



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 12:15 AM UTC

PDB ID : 8CBD / pdb\_00008cbd  
Title : SARS-CoV-2 Delta-RBD complexed with BA.4/5-1 and EY6A Fabs  
Authors : Zhou, D.; Ren, J.; Stuart, D.I.  
Deposited on : 2023-01-25  
Resolution : 3.52 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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

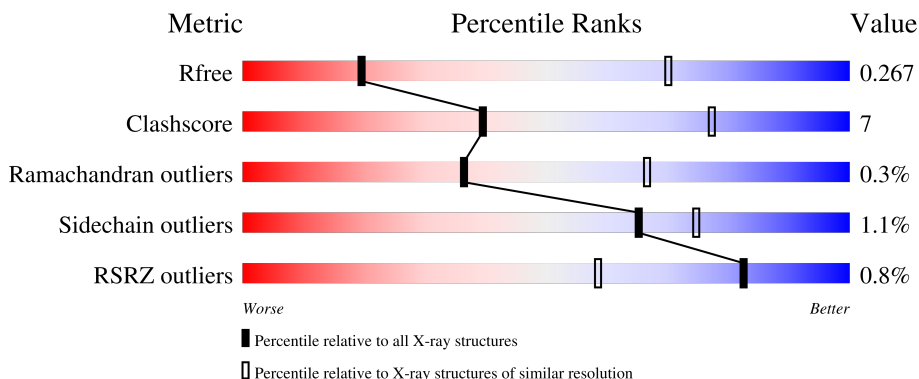
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.52 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	1025 (3.56-3.48)
Clashscore	190562	1079 (3.56-3.48)
Ramachandran outliers	187476	1052 (3.56-3.48)
Sidechain outliers	187428	1053 (3.56-3.48)
RSRZ outliers	180081	1024 (3.56-3.48)

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  $\geq 3$ , 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	R	202	 78% 18% .
1	X	202	 76% 20% .
1	Y	202	 78% 18% .
2	A	222	 79% 18% .
2	C	222	 78% 18% .

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Mol	Chain	Length	Quality of chain
2	H	222	 80% 17%
3	B	214	 78% 21%
3	D	214	 2% 82% 17%
3	L	214	 85% 14%
4	E	226	 80% 15% 5%
4	G	226	 1% 79% 16% 5%
4	J	226	 1% 80% 15% 5%
5	F	215	 1% 83% 15%
5	I	215	 82% 17%
5	K	215	 84% 14%

## 2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 24092 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	R	194	1539	985	260	286	8	0	0	0
1	X	194	1539	985	260	286	8	0	0	0
1	Y	194	1539	985	260	286	8	0	0	0

There are 30 discrepancies between the modelled and reference sequences:

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

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

- Molecule 2 is a protein called BA.4/5-1 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	216	Total	C	N	O	S	0	0	0
			1599	1016	258	320	5			
2	A	216	Total	C	N	O	S	0	0	0
			1599	1016	258	320	5			
2	C	216	Total	C	N	O	S	0	0	0
			1599	1016	258	320	5			

- Molecule 3 is a protein called BA.4/5-1 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	L	213	Total	C	N	O	S	0	0	0
			1639	1027	270	338	4			
3	B	213	Total	C	N	O	S	0	0	0
			1639	1027	270	338	4			
3	D	213	Total	C	N	O	S	0	0	0
			1639	1027	270	338	4			

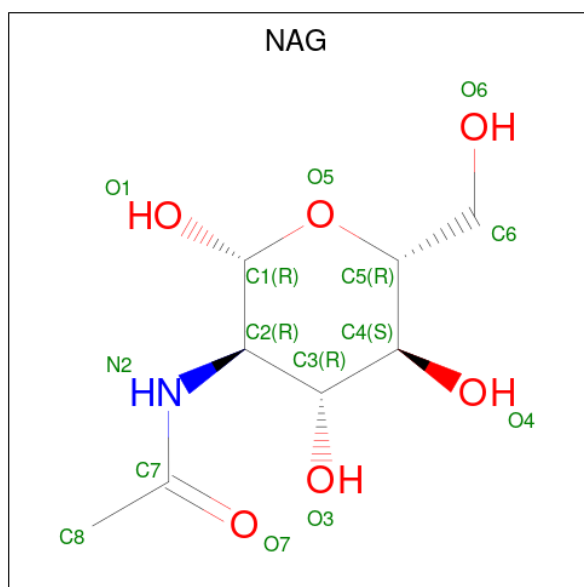
- Molecule 4 is a protein called EY6A heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	E	214	Total	C	N	O	S	0	0	0
			1631	1038	272	315	6			
4	G	214	Total	C	N	O	S	0	0	0
			1631	1038	272	315	6			
4	J	214	Total	C	N	O	S	0	0	0
			1631	1038	272	315	6			

