



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:24 PM GMT

PDB ID : 4ORG
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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

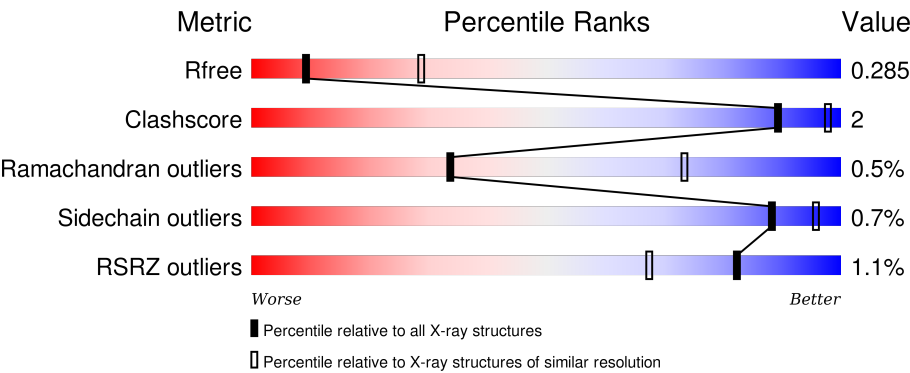
MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

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 3.12 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}	91344	1112 (3.16-3.08)
Clashscore	102246	1218 (3.16-3.08)
Ramachandran outliers	100387	1175 (3.16-3.08)
Sidechain outliers	100360	1175 (3.16-3.08)
RSRZ outliers	91569	1114 (3.16-3.08)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	<div><div></div><div>93%</div><div></div></div>
1	D	216	<div><div>%</div><div>93%</div><div></div></div>
1	F	216	<div><div></div><div>93%</div><div></div></div>
1	L	216	<div><div>%</div><div>93%</div><div>5%</div></div>
2	A	256	<div><div>%</div><div>84%</div><div>7%</div><div>9%</div></div>

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Mol	Chain	Length	Quality of chain
2	C	256	<div><div>%</div><div><div></div><div>86%</div><div>6%</div><div>7%</div></div></div>
2	E	256	<div><div>3%</div><div><div></div><div>82%</div><div>9%</div><div>8%</div></div></div>
2	H	256	<div><div>%</div><div><div></div><div>82%</div><div>10%</div><div>7%</div></div></div>

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

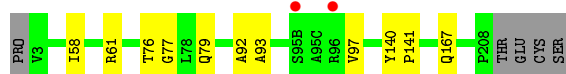
- Molecule 2 is a protein called CAP256-VRC26.04 heavy chain.

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

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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



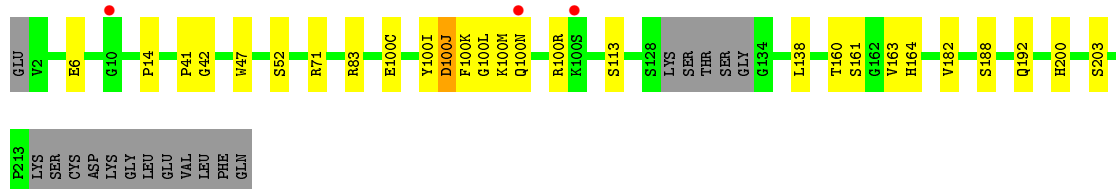
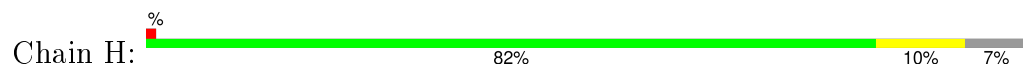
- Molecule 1: CAP256-VRC26.04 light chain



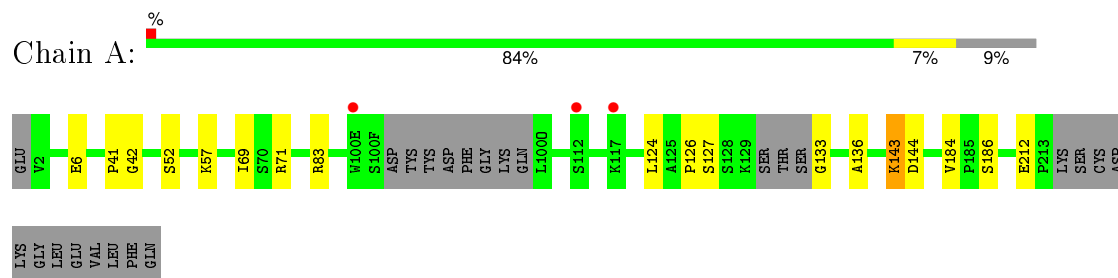
- Molecule 1: CAP256-VRC26.04 light chain



