



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:32 AM UTC

PDB ID : 4ORG / pdb\_00004org  
Title : Crystal structure of human Fab CAP256-VRC26.04, a potent V1V2-directed HIV-1 neutralizing antibody  
Authors : Gorman, J.; Doria-Rose, N.A.; Schramm, C.A.; Moore, P.L.; Mascola, J.R.; Shapiro, L.; Morris, L.; Kwong, P.D.  
Deposited on : 2014-02-11  
Resolution : 3.12 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](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

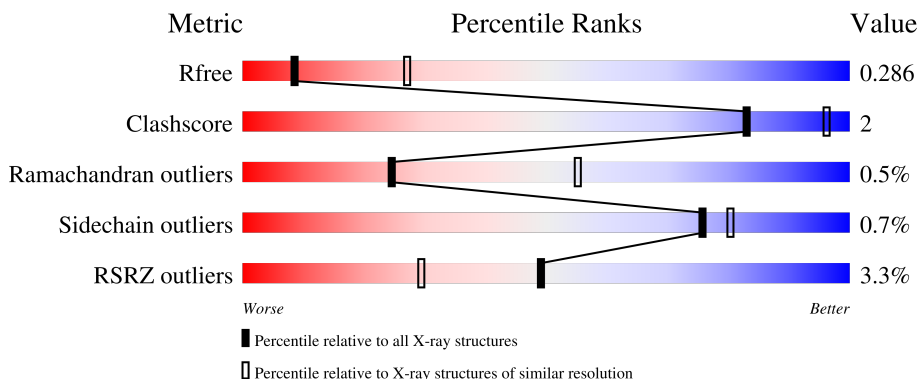
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.12 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.



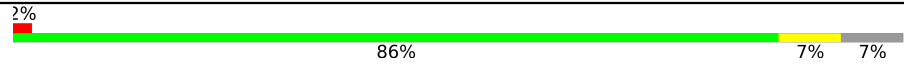

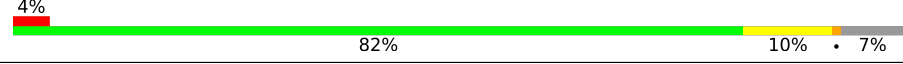
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1816 (3.14-3.10)
Clashscore	190562	1906 (3.14-3.10)
Ramachandran outliers	187476	1802 (3.14-3.10)
Sidechain outliers	187428	1802 (3.14-3.10)
RSRZ outliers	180081	1816 (3.14-3.10)

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	B	216	 4% 93% • •
1	D	216	 6% 93% • •
1	F	216	 3% 93% • •
1	L	216	 3% 93% 5% •
2	A	256	 2% 84% 7% 9%

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Mol	Chain	Length	Quality of chain
2	C	256	 <p>2% 86% 7% 7%</p>
2	E	256	 <p>2% 81% 9% 8%</p>
2	H	256	 <p>4% 82% 10% 7%</p>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 26405 atoms, of which 13008 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 CAP256-VRC26.04 light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	L	211	3093	979	1529	264	317	4	0	0	0
1	B	208	3061	970	1513	261	313	4	0	0	0
1	D	208	3047	967	1505	258	313	4	0	0	0
1	F	209	3062	972	1511	259	316	4	0	0	0

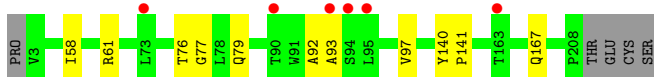
- Molecule 2 is a protein called CAP256-VRC26.04 heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	H	238	3565	1146	1751	314	345	9	0	0	0
2	A	232	3484	1117	1714	306	338	9	0	0	0
2	C	237	3547	1136	1743	312	347	9	0	0	0
2	E	235	3546	1136	1742	310	348	10	0	0	0

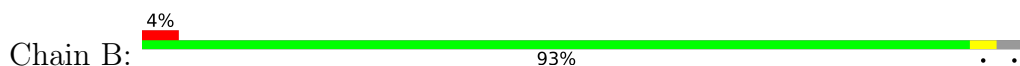
### 3 Residue-property plots [i](#)

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.

