



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 17, 2026 – 01:49 pm BST

PDB ID : 28JE / pdb_000028je
Title : BKP_yV VP1 IN COMPLEX WITH VHH017
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Weeks, S.D.
Deposited on : 2026-02-03
Resolution : 2.49 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

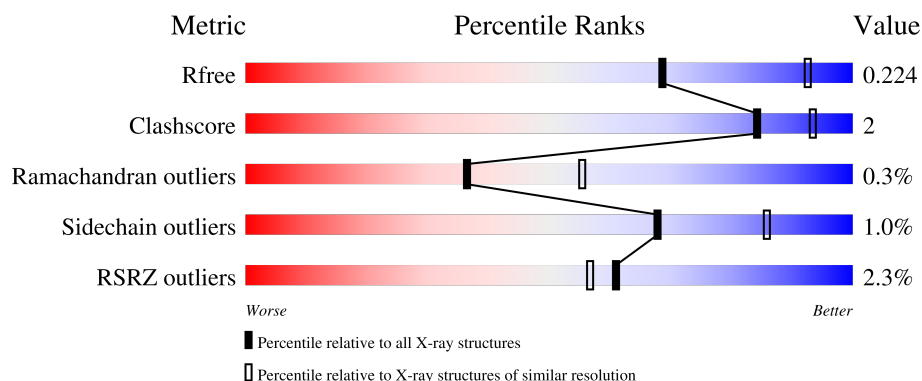
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	273	3% 90% 6% .
1	B	273	4% 88% 8% .
1	C	273	2% 90% 6% .
1	D	273	% 89% 7% .
1	E	273	90% 7% .

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Mol	Chain	Length	Quality of chain
2	F	131	
2	G	131	
2	H	131	
2	I	131	
2	J	131	

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
3	GOL	E	301	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 30750 atoms, of which 14874 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 Capsid protein VP1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	264	Total	C	H	N	O	S	61	2	0
			4095	1294	2037	359	393	12			
1	B	264	Total	C	H	N	O	S	62	2	0
			4083	1292	2029	355	394	13			
1	C	263	Total	C	H	N	O	S	65	1	0
			4034	1279	2000	352	391	12			
1	D	263	Total	C	H	N	O	S	61	1	0
			4060	1285	2018	354	391	12			
1	E	266	Total	C	H	N	O	S	61	1	0
			4103	1298	2036	359	398	12			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	GLY	-	expression tag	UNP A0A3G2SFE7
A	104	SER	CYS	engineered mutation	UNP A0A3G2SFE7
B	25	GLY	-	expression tag	UNP A0A3G2SFE7
B	104	SER	CYS	engineered mutation	UNP A0A3G2SFE7
C	25	GLY	-	expression tag	UNP A0A3G2SFE7
C	104	SER	CYS	engineered mutation	UNP A0A3G2SFE7
D	25	GLY	-	expression tag	UNP A0A3G2SFE7
D	104	SER	CYS	engineered mutation	UNP A0A3G2SFE7
E	25	GLY	-	expression tag	UNP A0A3G2SFE7
E	104	SER	CYS	engineered mutation	UNP A0A3G2SFE7

- Molecule 2 is a protein called VHH017.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	F	124	Total	C	H	N	O	S	32	0	0
			1857	598	904	166	185	4			
2	G	124	Total	C	H	N	O	S	33	0	0
			1851	596	901	166	184	4			

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	H	124	Total	C	H	N	O	S	30	0	0
			1870	601	913	167	185	4			
2	I	124	Total	C	H	N	O	S	30	0	0
			1873	602	915	167	185	4			
2	J	124	Total	C	H	N	O	S	30	0	0
			1867	600	911	167	185	4			

