



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 07:17 PM UTC

PDB ID : 4Y01 / pdb_00004y01
Title : Crystal structure of dipeptidyl peptidase 11 (DPP11) from Porphyromonas gingivalis
Authors : Sakamoto, Y.; Suzuki, Y.; Iizuka, I.; Tateoka, C.; Roppongi, S.; Fujimoto, M.; Nonaka, T.; Ogasawara, W.; Tanaka, N.
Deposited on : 2015-02-05
Resolution : 2.46 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 : 4-5-2 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

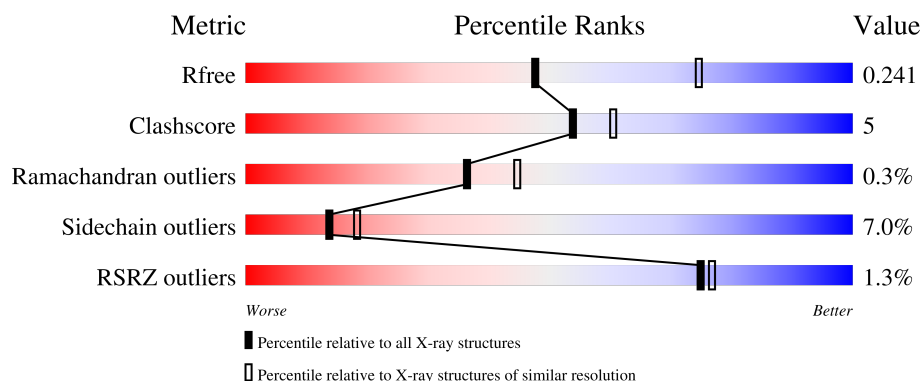
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.46 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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	A	720	2% 81% 14% ..
1	B	720	% 85% 11% ...

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 11408 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 Peptidase S46.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	699	Total	C	N	O	S	Se	0	0	0
			5608	3553	970	1058	4	23			
1	B	699	Total	C	N	O	S	Se	0	0	0
			5608	3553	970	1058	4	23			

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	61	Total	O	0	0
			61	61		

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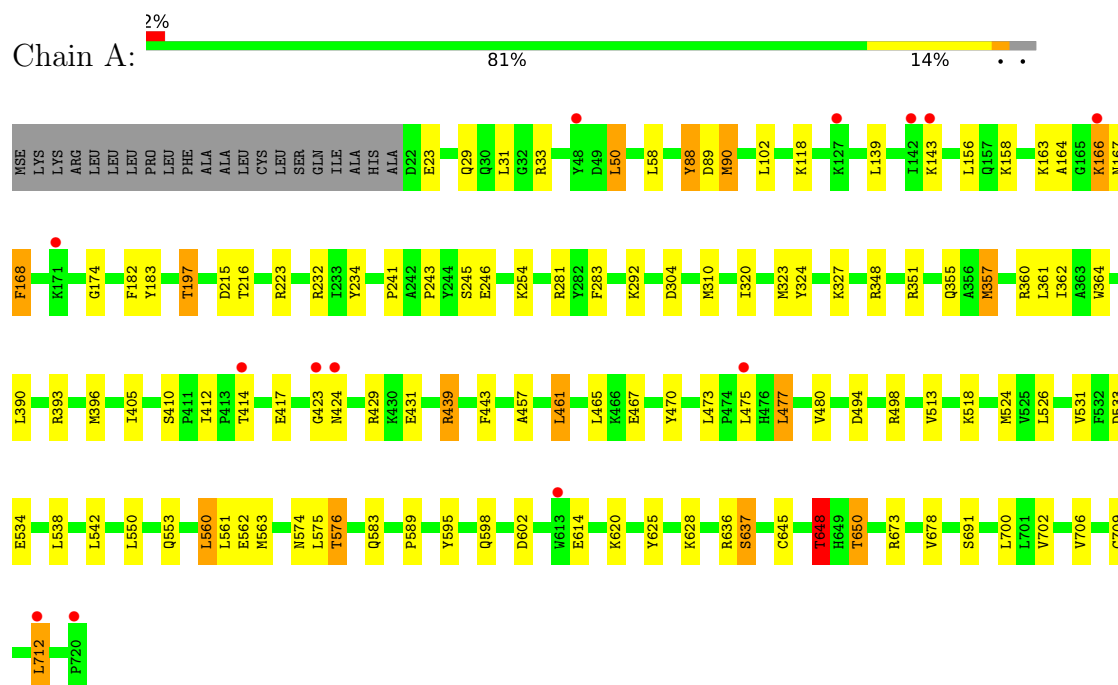
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	125	Total 125	O 125	0	0