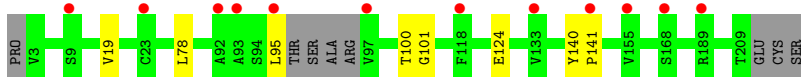
- Molecule 1: CAP256-VRC26.04 light chain



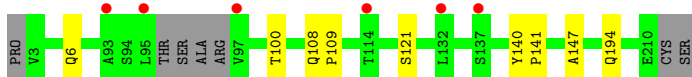
- Molecule 1: CAP256-VRC26.04 light chain



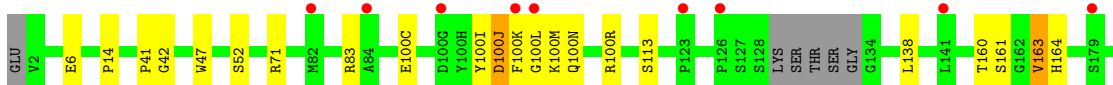
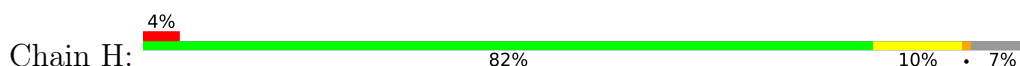
- Molecule 1: CAP256-VRC26.04 light chain

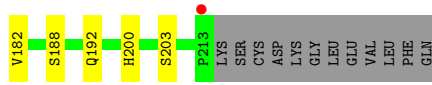


- Molecule 1: CAP256-VRC26.04 light chain

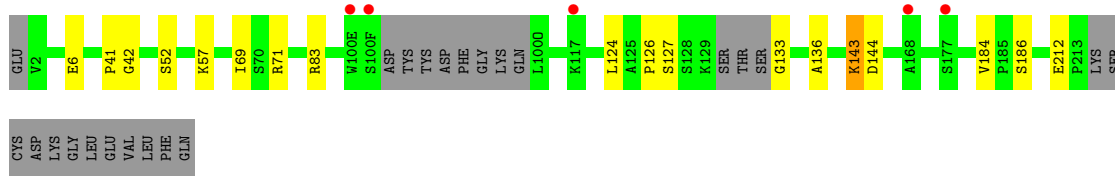
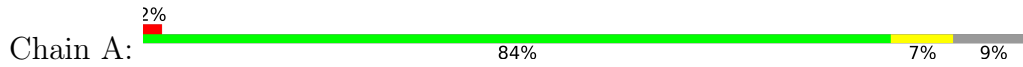


- Molecule 2: CAP256-VRC26.04 heavy chain

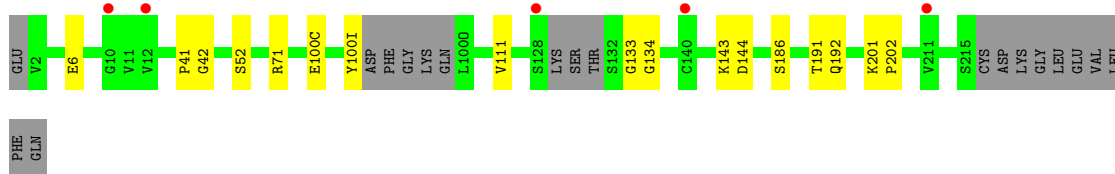
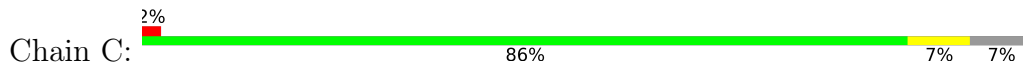