- Molecule 5 is a protein called EY6A light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	212	Total	C	N	O	S	0	0	0
			1618	1012	270	331	5			
5	I	212	Total	C	N	O	S	0	0	0
			1618	1012	270	331	5			
5	K	212	Total	C	N	O	S	0	0	0
			1618	1012	270	331	5			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula:  $C_8H_{15}NO_6$ ).

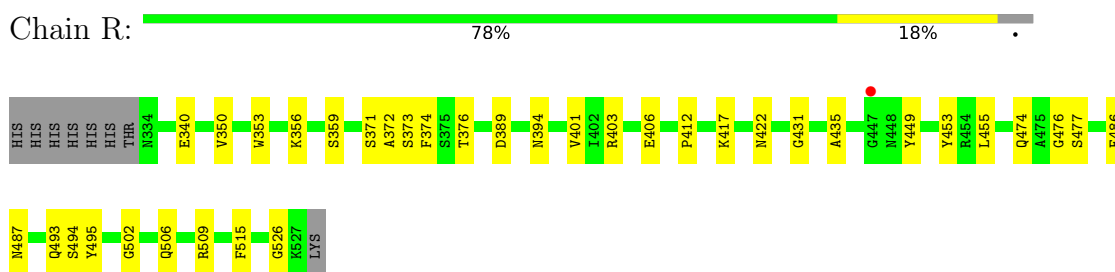


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	R	1	Total	C	N	O	0	0
			14	8	1	5		

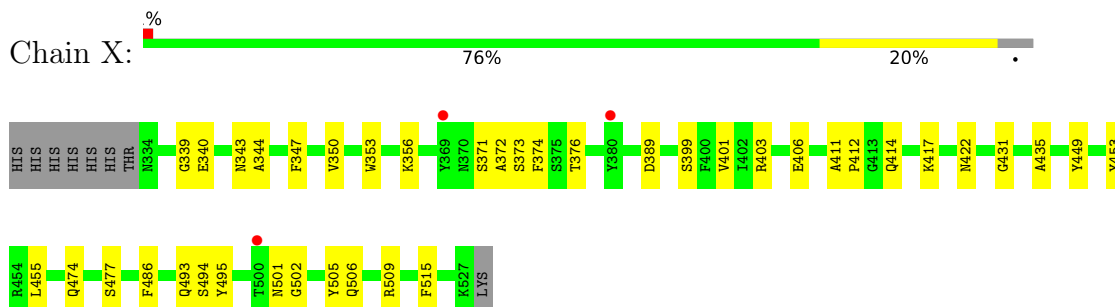
### 3 Residue-property plots [i](#)

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.

