



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:59 PM UTC

PDB ID : 8DCC / pdb_00008dcc
Title : SARS-CoV-2 Receptor-Binding Domain SPEEDesign Immunogen 3 Bound to P2B-2F6 Fab
Authors : Dickey, T.D.; Tolia, N.H.
Deposited on : 2022-06-16
Resolution : 2.60 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
Mogul : 2022.3.0, CSD as543be (2022)
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

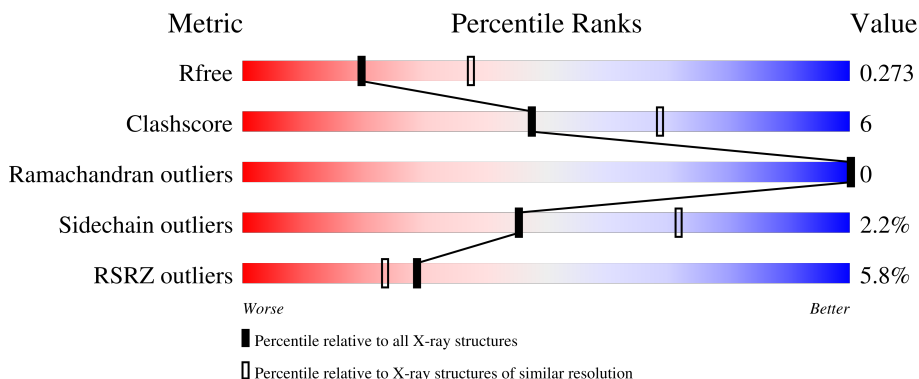
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	E	211	 6% 76% 14% 8%
2	L	216	 7% 83% 14% ..
3	H	242	 3% 82% 12% 5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4861 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 Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	E	194	1550	998	254	290	8	0	0	0

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	330	GLU	-	expression tag	UNP P0DTC2
E	331	THR	-	expression tag	UNP P0DTC2
E	332	GLY	-	expression tag	UNP P0DTC2
E	333	LYS	THR	engineered mutation	UNP P0DTC2
E	363	TYR	ALA	engineered mutation	UNP P0DTC2
E	388	LYS	ASN	engineered mutation	UNP P0DTC2
E	394	TYR	ASN	engineered mutation	UNP P0DTC2
E	468	THR	ILE	engineered mutation	UNP P0DTC2
E	514	THR	SER	engineered mutation	UNP P0DTC2
E	519	ASP	HIS	engineered mutation	UNP P0DTC2
E	522	PRO	ALA	engineered mutation	UNP P0DTC2
E	527	GLY	-	expression tag	UNP P0DTC2
E	528	THR	-	expression tag	UNP P0DTC2
E	529	GLY	-	expression tag	UNP P0DTC2
E	530	GLY	-	expression tag	UNP P0DTC2
E	531	GLY	-	expression tag	UNP P0DTC2
E	532	GLY	-	expression tag	UNP P0DTC2
E	533	SER	-	expression tag	UNP P0DTC2
E	534	LYS	-	expression tag	UNP P0DTC2
E	535	HIS	-	expression tag	UNP P0DTC2
E	536	HIS	-	expression tag	UNP P0DTC2
E	537	HIS	-	expression tag	UNP P0DTC2
E	538	HIS	-	expression tag	UNP P0DTC2
E	539	HIS	-	expression tag	UNP P0DTC2
E	540	HIS	-	expression tag	UNP P0DTC2

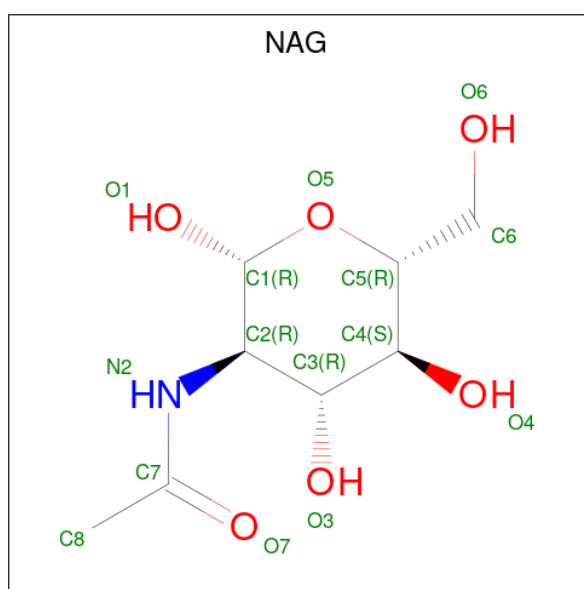
- Molecule 2 is a protein called P2B-2F6 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	213	Total 1568	C 978	N 261	O 324	S 5	0	0	0