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



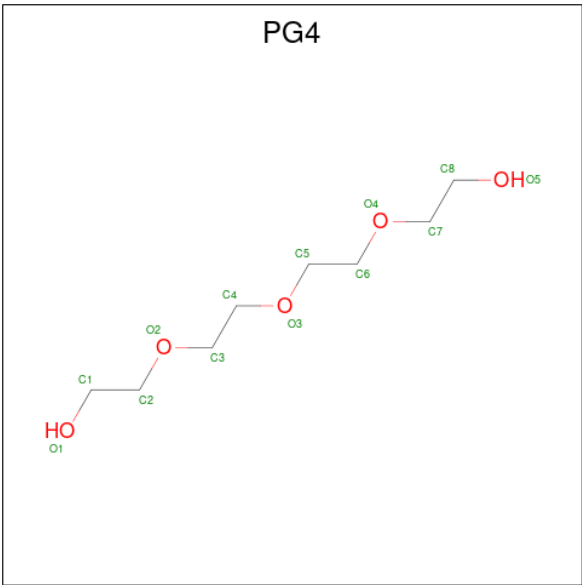
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	3	0
			14	3	8	3		
3	A	1	Total	C	H	O	3	0
			14	3	8	3		
3	A	1	Total	C	H	O	3	0
			14	3	8	3		
3	A	1	Total	C	H	O	3	0
			14	3	8	3		
3	B	1	Total	C	H	O	3	0
			14	3	8	3		
3	B	1	Total	C	H	O	3	0
			14	3	8	3		
3	C	1	Total	C	H	O	3	0
			14	3	8	3		
3	D	1	Total	C	H	O	3	0
			14	3	8	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	C	H	O	3	0
			14	3	8	3		
3	E	1	Total	C	H	O	3	0
			14	3	8	3		
3	E	1	Total	C	H	O	3	0
			14	3	8	3		
3	F	1	Total	C	H	O	3	0
			14	3	8	3		
3	F	1	Total	C	H	O	3	0
			14	3	8	3		
3	G	1	Total	C	H	O	3	0
			14	3	8	3		
3	G	1	Total	C	H	O	3	0
			14	3	8	3		
3	G	1	Total	C	H	O	3	0
			14	3	8	3		
3	H	1	Total	C	H	O	3	0
			14	3	8	3		
3	H	1	Total	C	H	O	3	0
			14	3	8	3		
3	H	1	Total	C	H	O	3	0
			14	3	8	3		
3	I	1	Total	C	H	O	3	0
			14	3	8	3		
3	I	1	Total	C	H	O	3	0
			14	3	8	3		
3	J	1	Total	C	H	O	3	0
			14	3	8	3		
3	J	1	Total	C	H	O	3	0
			14	3	8	3		
3	J	1	Total	C	H	O	3	0
			14	3	8	3		

- Molecule 4 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	E	1	Total	C	H	O	2	0
			31	8	18	5		

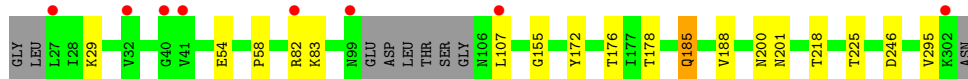
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	110	Total	O	0	0
			110	110		
5	B	99	Total	O	0	0
			99	99		
5	C	97	Total	O	0	0
			97	97		
5	D	102	Total	O	0	0
			102	102		
5	E	107	Total	O	0	0
			107	107		
5	F	41	Total	O	0	0
			41	41		
5	G	29	Total	O	0	0
			29	29		
5	H	41	Total	O	0	0
			41	41		
5	I	29	Total	O	0	0
			29	29		
5	J	35	Total	O	0	0
			35	35		

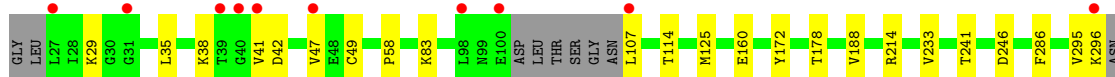
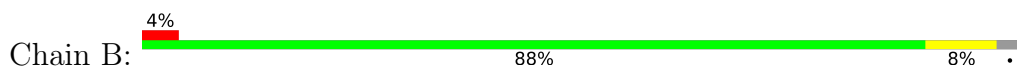
3 Residue-property plots [i](#)

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: Capsid protein VP1



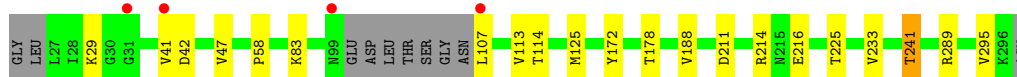
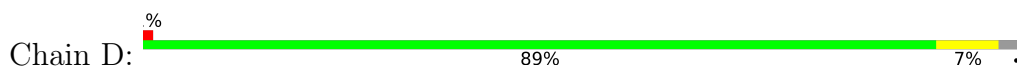
- Molecule 1: Capsid protein VP1