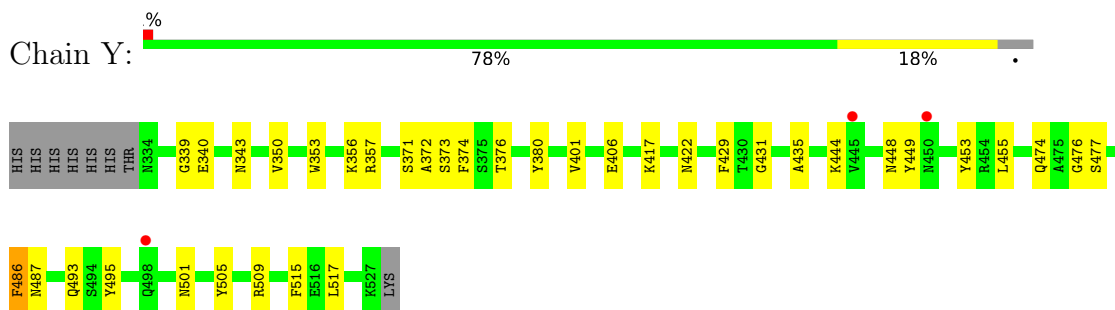
- Molecule 1: Spike protein S1



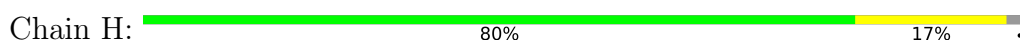
- Molecule 1: Spike protein S1

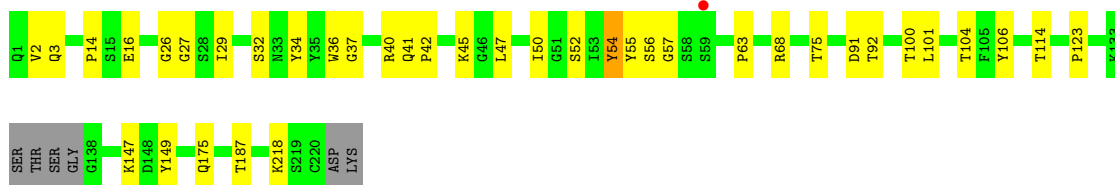


- Molecule 1: Spike protein S1



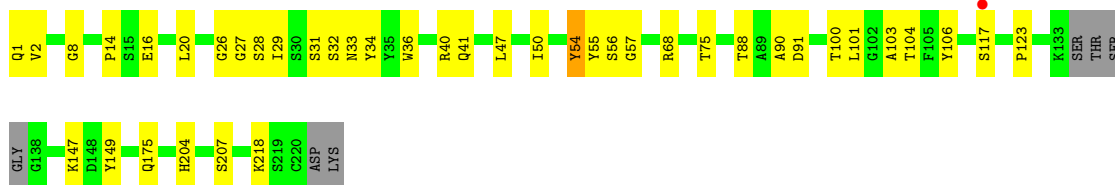
- Molecule 2: BA.4/5-1 heavy chain





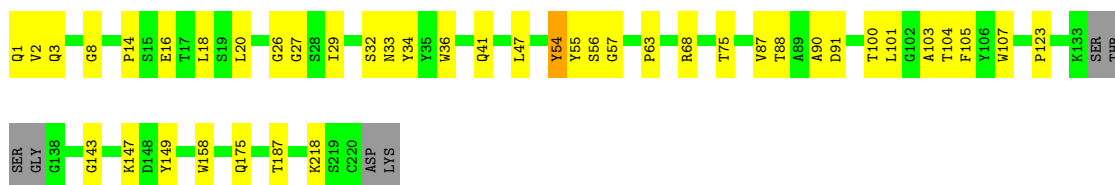
- Molecule 2: BA.4/5-1 heavy chain

Chain A: 79% 18%



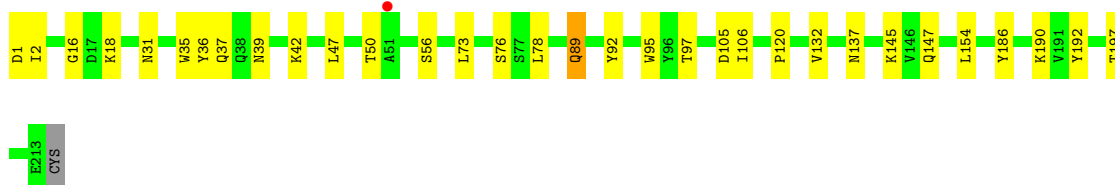
- Molecule 2: BA.4/5-1 heavy chain

Chain C: 78% 18%



