



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:14 PM UTC

PDB ID : 9BIW / pdb_00009biw
Title : Crystal structure of Chelona Toxin, a diphtheria toxin homolog, from *Austwickia chelonae*
Authors : Gill, S.K.; Sugiman-Marangos, S.N.; Melnyk, R.A.
Deposited on : 2024-04-24
Resolution : 2.50 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

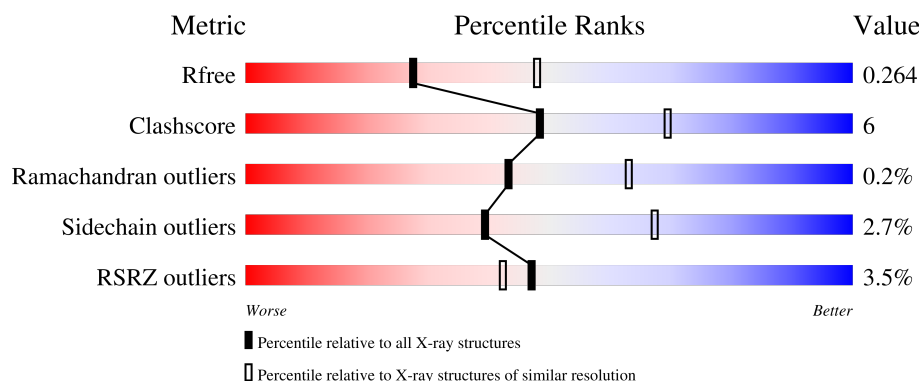
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	540	 3% 85% 12% ..
1	B	540	 4% 83% 15% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8218 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 Chelona Toxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	527	Total	C	N	O	S	0	0	0
			3899	2455	680	753	11			
1	B	528	Total	C	N	O	S	0	0	0
			3903	2459	683	750	11			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Ca	0	0
			4	4		
2	B	3	Total	Ca	0	0
			3	3		

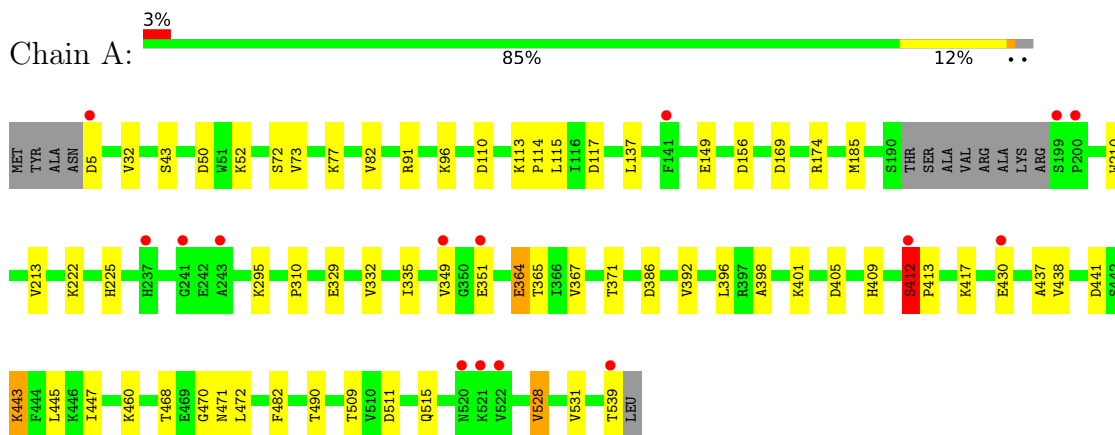
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	219	Total	O	0	0
			219	219		
3	B	190	Total	O	0	0
			190	190		