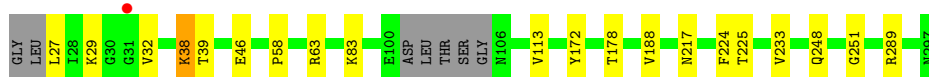
- Molecule 1: Capsid protein VP1



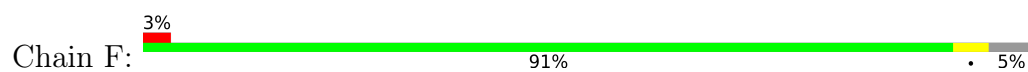
- Molecule 1: Capsid protein VP1



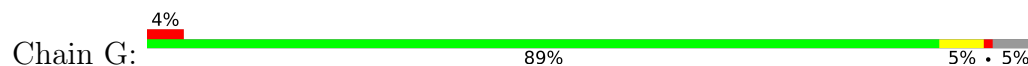
- Molecule 1: Capsid protein VP1



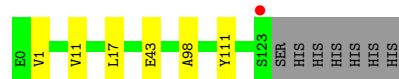
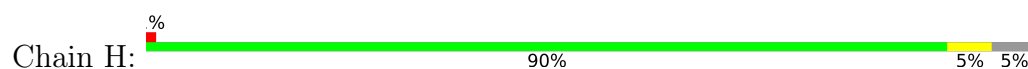
- Molecule 2: VHH017



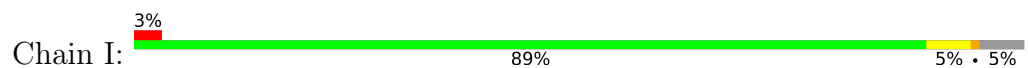
• Molecule 2: VHH017



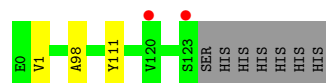
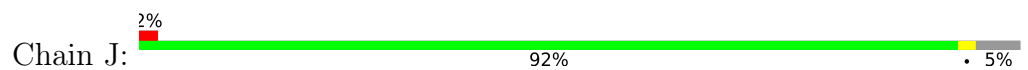
• Molecule 2: VHH017



• Molecule 2: VHH017



• Molecule 2: VHH017



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.83Å 152.36Å 91.93Å 90.00° 94.40° 90.00°	Depositor
Resolution (Å)	47.28 – 2.49 47.28 – 2.49	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.28-2.49) 99.3 (47.28-2.49)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.8.0430 (refmacat 0.4.105)	Depositor
R, R_{free}	0.193 , 0.225 0.192 , 0.224	Depositor DCC
R_{free} test set	2039 reflections (2.50%)	wwPDB-VP
Wilson B-factor (Å ²)	43.8	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 42.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	30750	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.52% 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: PG4, 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	0.50	0/2109	0.78	0/2862
1	B	0.49	0/2105	0.79	0/2857
1	C	0.49	0/2082	0.80	1/2829 (0.0%)
1	D	0.48	0/2090	0.78	0/2837
1	E	0.49	0/2115	0.78	0/2871
2	F	0.47	0/975	0.75	0/1322
2	G	0.48	0/972	0.75	0/1318
2	H	0.48	0/979	0.78	0/1326
2	I	0.47	0/980	0.76	0/1327
2	J	0.47	0/978	0.74	0/1325
All	All	0.48	0/15385	0.78	1/20874 (0.0%)

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	G	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	118	GLU	CB-CA-C	5.14	119.56	110.16

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	G	71	ARG	Sidechain

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	2058	2037	2029	12	0
1	B	2054	2029	2021	12	1
1	C	2034	2000	1988	11	0
1	D	2042	2018	2010	15	0
1	E	2067	2036	2028	14	0
2	F	953	904	899	2	0
2	G	950	901	898	4	1
2	H	957	913	910	2	0
2	I	958	915	912	3	0
2	J	956	911	908	1	0
3	A	24	32	32	1	0
3	B	12	16	16	0	0
3	C	6	8	8	0	0
3	D	12	16	16	2	0
3	E	12	16	16	4	0
3	F	12	16	16	0	0
3	G	18	24	24	1	0
3	H	18	24	24	0	0
3	I	12	16	16	0	0
3	J	18	24	24	0	0
4	E	13	18	18	0	0
5	A	110	0	0	0	0
5	B	99	0	0	0	0
5	C	97	0	0	0	0
5	D	102	0	0	1	0
5	E	107	0	0	0	0
5	F	41	0	0	0	0
5	G	29	0	0	0	0
5	H	41	0	0	0	0
5	I	29	0	0	1	0
5	J	35	0	0	0	0
All	All	15876	14874	14813	69	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 2.

