



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 11:48 PM EDT

PDB ID : 6FY2
Title : Crystal structure of a V2p-reactive RV144 vaccine-like antibody, CAP228-16H, in complex with a heterologous CAP225 V1V2
Authors : Wibmer, C.K.; Moore, P.L.; Morris, L.
Deposited on : 2018-03-10
Resolution : 2.30 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.37.1
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) : 2.37.1

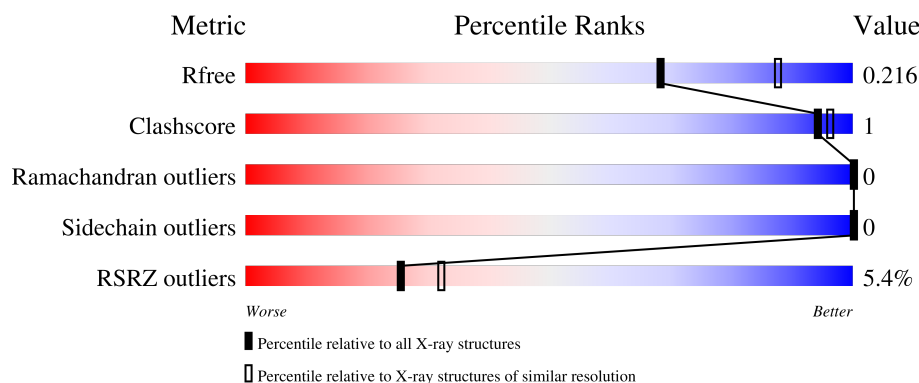
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	H	235	<div> <div>4%</div> <div>89%</div> <div>7%</div> </div>
1	X	235	<div> <div>6%</div> <div>90%</div> <div>7%</div> </div>
2	L	213	<div> <div>3%</div> <div>95%</div> <div>2%</div> </div>
2	Y	213	<div> <div>4%</div> <div>96%</div> <div>2%</div> </div>
3	P	137	<div> <div>6%</div> <div>16%</div> <div>84%</div> </div>

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Mol	Chain	Length	Quality of chain
3	Z	137	<div> <div>3%</div> <div>16%</div> <div>84%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GOL	L	303	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13906 atoms, of which 6669 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 CAP228-16H Heavy Chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	H	219	Total	C	H	N	O	S	0	0	0
			3260	1041	1614	280	318	7			
1	X	219	Total	C	H	N	O	S	0	0	0
			3261	1041	1615	280	318	7			

- Molecule 2 is a protein called CAP228-16H Light Chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	L	209	Total	C	H	N	O	S	0	0	0
			3077	981	1513	260	318	5			
2	Y	209	Total	C	H	N	O	S	0	0	0
			3075	981	1511	260	318	5			

- Molecule 3 is a protein called CAP225 Scaffolded V1V2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	22	Total	C	H	N	O	0	0	0
			378	119	192	34	33			
3	Z	22	Total	C	H	N	O	0	0	0
			378	119	192	34	33			

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	Z	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	L	1	Total	C	H	O	0	0
			14	3	8	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	L	1	Total	C	H	O	0	0
			14	3	8	3		
5	L	1	Total	C	H	O	0	0
			14	3	8	3		
5	Y	1	Total	C	H	O	0	0
			14	3	8	3		

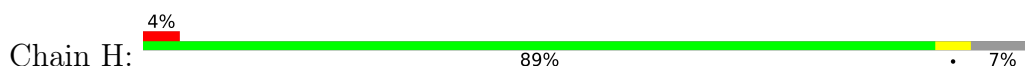
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	104	Total	O	0	0
			104	104		
6	L	102	Total	O	0	0
			102	102		
6	P	7	Total	O	0	0
			7	7		
6	X	94	Total	O	0	0
			94	94		
6	Y	89	Total	O	0	0
			89	89		
6	Z	10	Total	O	0	0
			10	10		

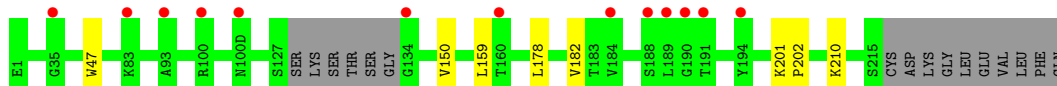
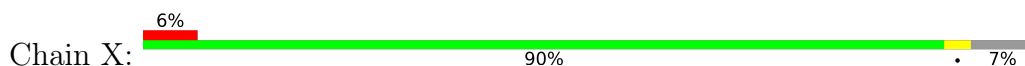
3 Residue-property plots [i](#)

