Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 06:37 pm BST

PDB ID	:	5JWF
Title	:	Crystal structure of Porphyromonas gingivalis DPP11
Authors	:	Bezerra, G.A.; Fedosyuk, S.; Ohara-Nemoto, Y.; Nemoto, T.K.; Djinovic-Carugo, K.
Deposited on	:	2016-05-12
Resolution	:	2.40 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 following versions of software and data (see references ⓘ) were used in the production of this report:

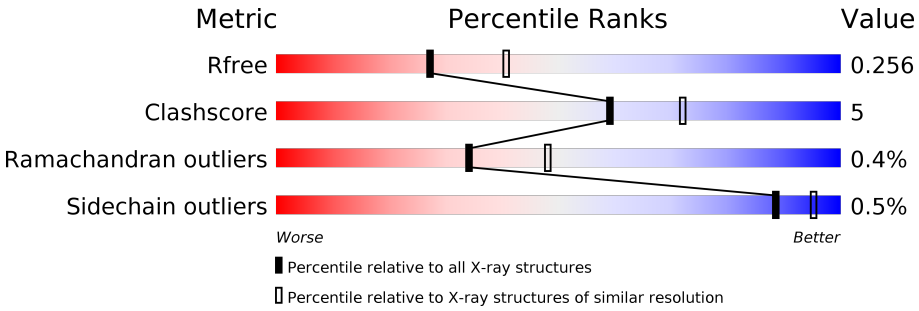
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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 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%

Mol	Chain	Length	Quality of chain
1	A	706	87% 11% ••
1	B	706	88% 10% •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 11516 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.

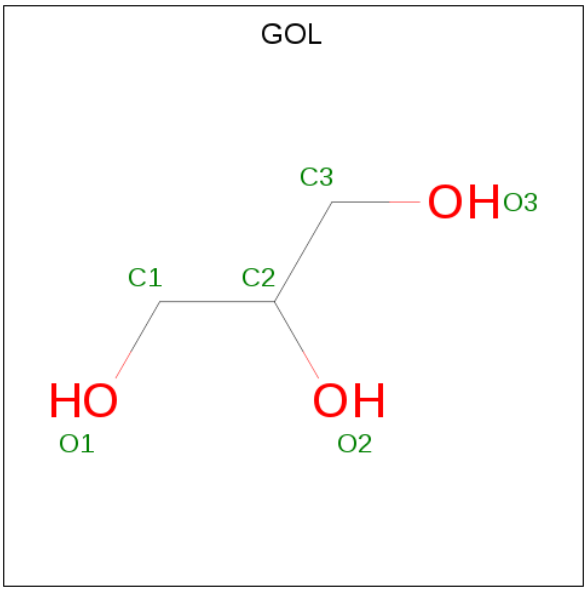
- Molecule 1 is a protein called Asp/Glu-specific dipeptidyl-peptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	700	Total	C	N	O	S	0	0	0
			5565	3531	958	1049	27			
1	B	698	Total	C	N	O	S	0	1	0
			5567	3532	962	1046	27			

There are 16 discrepancies between the modelled and reference sequences:

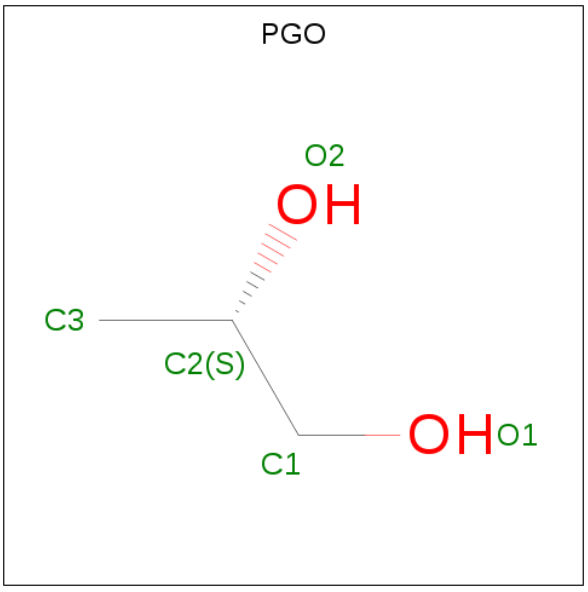
Chain	Residue	Modelled	Actual	Comment	Reference
A	21	MET	-	initiating methionine	UNP B2RID1
A	655	ALA	SER	conflict	UNP B2RID1
A	721	HIS	-	expression tag	UNP B2RID1
A	722	HIS	-	expression tag	UNP B2RID1
A	723	HIS	-	expression tag	UNP B2RID1
A	724	HIS	-	expression tag	UNP B2RID1
A	725	HIS	-	expression tag	UNP B2RID1
A	726	HIS	-	expression tag	UNP B2RID1
B	21	MET	-	initiating methionine	UNP B2RID1
B	655	ALA	SER	engineered mutation	UNP B2RID1
B	721	HIS	-	expression tag	UNP B2RID1
B	722	HIS	-	expression tag	UNP B2RID1
B	723	HIS	-	expression tag	UNP B2RID1
B	724	HIS	-	expression tag	UNP B2RID1
B	725	HIS	-	expression tag	UNP B2RID1
B	726	HIS	-	expression tag	UNP B2RID1

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0

- Molecule 3 is S-1,2-PROPANEDIOL (three-letter code: PGO) (formula: $C_3H_8O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 5 3 2	0	0

- Molecule 4 is water.

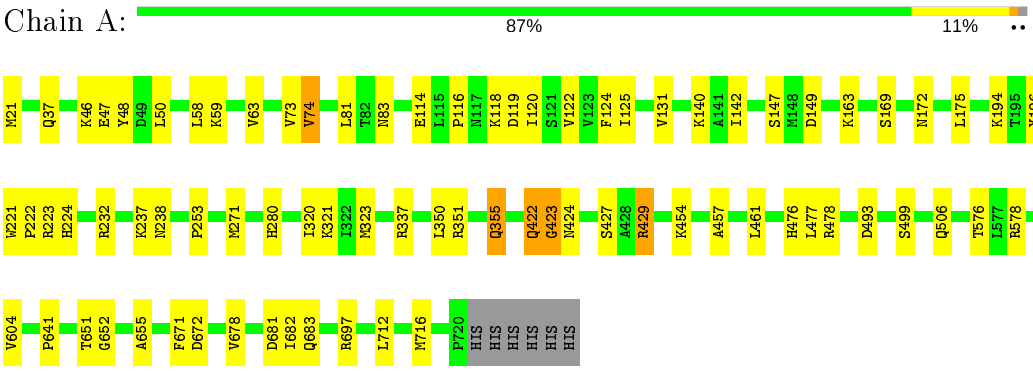
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	194	Total O 194 194	0	0
4	B	167	Total O 167 167	0	0

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 the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

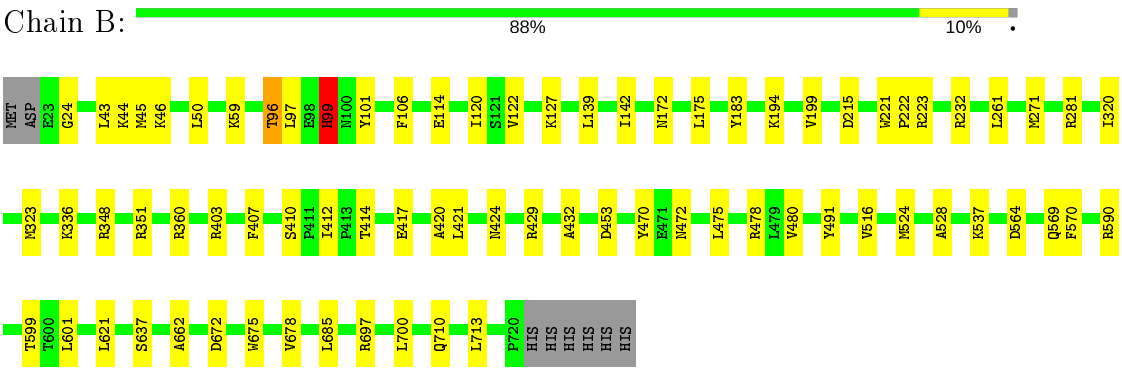
- Molecule 1: Asp/Glu-specific dipeptidyl-peptidase

