Full wwPDB X-ray Structure Validation Report (i)

Feb 19, 2024 – 12:54 pm GMT

PDB ID	:	8CMA
Title	:	SARS-CoV-2 Delta-RBD complexed with BA.4/5-35 Fab
Authors	:	Zhou, D.; Ren, J.; Stuart, D.I.
Deposited on	:	2023-02-18
Resolution	:	3.29 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 (i) 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 (1)) were used in the production of this report:

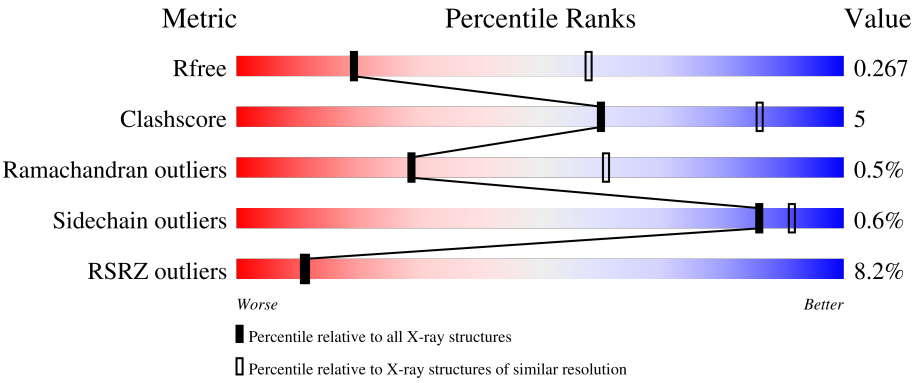
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.29 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}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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 <=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	H	223	7% 79% 17% .
2	E	202	13% 81% 10% 9%
3	L	216	4% 89% 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4732 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 BA.4/5-35 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	214	Total	C	N	O	S	0	0	0
			1584	1000	270	308	6			

- Molecule 2 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	184	Total	C	N	O	S	0	1	0
			1478	947	248	276	7			

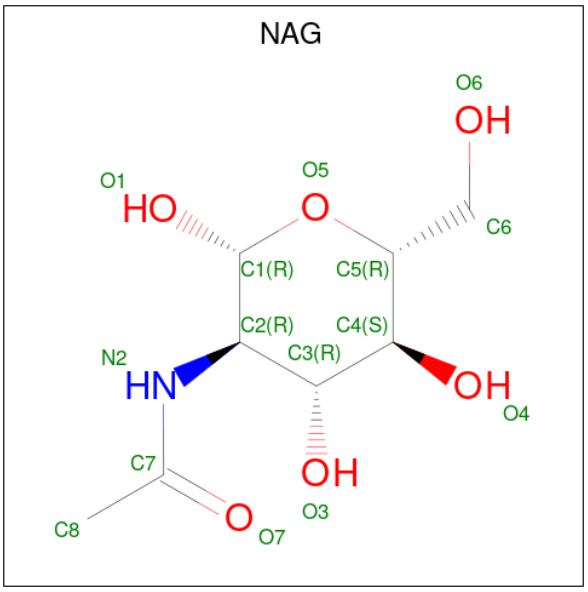
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	327	HIS	-	expression tag	UNP P0DTC2
E	328	HIS	-	expression tag	UNP P0DTC2
E	329	HIS	-	expression tag	UNP P0DTC2
E	330	HIS	-	expression tag	UNP P0DTC2
E	331	HIS	-	expression tag	UNP P0DTC2
E	332	HIS	-	expression tag	UNP P0DTC2
E	452	ARG	LEU	variant	UNP P0DTC2
E	478	LYS	THR	variant	UNP P0DTC2
E	527	LYS	-	expression tag	UNP P0DTC2
E	528	LYS	-	expression tag	UNP P0DTC2

- Molecule 3 is a protein called BA.4/5-35 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	215	Total	C	N	O	S	0	0	0
			1656	1038	280	332	6			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