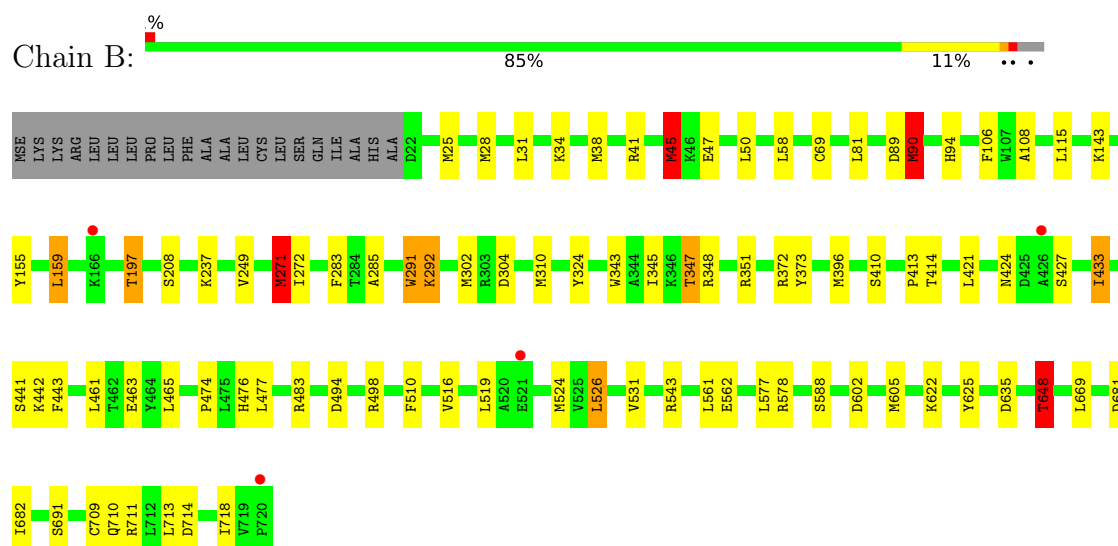
3 Residue-property plots

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: Peptidase S46



• Molecule 1: Peptidase S46



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.79Å 115.49Å 147.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.46 40.00 – 2.46	Depositor EDS
% Data completeness (in resolution range)	99.2 (40.00-2.46) 99.2 (40.00-2.46)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.184 , 0.233 0.198 , 0.241	Depositor DCC
R_{free} test set	2980 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	36.5	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 28.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11408	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	A	0.96	0/5710	1.08	7/7676 (0.1%)
1	B	1.00	2/5710 (0.0%)	1.08	9/7676 (0.1%)
All	All	0.98	2/11420 (0.0%)	1.08	16/15352 (0.1%)

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
1	A	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	25	MSE	CA-C	-5.32	1.46	1.53
1	B	588	SER	C-O	-5.18	1.18	1.24

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	271	MSE	CG-SE-CE	-8.46	80.31	98.92
1	B	710	GLN	N-CA-C	6.87	119.64	111.33
1	B	45	MSE	CG-SE-CE	-6.26	85.15	98.92
1	A	424	ASN	N-CA-C	6.02	120.31	111.34
1	A	88	TYR	N-CA-C	6.00	117.49	111.07
1	B	291	TRP	CA-CB-CG	5.92	124.85	113.60
1	B	69	CYS	N-CA-C	-5.77	100.54	109.14
1	A	648	THR	N-CA-CB	-5.53	102.21	110.17
1	A	118	LYS	N-CA-C	5.47	116.92	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	223	ARG	CG-CD-NE	-5.35	100.23	112.00
1	A	168	PHE	N-CA-C	5.29	117.04	111.28
1	B	90	MSE	CG-SE-CE	5.26	110.49	98.92
1	A	648	THR	CB-CA-C	5.22	119.15	109.54
1	B	709	CYS	CA-C-N	5.10	127.37	120.38
1	B	709	CYS	C-N-CA	5.10	127.37	120.38
1	B	249	VAL	N-CA-C	5.02	113.41	107.84