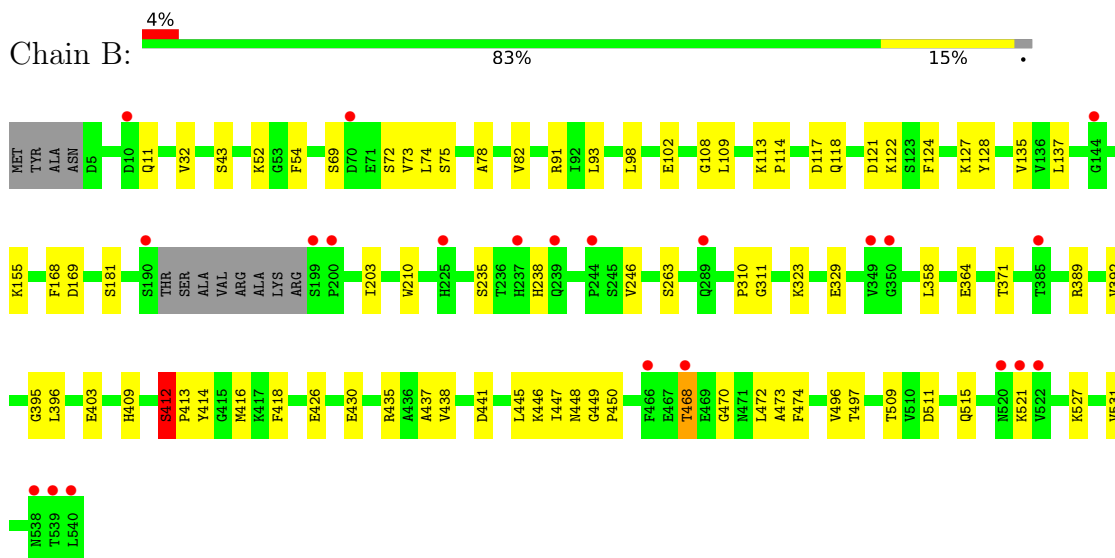
3 Residue-property plots

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: Chelona Toxin



• Molecule 1: Chelona Toxin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	48.24Å 138.84Å 152.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	51.27 – 2.50 51.27 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (51.27-2.50) 100.0 (51.27-2.50)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.16_3549: ???	Depositor
R, R_{free}	0.236 , 0.268 0.234 , 0.264	Depositor DCC
R_{free} test set	1801 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	31.1	Xtriage
Anisotropy	0.457	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 39.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8218	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 53.67 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.0752e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	0.15	0/3971	0.41	0/5393
1	B	0.15	0/3975	0.42	0/5395
All	All	0.15	0/7946	0.41	0/10788

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

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	3899	0	3859	39	0
1	B	3903	0	3870	47	0
2	A	4	0	0	0	0
2	B	3	0	0	0	0
3	A	219	0	0	7	0
3	B	190	0	0	5	0
All	All	8218	0	7729	86	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 6.

