B	95/96 (99%)	95 (100%)	0	100	100
2	G	184/196 (94%)	182 (99%)	2 (1%)	70	70
2	H	186/196 (95%)	183 (98%)	3 (2%)	58	57
3	D	179/182 (98%)	179 (100%)	0	100	100
3	L	176/182 (97%)	174 (99%)	2 (1%)	70	70
All	All	913/948 (96%)	906 (99%)	7 (1%)	81	80

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	133	THR
2	H	137[A]	SER
2	H	137[B]	SER
3	L	55	SER
3	L	182	SER
2	G	86	LEU
2	G	129	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	272	GLN
1	A	300	HIS
1	B	306	GLN
1	B	349	GLN
2	H	3	GLN
2	H	209	GLN
3	L	41	GLN
3	L	173	ASN
3	D	30	GLN
3	D	173	ASN

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Mol	Chain	Res	Type
2	G	119	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 [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%)	0.14	5 (4%)	40 42	19, 36, 51, 75	0
1	B	116/117 (99%)	-0.09	1 (0%)	81 83	21, 30, 50, 68	0
2	G	220/235 (93%)	0.11	3 (1%)	73 75	16, 33, 57, 73	1 (0%)
2	H	223/235 (94%)	0.26	8 (3%)	46 48	18, 34, 63, 117	1 (0%)
3	D	213/215 (99%)	0.16	0	100 100	15, 34, 60, 85	0
3	L	211/215 (98%)	0.43	22 (10%)	13 13	16, 36, 80, 98	0
All	All	1099/1134 (96%)	0.20	39 (3%)	47 49	15, 34, 64, 117	2 (0%)

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	105	ALA	4.7
1	A	364	PRO	4.3
3	L	188	TRP	3.9
3	L	133	ALA	3.3
3	L	183	LEU	3.3
3	L	194	TYR	3.3
2	H	150	GLY	3.2
3	L	158	VAL	3.1
2	H	205	SER	3.0
3	L	181	LEU	3.0
3	L	153	ALA	2.9
2	G	205	THR	2.9
3	L	132	LYS	2.8
2	H	144	SER	2.8
2	H	206	LEU	2.8
3	L	189	LYS	2.7
3	L	193	SER	2.7
1	A	363	PHE	2.6
3	L	182	SER	2.6

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Mol	Chain	Res	Type	RSRZ
3	L	128	LEU	2.6
3	L	134	THR	2.5
2	H	109	GLN	2.5
3	L	184	THR	2.5
3	L	108	VAL	2.4
1	A	293	ARG	2.4
3	L	161	GLY	2.3
1	A	282	THR	2.3
3	L	157	PRO	2.3
1	B	364	PRO	2.2
2	H	157	CYS	2.2
3	L	202	GLY	2.2
1	A	362	THR	2.2
3	L	160	ALA	2.2
2	G	56	SER	2.2
2	H	208	THR	2.2
3	L	192	ARG	2.2
2	G	154	CYS	2.1
3	L	191	HIS	2.1
3	L	204	THR	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.