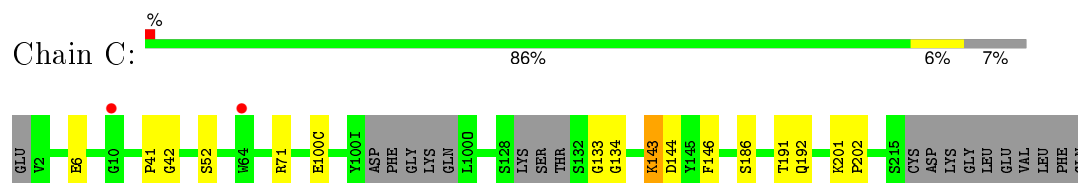
- Molecule 2: CAP256-VRC26.04 heavy chain



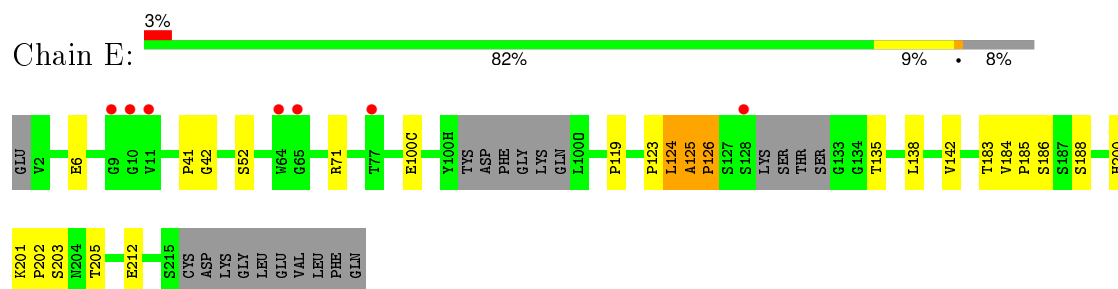
- Molecule 2: CAP256-VRC26.04 heavy chain



- 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, α , β , γ	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) 91.1 (35.63-3.12)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 3.12Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.275 , 0.289 0.276 , 0.285	Depositor DCC
R_{free} test set	1806 reflections (5.01%)	DCC
Wilson B-factor (Å ²)	60.6	Xtriage
Anisotropy	0.447	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 27.2	EDS
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 36109 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	26405	wwPDB-VP
Average B, all atoms (Å ²)	59.0	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 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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: 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	0.21	0/1585	0.40	0/2167
1	D	0.22	0/1579	0.41	0/2160
1	F	0.21	0/1588	0.40	0/2172
1	L	0.21	0/1602	0.40	0/2192
2	A	0.21	0/1813	0.40	0/2462
2	C	0.22	0/1837	0.39	0/2493
2	E	0.22	0/1831	0.40	0/2485
2	H	0.22	0/1848	0.39	0/2508
All	All	0.22	0/13683	0.40	0/18639

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	B	1548	1513	1515	5	0
1	D	1542	1505	1507	5	0
1	F	1551	1511	1513	5	0
1	L	1564	1529	1531	8	0
2	A	1770	1714	1718	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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:133:GLY:N	2:A:186:SER:HG	1.96	0.63
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:H:138:LEU:O	2:H:182:VAL:N	2.36	0.59
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:OE1	2:A:212:GLU:N	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:H:100(K):PHE:HA	2:H:100(L):GLY:C	2.31	0.51
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:E:200:HIS:CE1	2:E:203:SER:HG	2.28	0.48
2:H:52:SER:O	2:H:71:ARG:NH1	2.45	0.48
2:E:6:GLU:N	2:E:6:GLU:OE2	2.46	0.48
2:E:119:PRO:HB2	2:E:142:VAL:HG13	1.95	0.47
2:H:6:GLU:OE2	2:H:6:GLU:N	2.48	0.47
1:L:140:TYR:CG	1:L:141:PRO:HA	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:124:LEU:O	2:E:125:ALA:HB3	2.15	0.45
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: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:OE2	2:E:212:GLU:N	2.53	0.42
2:C:41:PRO:HA	2:C:42:GLY:HA2	1.78	0.42
2:C:191:THR:OG1	2:C:192:GLN:N	2.53	0.41
1:B:118:PHE:CB	2:A:124:LEU:HD22	2.49	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
2:E:201:LYS:N	2:E:202:PRO:CD	2.83	0.41
1:L:58:ILE:HD12	1:L:58:ILE:N	2.35	0.41
2:E:41:PRO:HA	2:E:42:GLY:HA2	1.77	0.41
2:A:41:PRO:HA	2:A:42:GLY:HA2	1.76	0.41
2:H:41:PRO:HA	2:H:42:GLY:HA2	1.76	0.41
2:H:100(C):GLU:HB3	2:H:100(R):ARG:HE	1.86	0.41
2:A:136:ALA:N	2:A:184:VAL:O	2.51	0.41
2:A:57:LYS:NZ	2:A:69:ILE:O	2.54	0.41
1:D:95:LEU:N	1:D:95:LEU:HD22	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