Chain A:



- Molecule 1: Asp/Glu-specific dipeptidyl-peptidase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	103.18Å 117.22Å 148.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.56 – 2.40 45.56 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.5 (45.56-2.40) 90.8 (45.56-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	1.31 (at 2.20Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.208 , 0.260 0.209 , 0.256	Depositor DCC
R_{free} test set	4177 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	29.3	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 34.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	11516	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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.

5 Model quality

5.1 Standard geometry

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

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	A	0.22	0/5690	0.39	0/7697
1	B	0.22	0/5695	0.40	1/7699 (0.0%)
All	All	0.22	0/11385	0.40	1/15396 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	99	HIS	CB-CA-C	5.49	121.39	110.40

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	A	5565	0	5401	51	0
1	B	5567	0	5425	52	0
2	B	18	0	24	0	0
3	B	5	0	8	0	0
4	A	194	0	0	0	0
4	B	167	0	0	8	0
All	All	11516	0	10858	103	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 5.

All (103) 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:A:83:ASN:ND2	1:A:655:ALA:O	2.15	0.79
1:A:422:GLN:O	1:A:424:ASN:N	2.16	0.78
1:B:421:LEU:HD12	1:B:429:ARG:HG3	1.68	0.73
1:B:424:ASN:HA	1:B:429:ARG:HH21	1.54	0.72
1:B:320:ILE:HD13	1:B:323:MET:HE3	1.72	0.72
1:A:427:SER:HA	1:A:429:ARG:HB2	1.71	0.71
1:A:114:GLU:OE2	1:A:232:ARG:NH1	2.24	0.70
1:B:424:ASN:HA	1:B:429:ARG:NH2	2.08	0.69
1:A:476:HIS:O	1:A:478:ARG:N	2.26	0.67
1:A:237:LYS:NZ	1:A:238:ASN:OD1	2.28	0.67
1:A:46:LYS:HZ3	1:A:48:TYR:H	1.43	0.67
1:B:99:HIS:O	1:B:99:HIS:HD2	1.77	0.66
1:A:223:ARG:NH1	1:A:672:ASP:OD2	2.29	0.65
1:B:590:ARG:NH2	4:B:902:HOH:O	2.32	0.62
1:B:281:ARG:NH2	4:B:906:HOH:O	2.34	0.61
1:A:476:HIS:C	1:A:478:ARG:H	2.05	0.60
1:B:403:ARG:NH2	4:B:905:HOH:O	2.34	0.59
1:B:99:HIS:CD2	1:B:99:HIS:O	2.56	0.59
1:A:351:ARG:NH1	1:A:355:GLN:HG2	2.18	0.58
1:B:281:ARG:NH1	4:B:908:HOH:O	2.36	0.58
1:B:44:LYS:HG2	1:B:662:ALA:HB1	1.86	0.58
1:B:101:TYR:HB3	1:B:106:PHE:HB2	1.86	0.57
1:B:601:LEU:HD11	1:B:621:LEU:HD11	1.84	0.57
1:A:351:ARG:HH12	1:A:355:GLN:HG2	1.68	0.57
1:A:131:VAL:HG12	1:A:163:LYS:NZ	2.20	0.56
1:A:122:VAL:HG12	1:A:196:TYR:HB2	1.88	0.56
1:A:21:MET:N	1:A:37:GLN:HB3	2.21	0.55
1:A:50:LEU:HD21	1:A:271:MET:HE1	1.88	0.55
1:A:83:ASN:HD21	1:A:671:PHE:HA	1.72	0.55
1:B:261:LEU:HD13	1:B:697:ARG:HG2	1.89	0.54
1:B:194:LYS:NZ	4:B:903:HOH:O	2.32	0.54
1:A:337:ARG:NH2	1:A:681:ASP:OD2	2.40	0.54
1:A:46:LYS:HZ1	1:A:48:TYR:HD1	1.55	0.54
1:B:470:TYR:CE2	1:B:478:ARG:HB2	2.44	0.53
1:A:221:TRP:CD2	1:A:222:PRO:HA	2.43	0.53
1:B:114:GLU:OE2	1:B:232:ARG:NH1	2.41	0.53
1:A:172:ASN:HB3	1:A:175:LEU:HD12	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:351:ARG:NH1	4:B:911:HOH:O	2.40	0.53