- Molecule 3 is a protein called P2B-2F6 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	H	229	Total 1698	C 1079	N 282	O 332	S 5	0	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

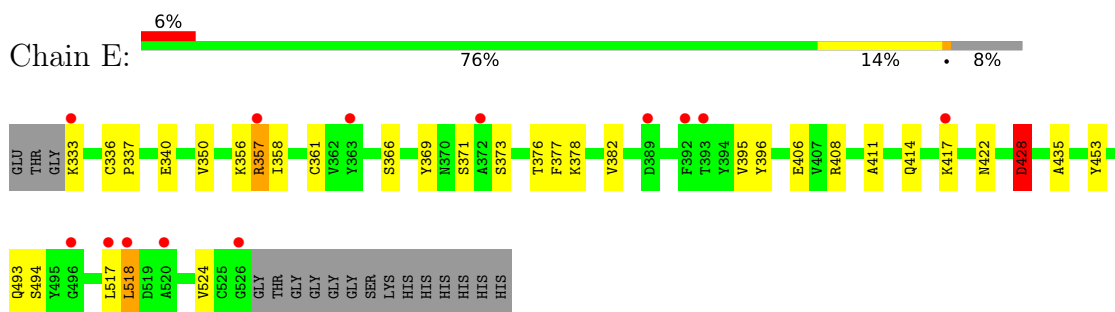
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	E	8	Total 8 8	0	0
5	L	9	Total 9 9	0	0
5	H	14	Total 14 14	0	0

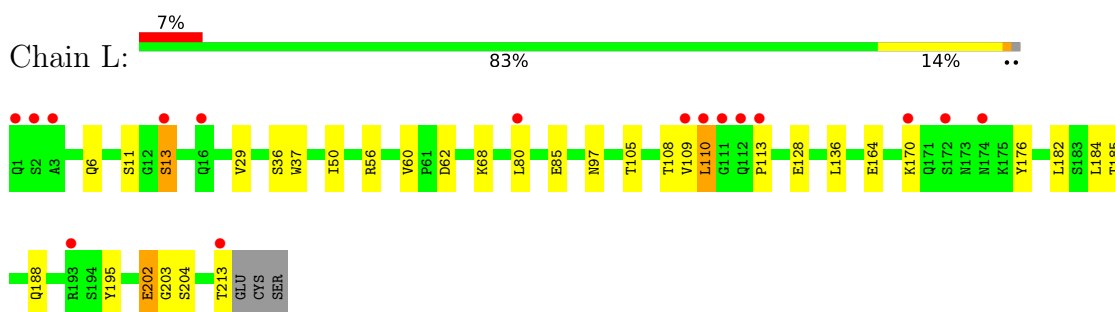
3 Residue-property plots [i](#)

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.

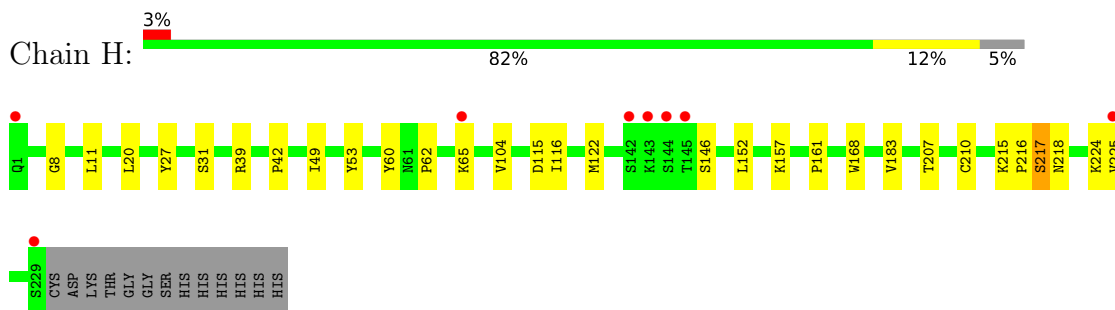
- Molecule 1: Spike protein S1



- Molecule 2: P2B-2F6 Fab light chain



- Molecule 3: P2B-2F6 Fab heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.06Å 91.97Å 111.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.23 – 2.60 56.23 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (56.23-2.60) 99.9 (56.23-2.60)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 2.61Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.221 , 0.272 0.221 , 0.273	Depositor DCC
R_{free} test set	2000 reflections (8.46%)	wwPDB-VP
Wilson B-factor (Å ²)	56.5	Xtrriage
Anisotropy	0.277	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4861	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.65% 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

