

Full wwPDB X-ray Structure Validation Report (i)

Mar 29, 2021 – 11:11 am BST

PDB ID : 6R6A

Title : Major aspartyl peptidase 1 from C. neoformans Authors : Krystufek, R.; Sacha, P.; Brynda, J.; Konvalinka, J.

Deposited on : 2019-03-26

Resolution : 1.80 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 (i) symbol.

The following versions of software and data (see references (1)) 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 : 2.18

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac: 5.8.0158

CCP4 : 7.0.044 (Gargrove) roteins) : Engh & Huber (2001)

Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

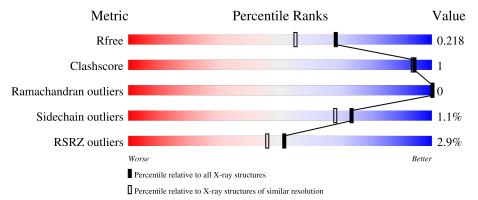
Validation Pipeline (wwPDB-VP) : 2.18

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 1.80 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	Similar resolution		
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{resolution range}(ext{Å}))$		
R_{free}	130704	5950 (1.80-1.80)		
Clashscore	141614	6793 (1.80-1.80)		
Ramachandran outliers	138981	6697 (1.80-1.80)		
Sidechain outliers	138945	6696 (1.80-1.80)		
RSRZ outliers	127900	5850 (1.80-1.80)		

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 <=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	A	350	96%					
2	D	6	67% 33%					
3	В	2	100%					



2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 3006 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 Endopeptidase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	345	Total 2617	C 1646	N 403	O 549	S 19	0	17	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Α	183	LYS	PHE	conflict	UNP J9VS02

• Molecule 2 is a protein called Pepstatin.

Mo	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	D	6	Total 60	C 42	N 6	O 12	0	1	0

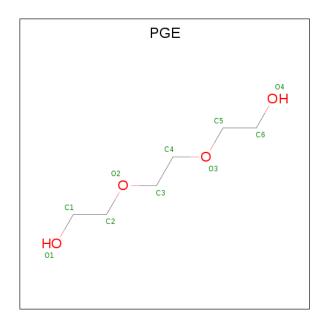
• Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
3	В	2	Total	C	N	0	0	0	0
			28	10	2	10			

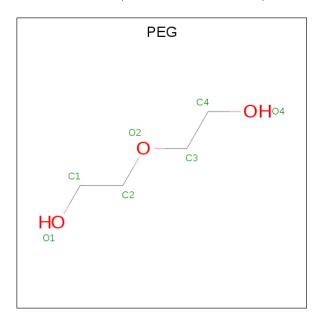
• Molecule 4 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
4	A	1	Total 10	C 6	O 4	0	0

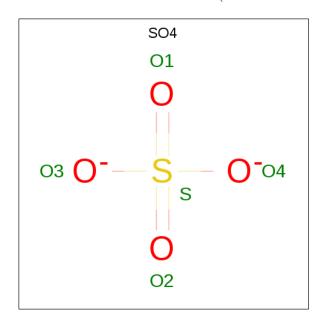
 $\bullet \ \, \text{Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$)}. \\$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 7 4 3	0	0
5	A	1	Total C O 7 4 3	0	0
5	A	1	Total C O 7 4 3	0	0



 \bullet Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



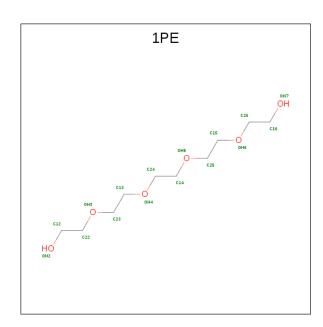
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O S 5 4 1	0	0
6	A	1	Total O S 5 4 1	0	0
6	A	1	Total O S 5 4 1	0	0
6	A	1	Total O S 5 4 1	0	0
6	A	1	Total O S 5 4 1	0	0
6	A	1	Total O S 5 4 1	0	0

• Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Na 1 1	0	0

• Molecule 8 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C O 13 8 5	0	0
8	A	1	Total C O 16 10 6	0	0

• Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	203	Total O 210 210	0	7



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: Endopeptidase

Chain A:

96%

• Molecule 2: Pepstatin

Chain D:

67%

33%

• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	97.36Å 112.64Å 91.03Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	73.66 - 1.80	Depositor
Resolution (A)	38.72 - 1.80	EDS
% Data completeness	84.3 (73.66-1.80)	Depositor
(in resolution range)	84.3 (38.72-1.80)	EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.00 (at 1.79Å)	Xtriage
Refinement program	REFMAC	Depositor
D D.	0.177 , 0.207	Depositor
R, R_{free}	0.191 , 0.218	DCC
R_{free} test set	1710 reflections (4.35%)	wwPDB-VP
Wilson B-factor (Å ²)	20.0	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38, 56.1	EDS
L-test for twinning ²	$ < L > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3006	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.01% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $< L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: IVA, NAG, 1PE, STA, PEG, SO4, PGE, NA