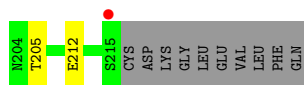
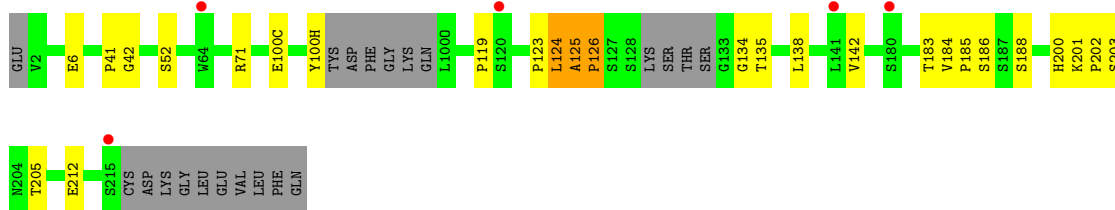
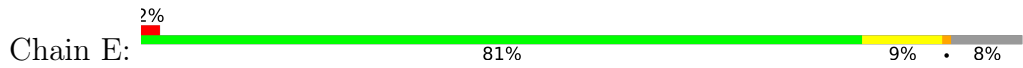
- Molecule 2: CAP256-VRC26.04 heavy chain



- Molecule 2: CAP256-VRC26.04 heavy chain



- Molecule 2: CAP256-VRC26.04 heavy chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.02Å 85.47Å 103.27Å 97.90° 107.72° 91.67°	Depositor
Resolution (Å)	35.63 – 3.12 35.63 – 3.12	Depositor EDS
% Data completeness (in resolution range)	92.7 (35.63-3.12) 92.8 (35.63-3.12)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.58 (at 3.12Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, $R_{free}$	0.275 , 0.289 0.278 , 0.286	Depositor DCC
$R_{free}$ test set	1811 reflections (4.65%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	60.6	Xtrriage
Anisotropy	0.447	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 28.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.25$	Xtrriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	26405	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 84.49 % 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 1.6411e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	B	0.29	0/1585	0.61	0/2167
1	D	0.29	0/1579	0.61	0/2160
1	F	0.28	0/1588	0.59	0/2172
1	L	0.30	0/1602	0.62	0/2192
2	A	0.26	0/1813	0.59	0/2462
2	C	0.28	0/1837	0.60	0/2493
2	E	0.28	0/1831	0.61	1/2485 (0.0%)
2	H	0.27	0/1848	0.61	0/2508
All	All	0.28	0/13683	0.61	1/18639 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	134	GLY	N-CA-C	5.16	117.01	110.20

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	B	1548	1513	1515	5	0
1	D	1542	1505	1507	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1551	1511	1513	5	0
1	L	1564	1529	1531	8	0
2	A	1770	1714	1718	10	0
2	C	1804	1743	1746	8	0
2	E	1804	1742	1746	15	0
2	H	1814	1751	1753	17	0
All	All	13397	13008	13029	64	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 2.