1:A:116:PRO:HA	1:A:200:ARG:HG2	1.90	0.52
1:A:320:ILE:HD13	1:A:323:MET:HE3	1.92	0.51
1:B:412:ILE:HD11	1:B:528:ALA:HB3	1.93	0.50
1:B:710:GLN:HA	1:B:713:LEU:HD23	1.93	0.50
1:B:99:HIS:NE2	1:B:101:TYR:OH	2.33	0.50
1:B:223:ARG:NH2	1:B:672:ASP:OD2	2.34	0.49
1:A:74:VAL:HG21	1:A:81:LEU:HD12	1.93	0.49
1:B:99:HIS:NE2	1:B:101:TYR:CZ	2.79	0.49
1:A:454:LYS:NZ	1:A:493:ASP:OD1	2.36	0.49
1:B:24:GLY:HA2	1:B:570:PHE:CD1	2.49	0.48
1:B:50:LEU:HD21	1:B:271:MET:HE1	1.95	0.48
1:A:46:LYS:HD2	1:A:47:GLU:H	1.78	0.48
1:B:43:LEU:HD11	1:B:45:MET:HB3	1.94	0.48
1:B:120:ILE:HD13	1:B:199:VAL:HB	1.95	0.48
1:B:221:TRP:CD2	1:B:222:PRO:HA	2.48	0.48
1:B:127:LYS:HB2	1:B:127:LYS:HE2	1.65	0.47
1:B:223:ARG:O	1:B:599:THR:HG21	2.15	0.47
1:A:422:GLN:HG3	1:A:423:GLY:N	2.30	0.47
1:A:321:LYS:HE2	1:A:321:LYS:HB3	1.76	0.46
1:A:350:LEU:HD22	1:A:683:GLN:HB3	1.98	0.46
1:B:417:GLU:HB3	1:B:432:ALA:HB1	1.97	0.46
1:A:59:LYS:HE3	1:A:125:ILE:O	2.17	0.45
1:B:472:ASN:ND2	4:B:917:HOH:O	2.48	0.45
1:B:348:ARG:HG3	1:B:685:LEU:HD13	1.97	0.45
1:B:96:THR:HG22	1:B:99:HIS:O	2.17	0.45
1:A:457:ALA:O	1:A:461:LEU:HB2	2.17	0.45
1:B:96:THR:HG23	1:B:97:LEU:N	2.31	0.45
1:B:96:THR:CG2	1:B:99:HIS:H	2.30	0.45
1:B:215:ASP:O	1:B:336:LYS:NZ	2.50	0.45
1:A:118:LYS:HG2	1:A:119:ASP:N	2.32	0.44
1:A:476:HIS:C	1:A:478:ARG:N	2.70	0.44
1:B:139:LEU:O	1:B:142:ILE:HG22	2.17	0.44
1:B:421:LEU:HB3	1:B:516:VAL:HG23	2.00	0.44
1:B:675:TRP:HA	1:B:678:VAL:HG23	1.99	0.44
1:A:120:ILE:HD13	1:A:199:VAL:HB	2.00	0.44
1:A:46:LYS:HD2	1:A:47:GLU:N	2.31	0.44
1:A:131:VAL:HG12	1:A:163:LYS:HZ3	1.83	0.43
1:A:124:PHE:HB2	1:A:194:LYS:HB3	2.00	0.43
1:B:475:LEU:O	1:B:478:ARG:HG2	2.18	0.43
1:A:140:LYS:C	1:A:142:ILE:H	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:LYS:NZ	1:A:48:TYR:HD1	2.16	0.42
1:B:407:PHE:HD2	1:B:453:ASP:OD2	2.03	0.42
1:A:147:SER:OG	1:A:149:ASP:OD2	2.38	0.42
1:A:224:HIS:HB3	1:A:604:VAL:HG22	2.02	0.42
1:B:537:LYS:NZ	4:B:922:HOH:O	2.52	0.42
1:A:499:SER:O	1:A:506:GLN:NE2	2.52	0.42
1:A:280:HIS:HB2	1:A:682:ILE:HD13	2.01	0.42
1:A:576:THR:O	1:A:578:ARG:HG2	2.19	0.42
1:A:337:ARG:HG3	1:A:678:VAL:HG21	2.02	0.41
1:A:63:VAL:HB	1:A:122:VAL:HG22	2.02	0.41
1:A:58:LEU:HA	1:A:58:LEU:HD12	1.92	0.41
1:B:59:LYS:HE3	1:B:59:LYS:HB3	1.92	0.41
1:B:360:ARG:NH2	1:B:564:ASP:OD2	2.52	0.41
1:A:712:LEU:O	1:A:716:MET:HG3	2.21	0.41
1:B:414:THR:OG1	1:B:417:GLU:HG3	2.21	0.41
1:A:73:VAL:HG11	1:A:253:PRO:HG3	2.03	0.41
1:B:261:LEU:HD21	1:B:700:LEU:HD12	2.03	0.41
1:B:480:VAL:HG12	1:B:491:TYR:CG	2.55	0.41
1:B:410:SER:HB3	1:B:524:MET:HE3	2.03	0.41
1:B:172:ASN:HB3	1:B:175:LEU:HD12	2.03	0.41
1:B:46:LYS:H	1:B:46:LYS:HG3	1.66	0.40
1:B:183:TYR:OH	1:B:569:GLN:O	2.36	0.40
1:A:589:PRO:HG3	1:A:595:TYR:CE2	2.56	0.40
1:A:651:THR:OG1	1:A:652:GLY:N	2.55	0.40
1:A:641:PRO:HG3	1:A:697:ARG:CZ	2.51	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	A	698/706 (99%)	673 (96%)	22 (3%)	3 (0%)	34 48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	697/706 (99%)	666 (96%)	28 (4%)	3 (0%)	34 48
All	All	1395/1412 (99%)	1339 (96%)	50 (4%)	6 (0%)	34 48