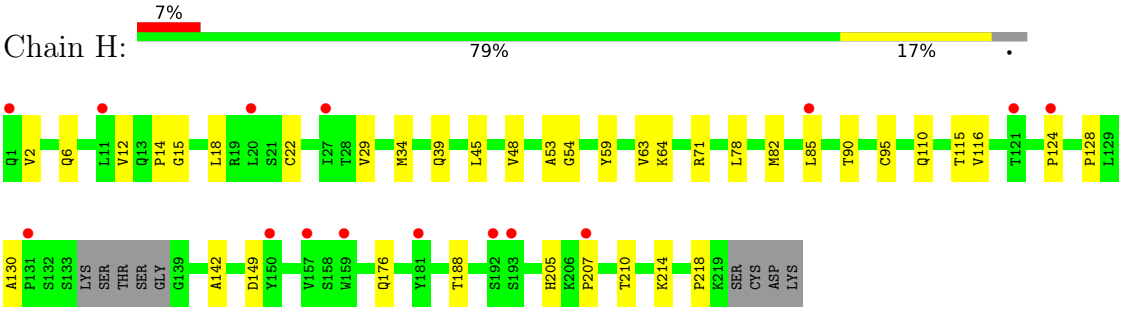


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	E	1	14	8	1	5	0	0

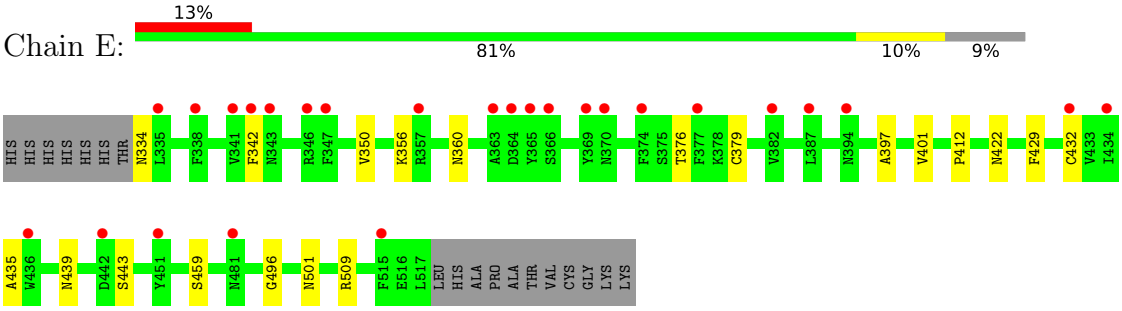
3 Residue-property plots (i)

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.

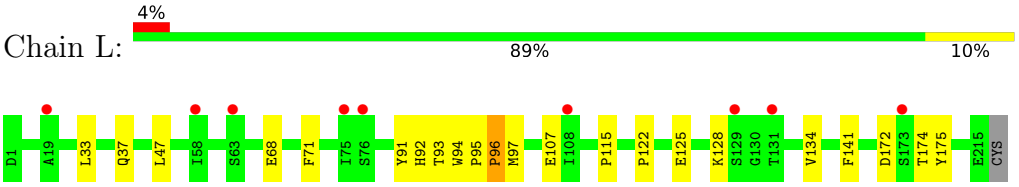
• Molecule 1: BA.4/5-35 heavy chain



• Molecule 2: Spike protein S1



• Molecule 3: BA.4/5-35 light chain



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	195.78Å 85.12Å 56.97Å 90.00° 102.03° 90.00°	Depositor
Resolution (Å)	47.87 – 3.29 47.87 – 3.29	Depositor EDS
% Data completeness (in resolution range)	98.4 (47.87-3.29) 98.5 (47.87-3.29)	Depositor EDS
R_{merge}	0.30	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.99 (at 3.25Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.231 , 0.268 0.233 , 0.267	Depositor DCC
R_{free} test set	681 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å^2)	105.1	Xtriage
Anisotropy	0.224	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 77.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	4732	wwPDB-VP
Average B, all atoms (Å^2)	124.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.58% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: NAG