All (64) 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:L:61:ARG:NH1	1:L:77:GLY:O	2.21	0.73
2:H:200:HIS:ND1	2:H:203:SER:OG	2.29	0.66
1:B:124:GLU:OE2	2:A:143:LYS:NZ	2.30	0.65
2:C:52:SER:O	2:C:71:ARG:NH1	2.31	0.64
1:D:124:GLU:OE2	2:C:143:LYS:NZ	2.31	0.64
2:A:6:GLU:N	2:A:6:GLU:OE2	2.32	0.63
2:A:83:ARG:NH2	2:E:100(C):GLU:OE1	2.31	0.63
1:L:167:GLN:OE1	2:H:164:HIS:NE2	2.32	0.62
2:E:52:SER:O	2:E:71:ARG:NH1	2.33	0.61
1:F:6:GLN:NE2	1:F:100:THR:O	2.34	0.61
2:A:133:GLY:N	2:A:186:SER:HG	2.00	0.59
2:H:138:LEU:O	2:H:182:VAL:N	2.36	0.59
2:H:100(K):PHE:HA	2:H:100(L):GLY:C	2.31	0.56
2:A:52:SER:O	2:A:71:ARG:NH1	2.40	0.55
2:H:163:VAL:HG22	2:H:182:VAL:HG22	1.89	0.54
1:L:79:GLN:NE2	1:B:186:LYS:O	2.39	0.54
2:A:212:GLU:N	2:A:212:GLU:OE1	2.42	0.52
2:E:125:ALA:HB1	2:E:126:PRO:CA	2.40	0.52
2:H:83:ARG:NH2	2:C:100(C):GLU:OE1	2.42	0.52
2:E:125:ALA:CB	2:E:138:LEU:HA	2.41	0.51
1:B:100:THR:N	1:B:101:GLY:HA2	2.26	0.50
1:D:100:THR:N	1:D:101:GLY:HA2	2.28	0.49
1:F:121:SER:OG	2:E:123:PRO:O	2.31	0.49
2:E:124:LEU:O	2:E:125:ALA:CB	2.61	0.48
2:H:52:SER:O	2:H:71:ARG:NH1	2.45	0.48
2:E:200:HIS:CE1	2:E:203:SER:HG	2.28	0.48
2:E:6:GLU:N	2:E:6:GLU:OE2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:119:PRO:HB2	2:E:142:VAL:HG13	1.95	0.47
2:H:6:GLU:N	2:H:6:GLU:OE2	2.48	0.47
1:L:140:TYR:CG	1:L:141:PRO:HA	2.51	0.46
2:C:6:GLU:OE1	2:C:6:GLU:N	2.48	0.45
1:F:140:TYR:CG	1:F:141:PRO:HA	2.51	0.45
2:H:188:SER:O	2:H:192:GLN:N	2.49	0.45
2:H:160:THR:O	2:H:160:THR:HG23	2.17	0.45
2:H:100(I):TYS:O	2:H:100(J):ASP:CB	2.65	0.45
1:L:76:THR:OG1	1:L:77:GLY:N	2.50	0.45
2:C:201:LYS:N	2:C:202:PRO:CD	2.80	0.45
1:L:97:VAL:HG11	2:H:47:TRP:HB3	2.00	0.44
2:E:124:LEU:O	2:E:125:ALA:HB3	2.15	0.44
2:E:184:VAL:HG13	2:E:185:PRO:HD2	1.99	0.44
1:F:108:GLN:N	1:F:109:PRO:CD	2.81	0.44
2:C:134:GLY:N	2:C:186:SER:OG	2.51	0.43
2:H:100(M):LYS:HA	2:H:100(N):GLN:HA	1.85	0.43
1:L:92:ALA:HB1	1:L:93:ALA:HB2	2.01	0.43
1:B:140:TYR:CG	1:B:141:PRO:HA	2.54	0.42
1:D:19:VAL:CG2	1:D:78:LEU:HD11	2.49	0.42
1:D:140:TYR:CG	1:D:141:PRO:HA	2.55	0.42
1:F:147:ALA:N	1:F:194:GLN:O	2.52	0.42
2:E:212:GLU:N	2:E:212:GLU:OE2	2.53	0.42
2:C:41:PRO:HA	2:C:42:GLY:HA2	1.78	0.42
1:B:118:PHE:CB	2:A:124:LEU:HD22	2.49	0.41
2:C:191:THR:OG1	2:C:192:GLN:N	2.53	0.41
2:H:100(K):PHE:HA	2:H:100(M):LYS:N	2.34	0.41
2:E:125:ALA:HB1	2:E:126:PRO:CB	2.50	0.41
1:L:58:ILE:N	1:L:58:ILE:HD12	2.35	0.41
2:E:201:LYS:N	2:E:202:PRO:CD	2.83	0.41
2:H:41:PRO:HA	2:H:42:GLY:HA2	1.76	0.41
2:A:41:PRO:HA	2:A:42:GLY:HA2	1.76	0.41
2:E:41:PRO:HA	2:E:42:GLY:HA2	1.77	0.41
2:H:100(C):GLU:HB3	2:H:100(R):ARG:HE	1.86	0.41
2:A:57:LYS:NZ	2:A:69:ILE:O	2.54	0.41
2:A:136:ALA:N	2:A:184:VAL:O	2.51	0.41
1:D:95:LEU:HD22	1:D:95:LEU:N	2.35	0.41
2:H:14:PRO:HG2	2:H:113:SER:HB3	2.03	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	B	204/216 (94%)	187 (92%)	17 (8%)	0	100	100
1	D	204/216 (94%)	187 (92%)	17 (8%)	0	100	100
1	F	205/216 (95%)	186 (91%)	19 (9%)	0	100	100
1	L	209/216 (97%)	184 (88%)	25 (12%)	0	100	100
2	A	226/256 (88%)	201 (89%)	23 (10%)	2 (1%)	14	42
2	C	230/256 (90%)	207 (90%)	21 (9%)	2 (1%)	14	42
2	E	229/256 (90%)	205 (90%)	22 (10%)	2 (1%)	14	42
2	H	232/256 (91%)	211 (91%)	19 (8%)	2 (1%)	14	42
All	All	1739/1888 (92%)	1568 (90%)	163 (9%)	8 (0%)	24	55