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	E	0.36	0/1595	0.69	5/2170 (0.2%)
2	L	0.50	0/1607	0.80	4/2194 (0.2%)
3	H	0.36	0/1741	0.62	4/2380 (0.2%)
All	All	0.41	0/4943	0.71	13/6744 (0.2%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	217	SER	N-CA-C	-7.82	98.36	110.17
2	L	203	GLY	N-CA-C	-7.40	106.02	115.42
2	L	113	PRO	N-CA-C	-7.07	99.50	110.95
3	H	217	SER	CA-C-N	-6.19	114.50	122.79
3	H	217	SER	C-N-CA	-6.19	114.50	122.79
2	L	13	SER	CA-C-O	-5.67	116.03	121.08
2	L	202	GLU	N-CA-C	-5.55	103.75	111.52
3	H	218	ASN	CB-CA-C	5.53	120.17	111.72
1	E	377	PHE	N-CA-C	-5.37	98.27	107.61
1	E	428	ASP	CA-C-N	5.34	128.46	120.87
1	E	428	ASP	C-N-CA	5.34	128.46	120.87
1	E	377	PHE	CB-CA-C	5.15	117.95	110.79
1	E	428	ASP	N-CA-C	-5.12	105.50	112.26

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	E	1550	0	1469	20	0
2	L	1568	0	1511	18	0
3	H	1698	0	1694	18	0
4	E	14	0	13	0	0
5	E	8	0	0	0	0
5	H	14	0	0	0	0
5	L	9	0	0	0	0
All	All	4861	0	4687	53	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 (53) 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)
2:L:85:GLU:HG3	2:L:108:THR:HA	1.46	0.94
3:H:60:TYR:HB2	3:H:65:LYS:HG2	1.73	0.70
1:E:406:GLU:OE2	1:E:417:LYS:NZ	2.26	0.69
2:L:185:THR:OG1	2:L:188:GLN:HG3	1.95	0.67
2:L:128:GLU:OE2	3:H:157:LYS:NZ	2.28	0.65
1:E:395:VAL:HG23	1:E:524:VAL:HG11	1.79	0.64
3:H:152:LEU:HD13	3:H:225:VAL:HG21	1.85	0.57
1:E:337:PRO:HD2	1:E:358:ILE:HD12	1.88	0.56
2:L:184:LEU:HD11	2:L:195:TYR:CZ	2.41	0.56
3:H:115:ASP:HB3	3:H:116:ILE:HD12	1.88	0.56
3:H:207:THR:HG23	3:H:224:LYS:HE3	1.88	0.56
1:E:350:VAL:HG22	1:E:422:ASN:HB3	1.89	0.54
1:E:417:LYS:HE2	1:E:453:TYR:CE2	2.44	0.54
2:L:97:ASN:HA	3:H:62:PRO:HG2	1.92	0.52
1:E:336:CYS:HB3	1:E:358:ILE:HG21	1.93	0.51
3:H:161:PRO:HD2	3:H:216:PRO:HB3	1.93	0.51
2:L:85:GLU:HB2	2:L:109:VAL:HG23	1.94	0.49
2:L:202:GLU:C	2:L:204:SER:H	2.21	0.49
1:E:376:THR:HB	1:E:435:ALA:HB3	1.96	0.48
2:L:202:GLU:O	2:L:204:SER:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:60:TYR:HB2	3:H:65:LYS:CG	2.40	0.47
1:E:340:GLU:OE2	1:E:356:LYS:HE2	2.14	0.47
3:H:42:PRO:HG3	3:H:122:MET:HE1	1.96	0.47
2:L:170:LYS:HA	2:L:176:TYR:HA	1.97	0.47
2:L:164:GLU:HB3	3:H:183:VAL:HG21	1.96	0.47
1:E:371:SER:C	1:E:373:SER:H	2.24	0.46
3:H:39:ARG:HB3	3:H:49:ILE:HD11	1.98	0.46
3:H:168:TRP:CH2	3:H:210:CYS:HB3	2.51	0.46
2:L:136:LEU:HD12	2:L:182:LEU:HD23	1.98	0.46
3:H:11:LEU:HD13	3:H:161:PRO:HG3	1.99	0.45
2:L:56:ARG:NH2	2:L:62:ASP:HB3	2.31	0.45
1:E:517:LEU:HA	1:E:517:LEU:HD12	1.71	0.45
2:L:37:TRP:HB2	2:L:50:ILE:HB	1.99	0.45
3:H:53:TYR:CE2	3:H:104:VAL:HG11	2.52	0.44
1:E:333:LYS:HB3	1:E:361:CYS:HA	1.99	0.44
1:E:337:PRO:O	1:E:340:GLU:HG2	2.18	0.44
2:L:56:ARG:HG2	2:L:60:VAL:HB	2.00	0.43
2:L:110:LEU:HD12	2:L:110:LEU:HA	1.85	0.43
2:L:85:GLU:OE2	2:L:170:LYS:NZ	2.50	0.43
1:E:357:ARG:HB3	1:E:396:TYR:CE1	2.54	0.43
3:H:27:TYR:CZ	3:H:31:SER:HB2	2.54	0.43
1:E:428:ASP:OD1	1:E:428:ASP:N	2.52	0.42
1:E:518:LEU:HD13	1:E:518:LEU:HA	1.83	0.42
1:E:376:THR:HG23	1:E:378:LYS:HE3	2.02	0.42
2:L:29:VAL:O	2:L:68:LYS:HD2	2.19	0.42
3:H:8:GLY:HA3	3:H:20:LEU:HD23	2.02	0.42
1:E:411:ALA:HB3	1:E:414:GLN:HG3	2.02	0.42
3:H:215:LYS:N	3:H:216:PRO:CD	2.83	0.41
3:H:215:LYS:C	3:H:217:SER:O	2.64	0.41
1:E:366:SER:HA	1:E:369:TYR:CE2	2.56	0.41
1:E:357:ARG:H	1:E:357:ARG:HG3	1.41	0.41
2:L:6:GLN:HG2	2:L:105:THR:OG1	2.21	0.40
1:E:493:GLN:HG2	1:E:494:SER:N	2.37	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	E	192/211 (91%)	184 (96%)	8 (4%)	0	100	100
2	L	211/216 (98%)	202 (96%)	9 (4%)	0	100	100
3	H	227/242 (94%)	219 (96%)	8 (4%)	0	100	100
All	All	630/669 (94%)	605 (96%)	25 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	E	169/180 (94%)	164 (97%)	5 (3%)	36	64
2	L	176/180 (98%)	170 (97%)	6 (3%)	32	60
3	H	194/205 (95%)	193 (100%)	1 (0%)	81	92
All	All	539/565 (95%)	527 (98%)	12 (2%)	45	72