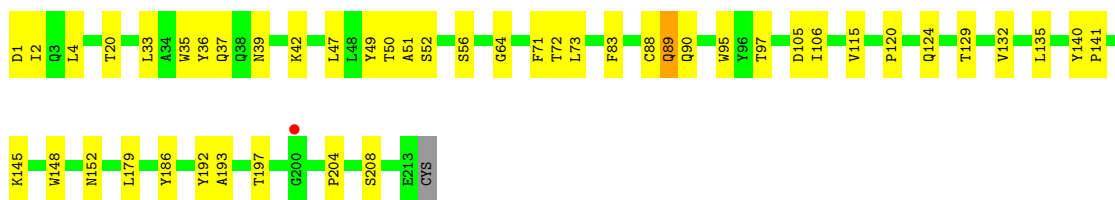
- Molecule 3: BA.4/5-1 light chain

Chain L: 85% 14%

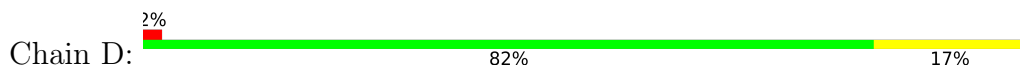


- Molecule 3: BA.4/5-1 light chain

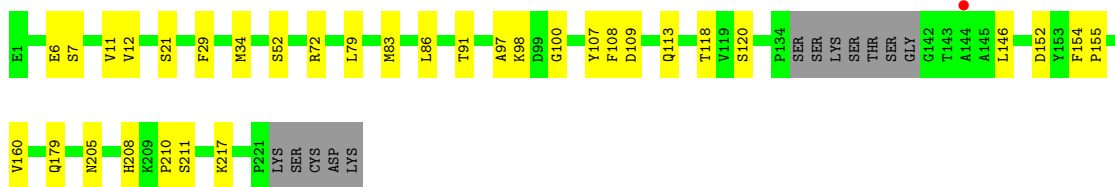
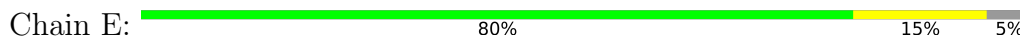
Chain B: 78% 21%



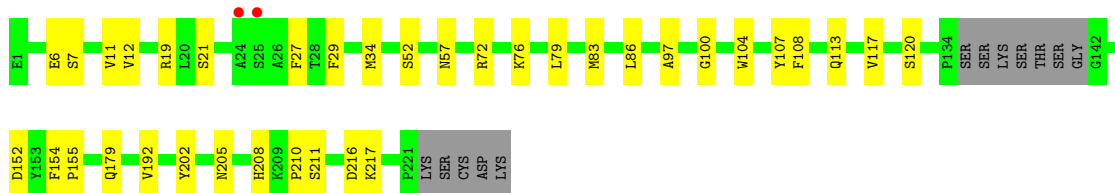
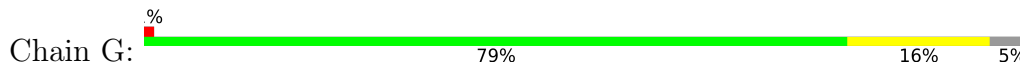
- Molecule 3: BA.4/5-1 light chain



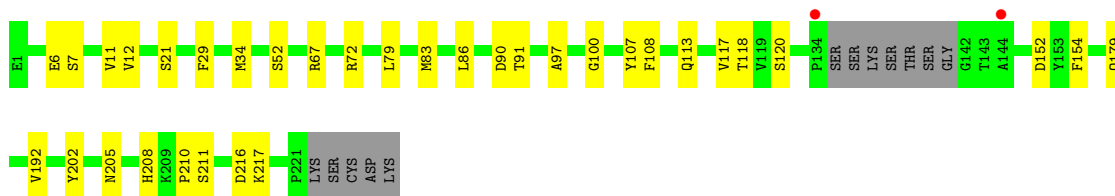
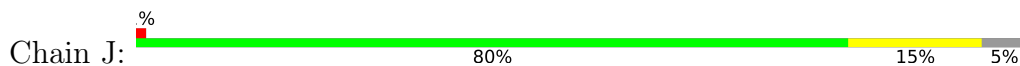
- Molecule 4: EY6A heavy chain