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	100(J)	ASP
2	A	126	PRO
2	A	144	ASP
2	C	144	ASP
2	E	125	ALA
2	E	126	PRO
2	H	161	SER
2	C	133	GLY

### 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	B	175/181 (97%)	175 (100%)	0	100	100
1	D	174/181 (96%)	174 (100%)	0	100	100
1	F	175/181 (97%)	175 (100%)	0	100	100
1	L	176/181 (97%)	176 (100%)	0	100	100
2	A	194/215 (90%)	192 (99%)	2 (1%)	68	77
2	C	198/215 (92%)	197 (100%)	1 (0%)	81	83
2	E	197/215 (92%)	191 (97%)	6 (3%)	36	63
2	H	197/215 (92%)	196 (100%)	1 (0%)	81	83
All	All	1486/1584 (94%)	1476 (99%)	10 (1%)	76	80

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	163	VAL
2	A	127	SER
2	A	143	LYS
2	C	111	VAL
2	E	124	LEU
2	E	135	THR
2	E	183	THR
2	E	186	SER
2	E	188	SER
2	E	205	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	27(B)	ASN
1	L	30	ASN
2	H	26	GLN
2	H	171	GLN
1	B	52	ASN
2	A	81	GLN
2	A	82(A)	ASN
1	D	194	GLN
2	C	204	ASN
1	F	170	ASN
1	F	184	GLN
1	F	194	GLN

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Mol	Chain	Res	Type
2	E	26	GLN
2	E	76	ASN
2	E	82(A)	ASN
2	E	171	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](#)

5 non-standard protein/DNA/RNA residues are 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	$\# Z  > 2$
2	TYS	C	100(H)	2	3,4,17	0.94	0	2,4,24	0.98	0
2	TYS	H	100(I)	2	3,4,17	0.90	0	2,4,24	1.02	0
2	TYS	E	100(H)	2	15,16,17	1.20	3 (20%)	15,22,24	0.60	0
2	TYS	H	100(H)	2	3,4,17	0.95	0	2,4,24	1.27	0
2	TYS	C	100(I)	2	3,4,17	0.92	0	2,4,24	1.46	1 (50%)

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
2	TYS	C	100(H)	2	-	0/1/2/13	-
2	TYS	H	100(I)	2	-	0/1/2/13	-
2	TYS	E	100(H)	2	-	7/10/11/13	0/1/1/1
2	TYS	H	100(H)	2	-	1/1/2/13	-
2	TYS	C	100(I)	2	-	1/1/2/13	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	100(H)	TYS	OH-CZ	-2.90	1.38	1.42
2	E	100(H)	TYS	O3-S	2.17	1.64	1.50
2	E	100(H)	TYS	OH-S	-2.09	1.54	1.58

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	100(I)	TYS	O-C-CA	-2.07	117.62	124.23