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	357	ARG
1	E	382	VAL
1	E	408	ARG
1	E	428	ASP
1	E	518	LEU

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Mol	Chain	Res	Type
2	L	11	SER
2	L	13	SER
2	L	36	SER
2	L	80	LEU
2	L	110	LEU
2	L	213	THR
3	H	146	SER

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

Mol	Chain	Res	Type
2	L	39	GLN
2	L	97	ASN
2	L	130	GLN
2	L	198	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](#)

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	1	14,14,15	0.24	0	17,19,21	0.85	1 (5%)

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	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	601	NAG	C1-O5-C5	3.04	116.26	112.19

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	601	NAG	C4-C5-C6-O6

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	E	194/211 (91%)	0.70	13 (6%) 24 19	44, 67, 104, 138	0
2	L	213/216 (98%)	0.53	16 (7%) 20 16	43, 61, 94, 133	0
3	H	229/242 (94%)	0.17	8 (3%) 47 41	42, 52, 72, 107	0
All	All	636/669 (95%)	0.45	37 (5%) 29 23	42, 58, 97, 138	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	213	THR	4.3
2	L	1	GLN	3.6
2	L	170	LYS	3.6
3	H	229	SER	3.5
3	H	145	THR	3.5
1	E	526	GLY	3.5
3	H	143	LYS	3.4
2	L	111	GLY	3.3
2	L	109	VAL	3.2
1	E	518	LEU	3.2
3	H	142	SER	3.0
1	E	372	ALA	3.0
3	H	144	SER	2.9
2	L	113	PRO	2.5
1	E	357	ARG	2.5
1	E	363	TYR	2.4
2	L	13	SER	2.4
2	L	2	SER	2.4
1	E	392	PHE	2.3
2	L	174	ASN	2.3
2	L	172	SER	2.3
1	E	333	LYS	2.3
3	H	225	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
2	L	112	GLN	2.2
2	L	80	LEU	2.2
2	L	110	LEU	2.2
1	E	520	ALA	2.2
2	L	3	ALA	2.2
1	E	496	GLY	2.2
1	E	517	LEU	2.2
3	H	65	LYS	2.1
1	E	389	ASP	2.1
2	L	16	GLN	2.1
1	E	417	LYS	2.0
3	H	1	GLN	2.0
2	L	193	ARG	2.0
1	E	393	THR	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(Å ²)	Q<0.9
4	NAG	E	601	14/15	0.79	0.14	75,91,104,105	0

6.5 Other polymers [i](#)

There are no such residues in this entry.