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	23	GLU	Peptide
1	A	423	GLY	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	5608	0	5491	51	0
1	B	5608	0	5491	58	0
2	A	6	0	8	0	0
3	A	61	0	0	1	0
3	B	125	0	0	1	0
All	All	11408	0	10990	109	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 (109) 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:B:410:SER:CB	1:B:524:MSE:HE3	1.88	1.04
1:A:410:SER:CB	1:A:524:MSE:HE3	1.87	1.04
1:B:302:MSE:HE3	1:B:396:MSE:SE	2.24	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:474:PRO:HG2	1:B:477:LEU:HD12	1.59	0.84
1:B:410:SER:HB2	1:B:524:MSE:CE	2.07	0.84
1:B:310:MSE:HE3	1:B:324:TYR:HD1	1.45	0.82
1:B:31:LEU:HD12	1:B:38:MSE:HE1	1.65	0.79
1:B:410:SER:HB2	1:B:524:MSE:HE3	1.65	0.78
1:B:410:SER:CB	1:B:524:MSE:CE	2.62	0.75
1:A:310:MSE:HE3	1:A:324:TYR:HD2	1.50	0.75
1:A:410:SER:HB2	1:A:524:MSE:HE3	1.68	0.75
1:B:410:SER:HB3	1:B:524:MSE:HE3	1.73	0.65
1:A:410:SER:HB3	1:A:524:MSE:HE3	1.76	0.64
1:B:34:LYS:HB2	1:B:38:MSE:CE	2.28	0.64
1:B:108:ALA:O	1:B:711:ARG:NH1	2.33	0.62
1:A:410:SER:HB2	1:A:524:MSE:CE	2.30	0.61
1:B:302:MSE:HE1	1:B:463:GLU:HG3	1.84	0.58
1:A:443:PHE:CE2	1:A:524:MSE:HE1	2.39	0.58
1:B:34:LYS:C	1:B:38:MSE:HE3	2.29	0.57
1:A:174:GLY:HA3	1:A:241:PRO:HG2	1.86	0.57
1:A:89:ASP:HB2	1:A:90:MSE:HE2	1.86	0.56
1:A:414:THR:HG22	1:A:417:GLU:OE1	2.05	0.56
1:B:94:HIS:CG	1:B:115:LEU:HD23	2.40	0.56
1:B:343:TRP:O	1:B:347:THR:HB	2.05	0.56
1:A:310:MSE:HE3	1:A:324:TYR:CD2	2.37	0.56
1:B:421:LEU:HD21	1:B:433:ILE:HD13	1.86	0.56
1:A:412:ILE:O	1:A:439:ARG:NH2	2.39	0.56
1:B:197:THR:HB	3:B:828:HOH:O	2.06	0.55
1:B:302:MSE:HE1	1:B:463:GLU:CG	2.37	0.54
1:B:413:PRO:HD3	1:B:519:LEU:HD21	1.89	0.54
1:A:320:ILE:HD13	1:A:323:MSE:CE	2.37	0.54
1:B:272:ILE:HD12	1:B:648:THR:HG21	1.89	0.54
1:B:292:LYS:HB2	1:B:345:ILE:HD13	1.90	0.54
1:B:413:PRO:HG3	1:B:519:LEU:CD2	2.37	0.54
1:A:429:ARG:NH1	3:A:901:HOH:O	2.36	0.54
1:B:34:LYS:HB2	1:B:38:MSE:HE2	1.89	0.54
1:A:320:ILE:HD13	1:A:323:MSE:HE2	1.89	0.54
1:A:410:SER:OG	1:A:524:MSE:HE3	2.08	0.53
1:B:89:ASP:HB2	1:B:90:MSE:HE3	1.90	0.53
1:B:577:LEU:O	1:B:578:ARG:HD3	2.09	0.53
1:B:413:PRO:HG3	1:B:519:LEU:HD21	1.91	0.52
1:A:589:PRO:HG3	1:A:595:TYR:CE2	2.45	0.52
1:A:351:ARG:HH12	1:A:355:GLN:HE21	1.56	0.52
1:B:648:THR:HG22	1:B:691:SER:OG	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:414:THR:HG22	1:A:417:GLU:CD	2.36	0.50
1:A:281:ARG:HH22	1:A:357:MSE:HE1	1.76	0.50
1:B:347:THR:CG2	1:B:348:ARG:NH1	2.75	0.50
1:A:31:LEU:HD21	1:A:50:LEU:HD13	1.92	0.50
1:B:155:TYR:CE2	1:B:159:LEU:HD21	2.47	0.50
1:B:285:ALA:HB1	1:B:351:ARG:NH1	2.26	0.49
1:B:28:MSE:HE3	1:B:577:LEU:HG	1.94	0.49
1:B:50:LEU:HD21	1:B:271:MSE:HE1	1.94	0.49