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		
IVIOI	Chain	RMSZ	# Z >5	RMSZ	# Z > 5	
1	A	0.62	0/2714	0.75	0/3692	
2	D	0.90	0/17	0.79	0/21	
All	All	0.62	0/2731	0.75	0/3713	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	D	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	403	STA	Mainchain,Peptide

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	A	2617	0	2494	6	0
2	D	60	0	74	1	0
3	В	28	0	25	0	0
4	A	10	0	14	0	0
5	A	21	0	30	0	0
6	A	30	0	0	0	0
7	A	1	0	0	0	0
8	A	29	0	39	0	0
9	A	210	0	0	1	1
All	All	3006	0	2676	7	1

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 (7) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{array}{ll} ext{Interatomic} \ ext{distance } (ext{Å}) \end{array}$	Clash overlap (Å)
1:A:265[A]:SER:O	1:A:266[A]:ALA:CB	2.31	0.79
1:A:321:MET:HG2	9:A:540:HOH:O	1.92	0.67
1:A:265[A]:SER:O	1:A:266[A]:ALA:HB3	1.97	0.63
1:A:265[A]:SER:O	1:A:266[A]:ALA:HB2	2.11	0.47
1:A:10:THR:HG23	1:A:180:GLN:HG3	1.97	0.47
2:D:405[A]:STA:HB2	2:D:405[A]:STA:HM1	1.73	0.44
1:A:319:MET:HB3	1:A:319:MET:HE2	1.61	0.43

All (1) 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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} ({\rm \AA}) \end{array}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
9:A:542:HOH:O	9:A:542:HOH:O[3_555]	1.93	0.27

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	Perce	\mathbf{ntiles}
1	A	$358/350 \; (102\%)$	350 (98%)	8 (2%)	0	100	100
2	D	3/6~(50%)	3 (100%)	0	0	100	100
All	All	361/356 (101%)	353 (98%)	8 (2%)	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	Analysed Rotameric Outliers		Percentiles		
1	A	291/282 (103%)	288 (99%)	3 (1%)	76	71	
2	D	2/2~(100%)	2 (100%)	0	100	100	
All	All	293/284 (103%)	290 (99%)	3 (1%)	73	71	

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	SER
1	A	192	ASN
1	A	206	ASP

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

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

3 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	Tuna	Chain	Res	Link	В	ond leng	$_{ m ths}$	Е	Bond ang	gles
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	STA	D	403	2	10,10,11	0.74	0	9,12,14	1.32	1 (11%)
2	STA	D	405[A]	2	8,11,11	0.63	0	7,14,14	1.80	1 (14%)
2	STA	D	405[B]	2	8,11,11	0.50	0	7,14,14	0.50	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	${f Torsions}$	Rings
2	STA	D	403	2	-	2/11/11/12	-
2	STA	D	405[A]	2	-	7/10/12/12	-
2	STA	D	405[B]	2	-	3/10/12/12	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
2	D	405[A]	STA	CG-CB-CA	-4.26	106.66	115.82
2	D	403	STA	O-C-CM	-3.18	116.16	125.43

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	403	STA	O-C-CM-CH
2	D	405[A]	STA	CB-CA-CH-OH
2	D	405[A]	STA	CA-CH-CM-C
2	D	405[A]	STA	OH-CH-CM-C
2	D	405[B]	STA	N-CA-CB-CG
2	D	405[A]	STA	CA-CB-CG-CD1
2	D	405[A]	STA	CA-CB-CG-CD2
2	D	405[B]	STA	CA-CB-CG-CD1
2	D	405[A]	STA	N-CA-CH-OH

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Mol	Chain	Res	Type	Atoms
2	D	405[B]	STA	CH-CA-CB-CG
2	D	405[A]	STA	N-CA-CH-CM
2	D	403	STA	OH-CH-CM-C

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	405[A]	STA	1	0

5.5 Carbohydrates (i)

2 monosaccharides 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).

Mo	.1 70		Chain	Dog Link		Во	nd leng	$ ag{ths}$	Bond angles		
1010	ol Ty	рe	Chain	Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	N.A	ΔG	В	1	3,1	14,14,15	0.49	0	17,19,21	1.27	2 (11%)
3	N.A	$^{\Lambda}\mathrm{G}$	В	2	3	14,14,15	0.45	0	17,19,21	1.45	2 (11%)

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
3	NAG	В	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	В	2	3	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
3	В	2	NAG	C1-O5-C5	4.36	118.11	112.19

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Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
3	В	1	NAG	C1-O5-C5	3.25	116.60	112.19
3	В	1	NAG	O5-C1-C2	3.00	116.03	111.29
3	В	2	NAG	O5-C5-C6	2.18	110.62	107.20

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	В	2	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry (i)

Of 13 ligands modelled in this entry, 1 is monoatomic - leaving 12 for Mogul analysis.

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).