All (86) 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:412:SER:HB3	1:B:413:PRO:HD2	1.57	0.85
1:A:409:HIS:O	3:A:701:HOH:O	1.96	0.84
1:A:412:SER:HB3	1:A:413:PRO:HD2	1.67	0.76
1:A:149:GLU:OE2	1:A:460:LYS:NZ	2.19	0.76
1:B:113:LYS:HB2	1:B:118:GLN:OE1	1.86	0.75
1:B:364:GLU:OE1	3:B:701:HOH:O	2.10	0.70
1:A:114:PRO:HB2	1:A:117:ASP:HB2	1.76	0.68
1:B:11:GLN:NE2	3:B:709:HOH:O	2.28	0.66
1:B:509:THR:HG22	1:B:531:VAL:HG22	1.80	0.64
1:A:509:THR:HG22	1:A:531:VAL:HG22	1.82	0.62
1:B:412:SER:HB3	1:B:413:PRO:CD	2.29	0.60
1:A:412:SER:OG	1:A:539:THR:N	2.35	0.59
1:B:121:ASP:HB3	1:B:124:PHE:HB3	1.84	0.59
1:B:109:LEU:HB3	1:B:118:GLN:HE22	1.68	0.58
1:B:108:GLY:O	3:B:702:HOH:O	2.18	0.57
1:B:437:ALA:HB3	1:B:511:ASP:HB2	1.87	0.57
1:A:490:THR:OG1	3:A:702:HOH:O	2.17	0.56
1:B:109:LEU:HD12	1:B:118:GLN:HE21	1.71	0.55
1:B:91:ARG:HB3	1:B:135:VAL:HG22	1.90	0.53
1:A:50:ASP:OD1	1:A:115:LEU:N	2.40	0.53
1:A:351:GLU:N	3:A:706:HOH:O	2.27	0.52
1:B:109:LEU:HB3	1:B:118:GLN:NE2	2.25	0.52
1:B:409:HIS:NE2	1:B:412:SER:HB2	2.25	0.52
1:A:310:PRO:HD3	1:A:515:GLN:HB2	1.92	0.52
1:A:468:THR:OG1	1:A:472:LEU:O	2.27	0.51
1:B:438:VAL:HG21	1:B:447:ILE:HD13	1.94	0.50
1:A:437:ALA:HB3	1:A:511:ASP:HB2	1.94	0.50
1:B:203:ILE:HD11	1:B:323:LYS:HE3	1.95	0.49
1:A:417:LYS:HE3	3:A:701:HOH:O	2.13	0.49
1:A:222:LYS:HA	1:A:225:HIS:CE1	2.46	0.49
1:A:438:VAL:HG21	1:A:447:ILE:HD13	1.95	0.49
1:B:114:PRO:HB2	1:B:117:ASP:HB2	1.95	0.49
1:A:364:GLU:HG3	1:A:365:THR:N	2.28	0.49
1:A:156:ASP:OD1	3:A:703:HOH:O	2.19	0.48
1:A:412:SER:HB3	1:A:413:PRO:CD	2.36	0.48
1:B:98:LEU:HD13	1:B:102:GLU:HG2	1.95	0.48
1:A:443:LYS:HA	1:A:443:LYS:HD3	1.57	0.48
1:A:392:VAL:HA	1:A:396:LEU:O	2.14	0.47
1:A:441:ASP:H	1:A:445:LEU:HB3	1.79	0.47
1:B:468:THR:HG22	1:B:470:GLY:H	1.78	0.47
1:A:210:TRP:CD2	1:A:371:THR:HG22	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:93:LEU:O	1:B:137:LEU:HD12	2.15	0.47
1:B:169:ASP:N	1:B:169:ASP:OD1	2.47	0.47
1:B:416:MET:HE2	1:B:418:PHE:CE1	2.49	0.47
1:B:210:TRP:CD2	1:B:371:THR:HG22	2.51	0.46
1:B:441:ASP:H	1:B:445:LEU:HB3	1.80	0.46
1:B:210:TRP:CE2	1:B:371:THR:HG22	2.51	0.46
1:A:110:ASP:HB3	1:A:113:LYS:HD2	1.99	0.45
1:A:430:GLU:HG2	1:A:482:PHE:HB3	1.96	0.45
1:A:401:LYS:HB3	1:A:405:ASP:OD2	2.16	0.45
1:B:438:VAL:O	1:B:472:LEU:HD22	2.17	0.45
1:B:435:ARG:HD2	1:B:474:PHE:CD1	2.51	0.44
1:B:54:PHE:HA	3:B:771:HOH:O	2.17	0.44
1:B:235:SER:HA	1:B:238:HIS:O	2.18	0.44
1:B:32:VAL:HG12	1:B:82:VAL:HG11	2.00	0.44
1:B:155:LYS:HD2	1:B:155:LYS:HA	1.83	0.44
1:A:210:TRP:CE2	1:A:371:THR:HG22	2.53	0.44
1:A:43:SER:O	1:A:52:LYS:NZ	2.51	0.44
1:B:43:SER:O	1:B:52:LYS:NZ	2.51	0.43
1:B:389:ARG:NH1	1:B:403:GLU:OE2	2.42	0.43
1:A:5:ASP:O	1:A:96:LYS:HE3	2.19	0.43
1:B:448:ASN:HB2	1:B:496:VAL:HG23	2.01	0.42
1:B:310:PRO:HD3	1:B:515:GLN:HB2	2.00	0.42
1:B:392:VAL:HA	1:B:396:LEU:O	2.19	0.42
1:A:412:SER:CB	1:A:413:PRO:HD2	2.46	0.42
1:B:74:LEU:HD23	1:B:74:LEU:HA	1.85	0.42
1:A:32:VAL:HG12	1:A:82:VAL:HG11	2.02	0.42
1:B:449:GLY:N	1:B:450:PRO:HD2	2.34	0.42
1:B:122:LYS:HD3	1:B:122:LYS:HA	1.65	0.42
1:A:213:VAL:HA	1:A:332:VAL:HG22	2.02	0.41
1:A:398:ALA:HB3	1:A:528:VAL:HG11	2.02	0.41
1:B:395:GLY:HA2	1:B:426:GLU:HG3	2.01	0.41
1:B:78:ALA:HB3	1:B:168:PHE:HB2	2.01	0.41
1:A:169:ASP:OD1	1:A:169:ASP:N	2.52	0.41
1:B:414:TYR:HB3	1:B:497:THR:HG22	2.03	0.41
1:A:77:LYS:NZ	3:A:717:HOH:O	2.40	0.41
1:A:295:LYS:HD3	1:A:295:LYS:HA	1.79	0.41
1:A:174:ARG:HD3	1:A:174:ARG:HA	1.62	0.41
1:B:311:GLY:HA2	1:B:430:GLU:HB3	2.02	0.41
1:B:472:LEU:HD13	1:B:473:ALA:N	2.36	0.41
1:B:72:SER:HB3	1:B:75:SER:HB3	2.03	0.41
1:B:127:LYS:HD3	1:B:128:TYR:CE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:MET:HE2	3:A:819:HOH:O	2.21	0.41
1:A:335:ILE:HD13	1:A:367:VAL:HG22	2.03	0.40
1:B:358:LEU:HD22	3:B:736:HOH:O	2.20	0.40
1:A:470:GLY:O	1:A:471:ASN:HB2	2.21	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	523/540 (97%)	512 (98%)	10 (2%)	1 (0%)	43	63
1	B	524/540 (97%)	512 (98%)	11 (2%)	1 (0%)	43	63
All	All	1047/1080 (97%)	1024 (98%)	21 (2%)	2 (0%)	43	63