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: CAP228-16H Heavy Chain



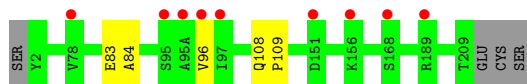
- Molecule 1: CAP228-16H Heavy Chain



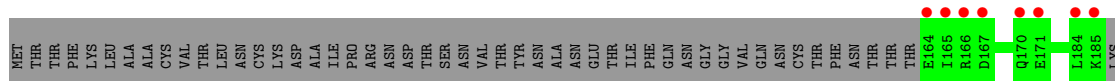
- Molecule 2: CAP228-16H Light Chain



- Molecule 2: CAP228-16H Light Chain



- Molecule 3: CAP225 Scaffolded V1V2



GLU
ASP
ASN
ASN
SER
ASN
SER
SER
GLU
TYR
ILE
LEU
ILE
ASN
ASN
CYS
GLN
THR
THR
THR
GLU
ALA
VAL
ASP
ALA
ALA
THR
ALA
LYS
VAL
PHE
LYS
GLN
TYR
ALA
ASN
ASP
ASN
GLY
ILE
ASP
GLY
GLU
TRP
THR
TYR
ASP
ASP
ALA
THR
LYS
THR
THR
THR
THR
THR
GLY
GLU
LEU

GLU
VAL
PHE
GLN

● Molecule 3: CAP225 Scaffolded V1V2



MET
THR
THR
PHE
LYS
LEU
ALA
ALA
CYS
VAL
THR
CYS
ASN
LEU
THR
CYS
LYS
ASP
ALA
ILE
PRO
ARG
ASN
ASP
THR
THR
TYR
ASN
ALA
LYS
ASN
GLU
THR
ILE
PHE
GLN
GLY
ASN
GLY
GLY
VAL
GLN
ASN
CYS
THR
PHE
ASN
THR
THR
THR
THR
E164
I165
R166
L184
K185
LYS
GLU
ASP
ASN
ASN

SER
ASN
SER
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GLU
TYR
ILE
LEU
ILE
ASN
CYS
GLN
THR
THR
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VAL
ASP
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GLN
TYR
ALA
ASN
ASP
ASN
GLY
ILE
ASP
GLY
GLU
TRP
THR
TYR
ASP
ASP
ALA
THR
THR
LYS
PHE
THR
VAL
THR
GLU
GLY
LEU
GLU
VAL
LEU
PHE

GLN

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	110.35Å 41.76Å 144.52Å 90.00° 96.81° 90.00°	Depositor
Resolution (Å)	36.09 – 2.30 36.09 – 2.30	Depositor EDS
% Data completeness (in resolution range)	95.2 (36.09-2.30) 95.1 (36.09-2.30)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	15.32 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.13.2998	Depositor
R, R_{free}	0.190 , 0.216 0.190 , 0.216	Depositor DCC
R_{free} test set	1999 reflections (3.40%)	wwPDB-VP
Wilson B-factor (Å ²)	32.9	Xtriage
Anisotropy	0.976	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 46.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13906	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.05% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, GOL

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	0.26	0/1687	0.50	0/2295
1	X	0.25	0/1687	0.49	0/2295
2	L	0.25	0/1604	0.46	0/2198
2	Y	0.26	0/1604	0.46	0/2198
3	P	0.23	0/188	0.37	0/251
3	Z	0.23	0/188	0.38	0/251
All	All	0.25	0/6958	0.47	0/9488

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 [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	H	1646	1614	1613	7	0
1	X	1646	1615	1613	7	0
2	L	1564	1513	1511	4	0
2	Y	1564	1511	1511	3	0
3	P	186	192	191	0	0
3	Z	186	192	191	0	0
4	H	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	Z	5	0	0	0	0
5	L	18	24	24	0	0
5	Y	6	8	8	0	0
6	H	104	0	0	0	0
6	L	102	0	0	0	0
6	P	7	0	0	0	0
6	X	94	0	0	0	0
6	Y	89	0	0	0	0
6	Z	10	0	0	0	0
All	All	7237	6669	6662	17	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 1.

All (17) 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:X:150:VAL:CG2	1:X:178:LEU:HD21	2.38	0.54
1:H:150:VAL:CG2	1:H:178:LEU:HD21	2.42	0.49
1:X:150:VAL:HG23	1:X:178:LEU:HD21	1.97	0.47
1:H:181:VAL:HB	2:L:135:LEU:HD13	1.98	0.46
1:H:204:ASN:HB3	1:X:210:LYS:HB3	1.98	0.46
1:X:159:LEU:HD21	1:X:182:VAL:HG21	1.99	0.45
2:Y:108:GLN:HB2	2:Y:109:PRO:HD2	2.00	0.44
2:L:83:GLU:O	2:L:84:ALA:HB2	2.17	0.44
2:Y:83:GLU:O	2:Y:84:ALA:HB2	2.17	0.44
1:H:178:LEU:C	1:H:178:LEU:HD12	2.38	0.43
1:X:178:LEU:C	1:X:178:LEU:HD12	2.39	0.43
1:X:47:TRP:CD2	2:Y:96:VAL:HB	2.54	0.43
1:H:162:GLY:O	1:H:182:VAL:HA	2.19	0.42
1:H:201:LYS:N	1:H:202:PRO:CD	2.83	0.42
1:X:201:LYS:N	1:X:202:PRO:CD	2.83	0.41
1:H:47:TRP:CD2	2:L:96:VAL:HB	2.54	0.41
2:L:108:GLN:HB2	2:L:109:PRO:HD2	2.02	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	H	215/235 (92%)	213 (99%)	2 (1%)	0	100	100
1	X	215/235 (92%)	213 (99%)	2 (1%)	0	100	100
2	L	207/213 (97%)	204 (99%)	3 (1%)	0	100	100
2	Y	207/213 (97%)	204 (99%)	3 (1%)	0	100	100
3	P	20/137 (15%)	20 (100%)	0	0	100	100
3	Z	20/137 (15%)	20 (100%)	0	0	100	100
All	All	884/1170 (76%)	874 (99%)	10 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	H	182/197 (92%)	182 (100%)	0	100	100
1	X	182/197 (92%)	182 (100%)	0	100	100
2	L	176/180 (98%)	176 (100%)	0	100	100
2	Y	176/180 (98%)	176 (100%)	0	100	100
3	P	20/120 (17%)	20 (100%)	0	100	100
3	Z	20/120 (17%)	20 (100%)	0	100	100
All	All	756/994 (76%)	756 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