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	423	GLY
1	B	96	THR
1	B	420	ALA
1	B	637	SER
1	A	477	LEU
1	A	429	ARG

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	A	576/596 (97%)	572 (99%)	4 (1%)	84 92
1	B	578/596 (97%)	576 (100%)	2 (0%)	92 97
All	All	1154/1192 (97%)	1148 (100%)	6 (0%)	88 95

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	74	VAL
1	A	169	SER
1	A	355	GLN
1	A	422	GLN
1	B	99	HIS
1	B	122	VAL

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

Mol	Chain	Res	Type
1	A	99	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry

4 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	$\#\|Z\| > 2$
2	GOL	B	801	-	5,5,5	0.37	0	5,5,5	0.29	0
2	GOL	B	802	-	5,5,5	0.37	0	5,5,5	0.32	0
2	GOL	B	803	-	5,5,5	0.36	0	5,5,5	0.33	0
3	PGO	B	804	-	3,4,4	0.30	0	1,4,4	0.03	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
2	GOL	B	801	-	-	2/4/4/4	-
2	GOL	B	802	-	-	3/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	B	803	-	-	2/4/4/4	-
3	PGO	B	804	-	-	0/2/2/2	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	801	GOL	O1-C1-C2-C3
2	B	802	GOL	O1-C1-C2-C3
2	B	803	GOL	O1-C1-C2-C3
2	B	803	GOL	O1-C1-C2-O2
2	B	801	GOL	O1-C1-C2-O2
2	B	802	GOL	O1-C1-C2-O2
2	B	802	GOL	O2-C2-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.