1:A:197:THR:HG22	1:A:243:PRO:HA	1.94	0.49
1:A:405:ILE:HD11	1:A:461:LEU:HD13	1.95	0.48
1:A:457:ALA:O	1:A:461:LEU:HB2	2.13	0.48
1:A:393:ARG:NH2	1:A:534:GLU:OE2	2.46	0.48
1:B:89:ASP:HB2	1:B:90:MSE:CE	2.44	0.47
1:B:413:PRO:CG	1:B:519:LEU:HD21	2.43	0.47
1:A:396:MSE:HE3	1:A:467:GLU:HB3	1.97	0.47
1:A:709:CYS:O	1:A:712:LEU:CD2	2.63	0.47
1:A:88:TYR:CE1	1:A:102:LEU:HD11	2.51	0.46
1:B:413:PRO:CD	1:B:519:LEU:HD21	2.46	0.46
1:A:215:ASP:N	1:A:614:GLU:OE2	2.48	0.46
1:B:106:PHE:CZ	1:B:115:LEU:HD13	2.50	0.46
1:A:360:ARG:HG2	1:A:563:MSE:HE1	1.98	0.45
1:B:81:LEU:HD13	1:B:669:LEU:HD11	1.99	0.45
1:B:155:TYR:CE2	1:B:159:LEU:CD2	3.00	0.45
1:A:650:THR:HG22	1:A:673:ARG:HG3	1.99	0.45
1:A:164:ALA:HB1	1:A:168:PHE:CD2	2.53	0.44
1:B:648:THR:HG22	1:B:691:SER:CB	2.47	0.44
1:B:681:ASP:C	1:B:682:ILE:HD12	2.43	0.44
1:A:232:ARG:HD2	1:A:234:TYR:CE1	2.53	0.44
1:B:34:LYS:CB	1:B:38:MSE:CE	2.95	0.44
1:B:34:LYS:CB	1:B:38:MSE:HE2	2.48	0.44
1:B:519:LEU:C	1:B:519:LEU:HD23	2.44	0.43
1:B:648:THR:CG2	1:B:691:SER:OG	2.66	0.43
1:B:372:ARG:NH2	1:B:373:TYR:OH	2.52	0.43
1:A:216:THR:N	1:A:614:GLU:OE2	2.45	0.43
1:A:166:LYS:HA	1:A:167:ASN:HA	1.79	0.43
1:A:494:ASP:OD1	1:A:498:ARG:HD3	2.19	0.43
1:A:538:LEU:O	1:A:542:LEU:HB2	2.18	0.43
1:B:410:SER:OG	1:B:524:MSE:HE3	2.17	0.43
1:A:31:LEU:HD21	1:A:50:LEU:CD1	2.49	0.43
1:B:635:ASP:OD1	1:B:635:ASP:C	2.61	0.43
1:A:361:LEU:HD22	1:A:560:LEU:HD13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:405:ILE:CD1	1:A:461:LEU:HD13	2.49	0.42
1:A:589:PRO:HG3	1:A:595:TYR:CZ	2.55	0.42
1:B:476:HIS:CD2	1:B:526:LEU:HB3	2.54	0.42
1:B:718:ILE:HD12	1:B:718:ILE:N	2.34	0.42
1:B:272:ILE:CD1	1:B:648:THR:HG21	2.49	0.42
1:A:470:TYR:HA	1:A:473:LEU:HD12	2.01	0.42
1:B:443:PHE:CE2	1:B:524:MSE:HE1	2.54	0.42
1:B:605:MSE:HG3	1:B:625:TYR:CE2	2.55	0.42
1:A:182:PHE:O	1:A:183:TYR:C	2.63	0.42
1:A:477:LEU:O	1:A:480:VAL:HG12	2.20	0.42
1:B:433:ILE:HD12	1:B:433:ILE:HA	1.88	0.42
1:B:292:LYS:CB	1:B:345:ILE:HD13	2.50	0.42
1:A:702:VAL:O	1:A:706:VAL:HB	2.20	0.41
1:A:648:THR:HG22	1:A:691:SER:HB2	2.02	0.41
1:A:712:LEU:H	1:A:712:LEU:HD22	1.84	0.41
1:A:625:TYR:O	1:A:628:LYS:HD3	2.20	0.41
1:A:636:ARG:O	1:A:637:SER:CB	2.69	0.41
1:B:272:ILE:HD12	1:B:648:THR:CG2	2.51	0.41
1:B:510:PHE:CZ	1:B:519:LEU:HD12	2.56	0.41
1:A:574:ASN:OD1	1:A:576:THR:HB	2.21	0.40
1:A:645:CYS:HA	1:A:691:SER:O	2.21	0.40
1:A:364:TRP:HB2	1:A:563:MSE:HE3	2.04	0.40
1:B:45:MSE:HE1	1:B:58:LEU:HD22	2.03	0.40
1:B:494:ASP:OD1	1:B:498:ARG:HD3	2.22	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	697/720 (97%)	671 (96%)	25 (4%)	1 (0%)	48 61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	697/720 (97%)	671 (96%)	23 (3%)	3 (0%)	30	37
All	All	1394/1440 (97%)	1342 (96%)	48 (3%)	4 (0%)	36	45