Mal	Trens	Chain	Dog	Link	Bo	nd leng	ths	В	ond ang	les
Mol	Type	Chain	m Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PGE	A	403	-	9,9,9	0.63	0	8,8,8	0.47	0
6	SO4	A	412	_	4,4,4	0.42	0	6,6,6	0.28	0
6	SO4	A	408	-	4,4,4	0.24	0	6,6,6	0.66	0
5	PEG	A	405	-	6,6,6	0.35	0	5,5,5	0.51	0
5	PEG	A	406	-	6,6,6	0.52	0	5,5,5	0.31	0
6	SO4	A	407	-	4,4,4	0.39	0	6,6,6	0.44	0
8	1PE	A	415	-	15,15,15	0.44	0	14,14,14	0.55	0
6	SO4	A	409	-	4,4,4	0.33	0	6,6,6	0.87	0
6	SO4	A	410	-	4,4,4	0.25	0	6,6,6	0.30	0
8	1PE	A	414	7	12,12,15	0.57	0	11,11,14	0.68	0
6	SO4	A	411	-	4,4,4	0.50	0	6,6,6	0.29	0
5	PEG	A	404	-	6,6,6	0.27	0	5,5,5	0.62	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	${f Torsions}$	Rings
4	PGE	A	403	-	-	3/7/7/7	-
5	PEG	A	405	-	-	2/4/4/4	-
5	PEG	A	406	=	-	2/4/4/4	-
8	1PE	A	415	-	-	11/13/13/13	-
8	1PE	A	414	7	-	2/10/10/13	-
5	PEG	A	404	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	403	PGE	O2-C3-C4-O3
8	A	415	1PE	ОН4-С13-С23-ОН3
8	A	415	1PE	OH5-C14-C24-OH4
5	A	404	PEG	O2-C3-C4-O4
5	A	405	PEG	O1-C1-C2-O2
5	A	406	PEG	O2-C3-C4-O4
8	A	414	1PE	ОН4-С13-С23-ОН3
8	A	414	1PE	C13-C23-OH3-C22
8	A	415	1PE	C13-C23-OH3-C22
4	A	403	PGE	C4-C3-O2-C2
8	A	415	1PE	C25-C15-OH6-C26
8	A	415	1PE	C23-C13-OH4-C24
8	A	415	1PE	OH2-C12-C22-OH3
8	A	415	1PE	C16-C26-OH6-C15
8	A	415	1PE	C14-C24-OH4-C13
5	A	406	PEG	C4-C3-O2-C2
8	A	415	1PE	OH6-C15-C25-OH5
8	A	415	1PE	C24-C14-OH5-C25
4	A	403	PGE	C3-C4-O3-C5
5	A	405	PEG	O2-C3-C4-O4
8	A	415	1PE	ОН7-С16-С26-ОН6

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^{th} 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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(m \AA^2)$	Q<0.9
1	A	345/350 (98%)	-0.14	10 (2%) 51 46	16, 22, 36, 55	0
2	D	3/6 (50%)	0.07	0 100 100	21, 21, 21, 25	0
All	All	348/356 (97%)	-0.14	10 (2%) 51 46	16, 22, 36, 55	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	169	ASN	4.2
1	A	231	SER	3.9
1	A	170	THR	3.5
1	A	76	SER	3.3
1	A	307	ARG	3.0
1	Α	77	GLU	2.6
1	A	171	ALA	2.5
1	A	225	ALA	2.2
1	A	167	GLY	2.2
1	A	75	SER	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^{th} 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	${f B-factors}({f \AA}^2)$	Q < 0.9
2	STA	D	405[A]	12/12	0.89	0.22	28,38,54,54	12
2	STA	D	405[B]	12/12	0.89	0.22	28,36,40,40	12
2	STA	D	403	11/12	0.97	0.09	16,17,18,18	0



6.3 Carbohydrates (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^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
3	NAG	В	2	14/15	0.79	0.33	61,72,75,82	0
3	NAG	В	1	14/15	0.88	0.18	39,45,50,58	0

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^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
5	PEG	A	406	7/7	0.52	0.36	66,67,72,74	0
6	SO4	A	410	5/5	0.84	0.28	60,67,73,74	1
6	SO4	A	411	5/5	0.84	0.18	36,41,43,48	5
4	PGE	A	403	10/10	0.85	0.15	52,57,57,58	0
5	PEG	A	405	7/7	0.87	0.18	56,58,61,64	0
5	PEG	A	404	7/7	0.88	0.11	42,45,50,51	0
7	NA	A	413	1/1	0.88	0.18	52,52,52,52	0
6	SO4	A	408	5/5	0.91	0.15	34,38,50,51	1
8	1PE	A	415	16/16	0.91	0.14	27,32,36,38	16
8	1PE	A	414	13/16	0.93	0.10	31,35,46,49	0
6	SO4	A	407	5/5	0.93	0.30	63,63,68,73	0
6	SO4	A	412	5/5	0.95	0.32	56,59,64,70	0
6	SO4	A	409	5/5	0.96	0.11	28,29,36,38	1

6.5 Other polymers (i)

There are no such residues in this entry.