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	H	0.25	0/1620	0.48	0/2209
2	E	0.25	0/1522	0.46	0/2066
3	L	0.25	0/1694	0.48	0/2304
All	All	0.25	0/4836	0.47	0/6579

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	H	1584	0	1560	22	0
2	E	1478	0	1401	10	0
3	L	1656	0	1606	12	0
4	E	14	0	13	1	0
All	All	4732	0	4580	43	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 (43) 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:H:82:MET:HB3	1:H:85:LEU:HD21	1.72	0.71
1:H:29:VAL:HG13	1:H:34:MET:HG3	1.76	0.66
3:L:37:GLN:HB2	3:L:47:LEU:HD11	1.81	0.61
1:H:39:GLN:HB2	1:H:45:LEU:HD23	1.82	0.60
1:H:12:VAL:HG21	1:H:18:LEU:HB2	1.84	0.58
1:H:34:MET:HB3	1:H:78:LEU:HD22	1.85	0.58
3:L:95:PRO:HB2	3:L:96:PRO:HD3	1.85	0.58
3:L:107:GLU:OE1	3:L:175:TYR:OH	2.23	0.56
1:H:59:TYR:O	1:H:64:LYS:NZ	2.37	0.55
1:H:130:ALA:HB1	1:H:218:PRO:HA	1.88	0.54
3:L:93:THR:O	3:L:96:PRO:HD2	2.07	0.54
2:E:376:THR:HB	2:E:435:ALA:HB3	1.90	0.53
1:H:149:ASP:OD1	1:H:176:GLN:NE2	2.41	0.53
1:H:53:ALA:HA	1:H:71:ARG:HH12	1.75	0.51
2:E:350:VAL:HG22	2:E:422:ASN:HB3	1.93	0.50
3:L:125:GLU:HA	3:L:128:LYS:HE2	1.93	0.50
1:H:205:HIS:HB3	1:H:210:THR:HB	1.94	0.50
2:E:379:CYS:HA	2:E:432:CYS:HA	1.92	0.50
1:H:124:PRO:HD2	1:H:210:THR:HG21	1.95	0.48
1:H:48:VAL:HG13	1:H:63:VAL:HG21	1.96	0.48
3:L:94:TRP:N	3:L:95:PRO:HD2	2.29	0.47
1:H:15:GLY:N	1:H:85:LEU:O	2.44	0.47
3:L:94:TRP:HA	3:L:97:MET:O	2.14	0.47
2:E:496:GLY:O	2:E:501:ASN:ND2	2.47	0.47
1:H:128:PRO:HD3	1:H:214:LYS:NZ	2.31	0.46
1:H:90:THR:HG23	1:H:115:THR:HA	1.98	0.46
3:L:115:PRO:HB3	3:L:141:PHE:HB3	1.97	0.46
1:H:54:GLY:HA2	2:E:459:SER:HA	1.97	0.46
2:E:412:PRO:HG3	2:E:429:PHE:HB3	1.99	0.45
2:E:342:PHE:HB2	4:E:601:NAG:H82	1.99	0.45
1:H:205:HIS:CD2	1:H:207:PRO:HD2	2.52	0.44
1:H:6:GLN:H	1:H:110:GLN:HE22	1.66	0.44
2:E:439:ASN:O	2:E:443[A]:SER:OG	2.19	0.44
1:H:14:PRO:HG3	1:H:116:VAL:HG12	2.01	0.43
3:L:33:LEU:HD13	3:L:71:PHE:CD1	2.54	0.43
3:L:122:PRO:HD3	3:L:134:VAL:HG22	2.02	0.42
1:H:6:GLN:NE2	1:H:95:CYS:SG	2.81	0.42
1:H:142:ALA:HB2	1:H:188:THR:HG22	2.01	0.42
3:L:91:TYR:HB2	3:L:94:TRP:HB2	2.02	0.41
1:H:22:CYS:HB3	1:H:78:LEU:HB3	2.01	0.41
2:E:401:VAL:HG22	2:E:509:ARG:HG2	2.01	0.41
2:E:356:LYS:HB3	2:E:397:ALA:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:172:ASP:OD1	3:L:174:THR:OG1	2.28	0.41