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	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%)	21	62
2	C	230/256 (90%)	207 (90%)	21 (9%)	2 (1%)	21	62
2	E	229/256 (90%)	205 (90%)	22 (10%)	2 (1%)	21	62
2	H	232/256 (91%)	211 (91%)	19 (8%)	2 (1%)	21	62
All	All	1739/1888 (92%)	1568 (90%)	163 (9%)	8 (0%)	34	73

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

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%)	82	93
2	C	198/215 (92%)	196 (99%)	2 (1%)	82	93
2	E	197/215 (92%)	191 (97%)	6 (3%)	48	81
2	H	197/215 (92%)	197 (100%)	0	100	100
All	All	1486/1584 (94%)	1476 (99%)	10 (1%)	88	96

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

Mol	Chain	Res	Type
2	A	127	SER
2	A	143	LYS
2	C	143	LYS
2	C	146	PHE
2	E	124	LEU
2	E	135	THR
2	E	183	THR
2	E	186	SER
2	E	188	SER
2	E	205	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	184	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	0.79	0	0,4,24	0.00	-
2	TYS	C	100(I)	2	3,4,17	0.77	0	0,4,24	0.00	-
2	TYS	E	100(H)	2	15,16,17	1.70	3 (20%)	16,22,24	1.01	2 (12%)
2	TYS	H	100(H)	2	3,4,17	0.80	0	0,4,24	0.00	-
2	TYS	H	100(I)	2	3,4,17	0.76	0	0,4,24	0.00	-

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	-	0/0/2/13	0/0/0/1
2	TYS	C	100(I)	2	-	0/0/2/13	0/0/0/1
2	TYS	E	100(H)	2	-	0/9/11/13	0/1/1/1
2	TYS	H	100(H)	2	-	0/0/2/13	0/0/0/1
2	TYS	H	100(I)	2	-	0/0/2/13	0/0/0/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	100(H)	TYS	OH-S	-5.00	1.54	1.63
2	E	100(H)	TYS	OH-CZ	-2.89	1.38	1.42
2	E	100(H)	TYS	O3-S	2.60	1.64	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	100(H)	TYS	O-C-CA	-2.02	120.22	125.49
2	E	100(H)	TYS	CZ-OH-S	2.43	122.65	118.52

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
2	H	100(I)	TYS	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates 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, 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	B	208/216 (96%)	0.04	0 100 100	35, 55, 75, 85	0
1	D	208/216 (96%)	0.03	2 (0%) 84 70	33, 59, 77, 93	0
1	F	209/216 (96%)	-0.01	1 (0%) 91 84	24, 45, 64, 78	0
1	L	211/216 (97%)	0.00	2 (0%) 85 73	15, 52, 80, 90	0
2	A	232/256 (90%)	-0.01	3 (1%) 79 63	30, 52, 73, 84	0
2	C	235/256 (91%)	-0.06	2 (0%) 85 73	27, 55, 72, 82	0
2	E	234/256 (91%)	0.03	7 (2%) 54 30	33, 56, 73, 86	0
2	H	236/256 (92%)	0.06	3 (1%) 79 63	35, 54, 83, 93	0
All	All	1773/1888 (93%)	0.01	20 (1%) 82 67	15, 54, 74, 93	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	10	GLY	5.6
1	F	95	LEU	5.2
2	E	64	TRP	4.1
2	E	9	GLY	3.2
1	L	95(B)	SER	2.8
1	D	155	VAL	2.7
2	H	10	GLY	2.6
2	A	117	LYS	2.5
2	E	10	GLY	2.4
2	A	100(E)	TRP	2.4
2	C	64	TRP	2.3
2	A	112	SER	2.3
2	E	65	GLY	2.2
2	H	100(S)	LYS	2.2
2	E	128	SER	2.1
2	E	77	THR	2.1

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Mol	Chain	Res	Type	RSRZ
2	E	11	VAL	2.1
2	H	100(N)	GLN	2.0
1	L	96	ARG	2.0
1	D	157	ALA	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	TYS	C	100(H)	5/17	0.92	0.32	-	75,76,90,91	0
2	TYS	E	100(H)	16/17	0.81	0.26	-	44,71,92,95	0
2	TYS	H	100(H)	5/17	0.76	0.44	-	74,93,108,112	0
2	TYS	H	100(I)	5/17	0.66	0.56	-	81,93,108,111	0
2	TYS	C	100(I)	5/17	0.84	0.21	-	68,79,91,98	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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.