7 ligands 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	$\# Z > 2$
5	GOL	L	302	-	5,5,5	0.87	0	5,5,5	1.03	0
5	GOL	L	303	-	5,5,5	0.93	0	5,5,5	0.99	0
4	SO4	H	302	-	4,4,4	0.15	0	6,6,6	0.05	0
4	SO4	H	301	-	4,4,4	0.14	0	6,6,6	0.05	0
4	SO4	Z	301	-	4,4,4	0.14	0	6,6,6	0.05	0
5	GOL	Y	301	-	5,5,5	0.91	0	5,5,5	0.96	0
5	GOL	L	301	-	5,5,5	0.92	0	5,5,5	0.95	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
5	GOL	Y	301	-	-	0/4/4/4	-
5	GOL	L	303	-	-	0/4/4/4	-
5	GOL	L	301	-	-	4/4/4/4	-
5	GOL	L	302	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	L	301	GOL	O1-C1-C2-C3
5	L	301	GOL	C1-C2-C3-O3
5	L	301	GOL	O1-C1-C2-O2
5	L	301	GOL	O2-C2-C3-O3

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	H	219/235 (93%)	0.38	9 (4%)	37	44	24, 42, 79, 108	0
1	X	219/235 (93%)	0.54	13 (5%)	22	28	27, 43, 86, 104	0
2	L	209/213 (98%)	0.22	6 (2%)	51	58	23, 38, 71, 94	0
2	Y	209/213 (98%)	0.38	9 (4%)	35	42	30, 47, 82, 96	0
3	P	22/137 (16%)	1.63	8 (36%)	0	0	34, 49, 119, 136	0
3	Z	22/137 (16%)	1.19	4 (18%)	1	1	35, 49, 107, 131	0
All	All	900/1170 (76%)	0.43	49 (5%)	25	32	23, 43, 84, 136	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	P	166	ARG	6.7
3	Z	165	ILE	5.8
1	X	189	LEU	5.6
3	Z	164	GLU	5.5
3	Z	184	LEU	5.0
3	Z	166	ARG	4.7
3	P	167	ASP	4.5
1	H	191	THR	4.2
3	P	165	ILE	4.1
3	P	164	GLU	4.1
1	X	191	THR	3.7
3	P	170	GLN	3.7
2	L	94	THR	3.4
1	H	215	SER	3.4
2	L	186	LYS	3.4
2	L	95	SER	3.3
2	Y	156	LYS	3.2
2	L	189	ARG	3.2
1	H	158	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	X	100(D)	ASN	3.1
2	Y	96	VAL	3.0
3	P	185	LYS	3.0
1	X	134	GLY	3.0
1	H	35	GLY	2.9
2	Y	97	ILE	2.9
1	H	34	ILE	2.9
2	Y	95(A)	ALA	2.7
2	L	96	VAL	2.7
2	L	157	ALA	2.6
1	X	35	GLY	2.5
2	Y	189	ARG	2.5
1	X	190	GLY	2.5
2	Y	168	SER	2.5
2	Y	78	VAL	2.5
1	X	160	THR	2.5
1	X	93	ALA	2.4
1	X	188	SER	2.4
1	X	100	ARG	2.3
1	X	194	TYR	2.3
3	P	171	GLU	2.2
1	X	184	VAL	2.1
1	H	192	GLN	2.1
2	Y	151	ASP	2.1
2	Y	95	SER	2.1
1	H	201	LYS	2.1
1	H	190	GLY	2.1
1	X	83	LYS	2.0
3	P	184	LEU	2.0
1	H	93	ALA	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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, 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
5	GOL	L	303	6/6	0.50	0.56	135,162,165,167	0
5	GOL	Y	301	6/6	0.71	0.31	106,127,135,136	0
4	SO4	H	302	5/5	0.75	0.22	147,148,149,149	0
5	GOL	L	301	6/6	0.75	0.35	82,100,115,120	0
4	SO4	Z	301	5/5	0.77	0.19	146,146,148,149	0
5	GOL	L	302	6/6	0.82	0.29	142,170,180,184	0
4	SO4	H	301	5/5	0.97	0.15	57,57,62,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.