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	100(H)	TYS	O-C-CA-CB
2	C	100(I)	TYS	O-C-CA-CB
2	E	100(H)	TYS	C-CA-CB-CG
2	E	100(H)	TYS	CZ-OH-S-O1
2	E	100(H)	TYS	CZ-OH-S-O2
2	E	100(H)	TYS	CZ-OH-S-O3
2	E	100(H)	TYS	N-CA-CB-CG
2	E	100(H)	TYS	CA-CB-CG-CD1
2	E	100(H)	TYS	CA-CB-CG-CD2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	100(I)	TYS	1	0

## 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, 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	B	208/216 (96%)	0.58	9 (4%) 40 22	39, 61, 82, 93	0
1	D	208/216 (96%)	0.64	12 (5%) 29 15	35, 64, 84, 101	0
1	F	209/216 (96%)	0.36	6 (2%) 53 32	25, 50, 70, 84	0
1	L	211/216 (97%)	0.41	6 (2%) 55 34	17, 57, 88, 99	0
2	A	232/256 (90%)	0.37	5 (2%) 62 41	32, 57, 77, 91	0
2	C	235/256 (91%)	0.43	5 (2%) 63 42	28, 59, 79, 89	0
2	E	234/256 (91%)	0.46	5 (2%) 63 42	38, 62, 79, 92	0
2	H	236/256 (92%)	0.51	10 (4%) 40 22	38, 59, 89, 103	0
All	All	1773/1888 (93%)	0.47	58 (3%) 49 29	17, 59, 82, 103	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	95	LEU	4.4
1	B	199	GLY	4.3
2	H	100(G)	ASP	4.3
1	F	95	LEU	4.1
2	E	64	TRP	3.7
1	D	23	CYS	3.5
2	C	10	GLY	3.5
1	D	92	ALA	3.4
2	A	117	LYS	3.4
2	E	141	LEU	3.1
2	A	177	SER	3.0
2	H	82	MET	3.0
2	E	120	SER	3.0
2	H	141	LEU	2.9
1	L	94	SER	2.9
1	B	99	GLY	2.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	D	93	ALA	2.9
1	D	168	SER	2.8
2	H	179	SER	2.7
1	D	155	VAL	2.7
1	B	129	LYS	2.6
1	L	95	LEU	2.6
1	D	133	VAL	2.6
1	B	200	SER	2.6
2	C	128	SER	2.5
1	F	93	ALA	2.5
1	D	189	ARG	2.5
1	L	73	LEU	2.4
1	D	97	VAL	2.4
1	B	95	LEU	2.4
2	A	100(F)	SER	2.4
2	H	126	PRO	2.4
2	A	100(E)	TRP	2.4
1	L	93	ALA	2.3
2	C	211	VAL	2.3
2	E	180	SER	2.3
1	B	90	THR	2.3
2	H	213	PRO	2.3
1	L	90	THR	2.3
2	H	100(K)	PHE	2.3
1	F	97	VAL	2.3
1	F	132	LEU	2.2
2	H	123	PRO	2.2
2	E	215	SER	2.1
1	B	162	THR	2.1
1	F	114	THR	2.1
2	H	84	ALA	2.1
1	D	9	SER	2.1
1	F	137	SER	2.1
1	B	112	ASN	2.1
2	C	140	CYS	2.1
1	D	118	PHE	2.1
2	C	12	VAL	2.1
1	L	163	THR	2.1
1	B	95(C)	ALA	2.1
2	A	168	ALA	2.1
2	H	100(L)	GLY	2.1
1	D	141	PRO	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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(Å <sup>2</sup> )	Q<0.9
2	TYS	H	100(I)	5/17	0.28	0.27	81,93,108,111	0
2	TYS	H	100(H)	5/17	0.29	0.26	74,93,108,112	0
2	TYS	C	100(I)	5/17	0.60	0.24	68,79,91,98	0
2	TYS	E	100(H)	16/17	0.71	0.18	44,71,92,95	0
2	TYS	C	100(H)	5/17	0.87	0.10	75,76,90,91	0

## 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.