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	H	210/223 (94%)	199 (95%)	11 (5%)	0	100	100
2	E	183/202 (91%)	176 (96%)	6 (3%)	1 (0%)	29	61
3	L	213/216 (99%)	198 (93%)	13 (6%)	2 (1%)	17	48
All	All	606/641 (94%)	573 (95%)	30 (5%)	3 (0%)	29	61

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	L	96	PRO
3	L	68	GLU
2	E	360	ASN

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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	177/186 (95%)	176 (99%)	1 (1%)	86	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	E	161/175 (92%)	160 (99%)	1 (1%)	86 91
3	L	186/188 (99%)	185 (100%)	1 (0%)	88 93
All	All	524/549 (95%)	521 (99%)	3 (1%)	86 91

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

Mol	Chain	Res	Type
1	H	2	VAL
2	E	334	ASN
3	L	92	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	NAG	E	601	2	14,14,15	0.19	0	17,19,21	0.54	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	E	601	2	-	0/6/23/26	0/1/1/1

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	601	NAG	1	0

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, 95^{th} 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	H	214/223 (95%)	0.65	15 (7%) 16 16	86, 126, 172, 200	0
2	E	184/202 (91%)	0.87	26 (14%) 2 2	92, 127, 193, 227	0
3	L	215/216 (99%)	0.62	9 (4%) 36 34	82, 109, 145, 178	0
All	All	613/641 (95%)	0.70	50 (8%) 11 11	82, 120, 178, 227	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	387	LEU	6.9
1	H	124	PRO	5.6
2	E	434	ILE	4.6
2	E	374	PHE	4.5
2	E	366	SER	4.3
2	E	342	PHE	4.3
2	E	365	TYR	4.2
3	L	76	SER	3.8
1	H	121	THR	3.5
2	E	363	ALA	3.5
2	E	346	ARG	3.3
2	E	382	VAL	3.3
2	E	347	PHE	3.2
2	E	451	TYR	3.2
2	E	338	PHE	3.1
1	H	193	SER	3.0
2	E	515	PHE	3.0
1	H	85	LEU	2.9
2	E	335	LEU	2.9
2	E	343	ASN	2.9
3	L	173	SER	2.8
1	H	150	TYR	2.8
1	H	181	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
1	H	1	GLN	2.7
1	H	207	PRO	2.7
3	L	19	ALA	2.7
3	L	129	SER	2.6
2	E	436	TRP	2.6
2	E	341	VAL	2.6
3	L	58	ILE	2.6
3	L	75	ILE	2.6
1	H	20	LEU	2.6
3	L	131	THR	2.6
1	H	131	PRO	2.5
2	E	357	ARG	2.5
2	E	394	ASN	2.4
2	E	377	PHE	2.4
1	H	159	TRP	2.4
2	E	432	CYS	2.3
2	E	370	ASN	2.2
2	E	442	ASP	2.2
1	H	11	LEU	2.2
2	E	481	ASN	2.2
1	H	192	SER	2.2
2	E	369	TYR	2.1
3	L	63	SER	2.1
3	L	108	ILE	2.1
2	E	364	ASP	2.1
1	H	27	ILE	2.1
1	H	157	VAL	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 monosaccharides 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, 95^{th} 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(Å^2)	Q<0.9
4	NAG	E	601	14/15	0.73	0.39	137,196,210,217	0

6.5 Other polymers (i)

There are no such residues in this entry.