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	516	VAL
1	B	648	THR
1	B	143	LYS
1	A	637	SER

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	590/583 (101%)	540 (92%)	50 (8%)	10	11
1	B	590/583 (101%)	557 (94%)	33 (6%)	19	27
All	All	1180/1166 (101%)	1097 (93%)	83 (7%)	14	18

All (83) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	GLN
1	A	33	ARG
1	A	50	LEU
1	A	58	LEU
1	A	90	MSE
1	A	139	LEU
1	A	143	LYS
1	A	156	LEU
1	A	158	LYS
1	A	163	LYS
1	A	166	LYS
1	A	197	THR

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Mol	Chain	Res	Type
1	A	245	SER
1	A	246	GLU
1	A	254	LYS
1	A	283	PHE
1	A	292	LYS
1	A	304	ASP
1	A	327	LYS
1	A	348	ARG
1	A	357	MSE
1	A	362	ILE
1	A	390	LEU
1	A	431	GLU
1	A	439	ARG
1	A	461	LEU
1	A	465	LEU
1	A	475	LEU
1	A	477	LEU
1	A	513	VAL
1	A	518	LYS
1	A	526	LEU
1	A	531	VAL
1	A	533	ASP
1	A	550	LEU
1	A	553	GLN
1	A	560	LEU
1	A	561	LEU
1	A	562	GLU
1	A	575	LEU
1	A	576	THR
1	A	583	GLN
1	A	598	GLN
1	A	602	ASP
1	A	620	LYS
1	A	648	THR
1	A	650	THR
1	A	678	VAL
1	A	700	LEU
1	A	712	LEU
1	B	41	ARG
1	B	45	MSE
1	B	47	GLU
1	B	90	MSE

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Mol	Chain	Res	Type
1	B	159	LEU
1	B	197	THR
1	B	208	SER
1	B	237	LYS
1	B	271	MSE
1	B	283	PHE
1	B	291	TRP
1	B	292	LYS
1	B	304	ASP
1	B	347	THR
1	B	414	THR
1	B	424	ASN
1	B	427	SER
1	B	433	ILE
1	B	441	SER
1	B	442	LYS
1	B	461	LEU
1	B	465	LEU
1	B	483	ARG
1	B	526	LEU
1	B	531	VAL
1	B	543	ARG
1	B	561	LEU
1	B	562	GLU
1	B	602	ASP
1	B	622	LYS
1	B	648	THR
1	B	713	LEU
1	B	714	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	ASN
1	A	117	ASN
1	A	157	GLN
1	A	172	ASN
1	A	280	HIS
1	A	355	GLN
1	A	368	GLN
1	A	489	GLN
1	A	598	GLN

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Mol	Chain	Res	Type
1	B	83	ASN
1	B	117	ASN
1	B	157	GLN
1	B	186	ASN
1	B	240	ASN
1	B	280	HIS
1	B	307	GLN
1	B	353	ASN
1	B	422	GLN
1	B	472	ASN
1	B	506	GLN
1	B	553	GLN
1	B	569	GLN
1	B	598	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](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	A	801	-	5,5,5	0.73	0	5,5,5	0.77	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	A	801	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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, 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	A	676/720 (93%)	-0.06	13 (1%) 66 67	20, 42, 71, 115	0
1	B	676/720 (93%)	-0.33	4 (0%) 85 87	16, 34, 61, 99	0
All	All	1352/1440 (93%)	-0.19	17 (1%) 75 77	16, 38, 68, 115	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	613	TRP	2.5
1	A	143	LYS	2.4
1	A	414	THR	2.4
1	B	521	GLU	2.4
1	A	142	ILE	2.4
1	A	423	GLY	2.4
1	B	166	LYS	2.3
1	A	424	ASN	2.2
1	B	426	ALA	2.2
1	A	171	LYS	2.2
1	A	166	LYS	2.2
1	A	48	TYR	2.1
1	A	712	LEU	2.1
1	B	720	PRO	2.1
1	A	127	LYS	2.1
1	A	720	PRO	2.0
1	A	475	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	GOL	A	801	6/6	0.68	0.27	51,56,63,67	0

6.5 Other polymers [i](#)

There are no such residues in this entry.