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	412	SER
1	B	412	SER

5.3.2 Protein sidechains [i](#)

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	409/438 (93%)	398 (97%)	11 (3%)	39 67
1	B	408/438 (93%)	397 (97%)	11 (3%)	39 67
All	All	817/876 (93%)	795 (97%)	22 (3%)	39 67

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

Mol	Chain	Res	Type
1	A	72	SER
1	A	73	VAL
1	A	91	ARG
1	A	137	LEU
1	A	329	GLU
1	A	349	VAL
1	A	364	GLU
1	A	386	ASP
1	A	412	SER
1	A	443	LYS
1	A	528	VAL
1	B	69	SER
1	B	73	VAL
1	B	181	SER
1	B	246	VAL
1	B	263	SER
1	B	329	GLU
1	B	412	SER
1	B	446	LYS
1	B	468	THR
1	B	521	LYS
1	B	527	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	47	ASN
1	B	118	GLN
1	B	333	GLN
1	B	507	ASN

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](#)

Of 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	527/540 (97%)	0.27	15 (2%) 55 50	19, 31, 55, 67	0
1	B	528/540 (97%)	0.35	22 (4%) 40 36	19, 33, 60, 85	0
All	All	1055/1080 (97%)	0.31	37 (3%) 47 42	19, 32, 57, 85	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	520	ASN	3.8
1	B	539	THR	3.6
1	B	199	SER	3.5
1	A	200	PRO	3.4
1	A	237	HIS	3.3
1	B	190	SER	3.2
1	B	540	LEU	3.2
1	A	5	ASP	3.0
1	B	522	VAL	2.8
1	A	241	GLY	2.7
1	B	538	ASN	2.6
1	B	144	GLY	2.5
1	A	141	PHE	2.5
1	B	521	LYS	2.5
1	B	70	ASP	2.5
1	A	539	THR	2.4
1	A	521	LYS	2.4
1	A	430	GLU	2.4
1	B	244	PRO	2.3
1	B	468	THR	2.3
1	B	200	PRO	2.3
1	A	199	SER	2.2
1	A	412	SER	2.2
1	A	522	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	385	THR	2.2
1	A	349	VAL	2.2
1	A	351	GLU	2.2
1	B	225	HIS	2.2
1	B	239	GLN	2.2
1	B	520	ASN	2.1
1	B	350	GLY	2.1
1	B	237	HIS	2.1
1	B	10	ASP	2.1
1	B	466	PHE	2.1
1	B	349	VAL	2.0
1	A	243	ALA	2.0
1	B	289	GLN	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CA	A	602	1/1	0.72	0.17	97,97,97,97	0
2	CA	A	603	1/1	0.84	0.13	97,97,97,97	0
2	CA	A	604	1/1	0.85	0.23	109,109,109,109	0
2	CA	B	601	1/1	0.90	0.08	37,37,37,37	0
2	CA	A	601	1/1	0.93	0.12	35,35,35,35	0
2	CA	B	602	1/1	0.93	0.08	60,60,60,60	0
2	CA	B	603	1/1	0.95	0.05	58,58,58,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.