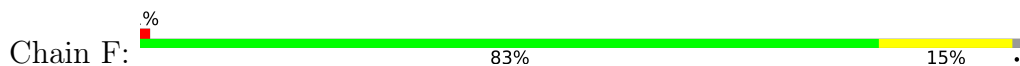
- Molecule 4: EY6A heavy chain



- Molecule 4: EY6A heavy chain



- Molecule 5: EY6A light chain





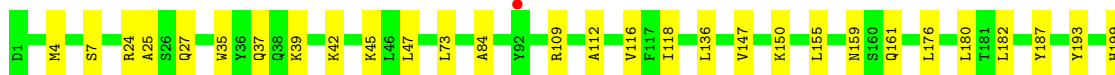
- Molecule 5: EY6A light chain

Chain I: 82% 17%



- Molecule 5: EY6A light chain

Chain K: 84% 14%



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	242.05Å 139.37Å 168.53Å 90.00° 115.58° 90.00°	Depositor
Resolution (Å)	74.69 – 3.52 74.69 – 3.52	Depositor EDS
% Data completeness (in resolution range)	99.1 (74.69-3.52) 99.3 (74.69-3.52)	Depositor EDS
$R_{merge}$	0.33	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.04 (at 3.49Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.218 , 0.266 0.218 , 0.267	Depositor DCC
$R_{free}$ test set	3035 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	123.4	Xtrriage
Anisotropy	0.345	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 169.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.37$ , $\langle L^2 \rangle = 0.21$	Xtrriage
Estimated twinning fraction	0.127 for $1/2^*h-3/2^*k,-1/2^*h-1/2^*k,-1/2^*h+1/2^*k-1$ 0.146 for $1/2^*h+3/2^*k,1/2^*h-1/2^*k,-1/2^*h-1/2^*k-1$	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	24092	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	167.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	R	0.15	0/1582	0.32	0/2150
1	X	0.15	0/1582	0.32	0/2150
1	Y	0.16	0/1582	0.33	0/2150
2	A	0.18	0/1640	0.34	0/2242
2	C	0.16	0/1640	0.33	0/2242
2	H	0.13	0/1640	0.33	0/2242
3	B	0.16	0/1675	0.37	0/2278
3	D	0.16	0/1675	0.38	0/2278
3	L	0.15	0/1675	0.36	0/2278
4	E	0.11	0/1673	0.27	0/2280
4	G	0.11	0/1673	0.26	0/2280
4	J	0.10	0/1673	0.26	0/2280
5	F	0.14	0/1651	0.34	0/2241
5	I	0.15	0/1651	0.35	0/2241
5	K	0.13	0/1651	0.36	0/2241
All	All	0.14	0/24663	0.33	0/33573

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	R	1539	0	1455	22	2
1	X	1539	0	1456	25	0
1	Y	1539	0	1456	25	0
2	A	1599	0	1571	23	0
2	C	1599	0	1571	26	0
2	H	1599	0	1571	22	0
3	B	1639	0	1580	31	0
3	D	1639	0	1580	27	0
3	L	1639	0	1580	24	0
4	E	1631	0	1586	18	0
4	G	1631	0	1586	21	2
4	J	1631	0	1586	20	0
5	F	1618	0	1582	18	0
5	I	1618	0	1582	22	0
5	K	1618	0	1582	17	0
6	R	14	0	13	0	0
All	All	24092	0	23337	319	2

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 7.

The worst 5 of 319 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)
5:I:196:GLU:HG3	5:I:205:PRO:HB3	1.64	0.80
5:F:196:GLU:HG3	5:F:205:PRO:HB3	1.65	0.77
5:F:120:PRO:HB3	5:F:210:PHE:CZ	2.24	0.73
2:H:63:PRO:HD2	3:L:95:TRP:CD1	2.23	0.72
5:I:37:GLN:HB2	5:I:47:LEU:HD11	1.71	0.72

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:389:ASP:OD1	4:G:76:LYS:NZ[3_545]	2.08	0.12
1:R:526:GLY:O	4:G:19:ARG:NH1[3_545]	2.18	0.02

## 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	R	192/202 (95%)	179 (93%)	13 (7%)	0	100	100
1	X	192/202 (95%)	179 (93%)	13 (7%)	0	100	100
1	Y	192/202 (95%)	179 (93%)	13 (7%)	0	100	100
2	A	212/222 (96%)	200 (94%)	9 (4%)	3 (1%)	9	38
2	C	212/222 (96%)	199 (94%)	10 (5%)	3 (1%)	9	38
2	H	212/222 (96%)	200 (94%)	9 (4%)	3 (1%)	9	38
3	B	211/214 (99%)	204 (97%)	7 (3%)	0	100	100
3	D	211/214 (99%)	203 (96%)	8 (4%)	0	100	100
3	L	211/214 (99%)	202 (96%)	9 (4%)	0	100	100
4	E	210/226 (93%)	200 (95%)	10 (5%)	0	100	100
4	G	210/226 (93%)	200 (95%)	10 (5%)	0	100	100
4	J	210/226 (93%)	200 (95%)	10 (5%)	0	100	100
5	F	210/215 (98%)	202 (96%)	8 (4%)	0	100	100
5	I	210/215 (98%)	199 (95%)	11 (5%)	0	100	100
5	K	210/215 (98%)	201 (96%)	9 (4%)	0	100	100
All	All	3105/3237 (96%)	2947 (95%)	149 (5%)	9 (0%)	36	66

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	101	LEU
2	A	101	LEU
2	C	101	LEU
2	H	56	SER
2	C	56	SER

### 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	R	166/175 (95%)	165 (99%)	1 (1%)	78	80
1	X	166/175 (95%)	164 (99%)	2 (1%)	63	73
1	Y	166/175 (95%)	165 (99%)	1 (1%)	78	80
2	A	185/191 (97%)	183 (99%)	2 (1%)	65	75
2	C	185/191 (97%)	183 (99%)	2 (1%)	65	75
2	H	185/191 (97%)	183 (99%)	2 (1%)	65	75
3	B	187/188 (100%)	185 (99%)	2 (1%)	65	75
3	D	187/188 (100%)	186 (100%)	1 (0%)	81	81
3	L	187/188 (100%)	186 (100%)	1 (0%)	81	81
4	E	180/191 (94%)	177 (98%)	3 (2%)	53	70
4	G	180/191 (94%)	178 (99%)	2 (1%)	65	75
4	J	180/191 (94%)	178 (99%)	2 (1%)	65	75
5	F	186/188 (99%)	183 (98%)	3 (2%)	55	70
5	I	186/188 (99%)	183 (98%)	3 (2%)	55	70
5	K	186/188 (99%)	183 (98%)	3 (2%)	55	70
All	All	2712/2799 (97%)	2682 (99%)	30 (1%)	65	75

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	I	182	LEU
2	C	54	TYR
5	K	45	LYS
3	D	89	GLN
3	B	89	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
3	B	152	ASN
2	C	41	GLN
3	D	38	GLN
2	C	196	GLN
5	I	34	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](#)

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$
6	NAG	R	601	1	14,14,15	0.52	0	17,19,21	0.75	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
6	NAG	R	601	1	-	0/6/23/26	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( $^{\circ}$ )	Ideal( $^{\circ}$ )
6	R	601	NAG	C1-O5-C5	2.70	115.80	112.19

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	R	194/202 (96%)	-0.20	1 (0%) 87 67	74, 118, 181, 234	0
1	X	194/202 (96%)	-0.05	3 (1%) 72 44	101, 146, 224, 263	0
1	Y	194/202 (96%)	-0.15	3 (1%) 72 44	83, 124, 188, 250	0
2	A	216/222 (97%)	-0.36	1 (0%) 87 67	90, 133, 193, 234	0
2	C	216/222 (97%)	-0.33	0 100 100	100, 160, 214, 246	0
2	H	216/222 (97%)	-0.41	1 (0%) 87 67	82, 133, 188, 231	0
3	B	213/214 (99%)	-0.49	1 (0%) 87 67	94, 125, 161, 190	0
3	D	213/214 (99%)	-0.25	4 (1%) 66 39	93, 148, 183, 272	0
3	L	213/214 (99%)	-0.42	1 (0%) 87 67	84, 124, 158, 198	0
4	E	214/226 (94%)	-0.34	1 (0%) 87 67	87, 155, 287, 312	0
4	G	214/226 (94%)	-0.24	2 (0%) 81 56	110, 177, 294, 335	0
4	J	214/226 (94%)	-0.24	2 (0%) 81 56	132, 214, 329, 374	0
5	F	212/215 (98%)	-0.20	3 (1%) 73 46	102, 190, 282, 313	0
5	I	212/215 (98%)	-0.23	1 (0%) 87 67	117, 210, 300, 356	0
5	K	212/215 (98%)	-0.25	1 (0%) 87 67	159, 275, 357, 389	0
All	All	3147/3237 (97%)	-0.28	25 (0%) 82 58	74, 149, 288, 389	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	G	25	SER	3.3
5	F	62	PHE	2.8
5	F	11	LEU	2.7
5	K	92	TYR	2.6
5	I	56	SER	2.6

## 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, 95<sup>th</sup> 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
6	NAG	R	601	14/15	0.66	0.12	152,211,232,233	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.