The worst 5 of 69 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:D:216:GLU:OE1	5:D:401:HOH:O	1.90	0.89
1:C:54:GLU:OE2	1:C:200:ASN:ND2	2.09	0.85
1:A:155:GLY:HA3	1:A:218:THR:HG22	1.62	0.82
1:A:54:GLU:OE2	1:A:200:ASN:ND2	2.16	0.78
2:I:52:TRP:O	2:I:71:ARG:NH1	2.26	0.66

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	Interatomic distance (Å)	Clash overlap (Å)
1:B:38:LYS:NZ	2:G:117:GLY:O[1_455]	2.06	0.14

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	A	262/273 (96%)	249 (95%)	12 (5%)	1 (0%)	30	49
1	B	262/273 (96%)	249 (95%)	12 (5%)	1 (0%)	30	49
1	C	260/273 (95%)	247 (95%)	12 (5%)	1 (0%)	30	49
1	D	260/273 (95%)	247 (95%)	12 (5%)	1 (0%)	30	49
1	E	263/273 (96%)	250 (95%)	12 (5%)	1 (0%)	30	49
2	F	122/131 (93%)	122 (100%)	0	0	100	100
2	G	122/131 (93%)	122 (100%)	0	0	100	100
2	H	122/131 (93%)	122 (100%)	0	0	100	100
2	I	122/131 (93%)	122 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	J	122/131 (93%)	122 (100%)	0	0	100	100
All	All	1917/2020 (95%)	1852 (97%)	60 (3%)	5 (0%)	36	55

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	188	VAL
1	B	188	VAL
1	C	188	VAL
1	D	188	VAL
1	E	188	VAL

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	229/234 (98%)	228 (100%)	1 (0%)	84	93
1	B	229/234 (98%)	228 (100%)	1 (0%)	84	93
1	C	225/234 (96%)	223 (99%)	2 (1%)	70	87
1	D	227/234 (97%)	225 (99%)	2 (1%)	70	87
1	E	230/234 (98%)	228 (99%)	2 (1%)	70	87
2	F	97/106 (92%)	96 (99%)	1 (1%)	68	86
2	G	97/106 (92%)	95 (98%)	2 (2%)	47	74
2	H	98/106 (92%)	96 (98%)	2 (2%)	48	75
2	I	98/106 (92%)	95 (97%)	3 (3%)	35	62
2	J	98/106 (92%)	97 (99%)	1 (1%)	68	86
All	All	1628/1700 (96%)	1611 (99%)	17 (1%)	68	86

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	43	GLU

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Mol	Chain	Res	Type
2	J	1	VAL
1	E	38	LYS
2	F	10	LEU
2	G	1	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	185	GLN
1	B	229	ASN
1	C	229	ASN
1	E	185	GLN
1	E	229	ASN

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](#)

25 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
3	GOL	F	201	-	5,5,5	0.10	0	5,5,5	0.25	0
3	GOL	J	1201	-	5,5,5	0.08	0	5,5,5	0.24	0
3	GOL	B	302	-	5,5,5	0.09	0	5,5,5	0.26	0
4	PG4	E	302	-	12,12,12	0.16	0	11,11,11	0.14	0
3	GOL	A	1102	-	5,5,5	0.11	0	5,5,5	0.32	0
3	GOL	J	1202	-	5,5,5	0.07	0	5,5,5	0.25	0
3	GOL	G	203	-	5,5,5	0.09	0	5,5,5	0.25	0
3	GOL	G	202	-	5,5,5	0.11	0	5,5,5	0.30	0
3	GOL	D	301	-	5,5,5	0.09	0	5,5,5	0.28	0
3	GOL	B	301	-	5,5,5	0.09	0	5,5,5	0.28	0
3	GOL	A	1104	-	5,5,5	0.11	0	5,5,5	0.28	0
3	GOL	J	1203	-	5,5,5	0.10	0	5,5,5	0.25	0
3	GOL	E	303	-	5,5,5	0.10	0	5,5,5	0.27	0
3	GOL	D	302	-	5,5,5	0.11	0	5,5,5	0.28	0
3	GOL	E	301	-	5,5,5	0.09	0	5,5,5	0.32	0
3	GOL	H	201	-	5,5,5	0.07	0	5,5,5	0.26	0
3	GOL	A	1103	-	5,5,5	0.08	0	5,5,5	0.22	0
3	GOL	A	1101	-	5,5,5	0.09	0	5,5,5	0.29	0
3	GOL	I	202	-	5,5,5	0.10	0	5,5,5	0.28	0
3	GOL	C	301	-	5,5,5	0.10	0	5,5,5	0.26	0
3	GOL	F	202	-	5,5,5	0.08	0	5,5,5	0.27	0
3	GOL	I	201	-	5,5,5	0.11	0	5,5,5	0.25	0
3	GOL	G	201	-	5,5,5	0.09	0	5,5,5	0.25	0
3	GOL	H	202	-	5,5,5	0.10	0	5,5,5	0.31	0
3	GOL	H	203	-	5,5,5	0.09	0	5,5,5	0.25	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
3	GOL	F	201	-	-	2/4/4/4	-
3	GOL	J	1201	-	-	3/4/4/4	-
3	GOL	B	302	-	-	0/4/4/4	-
4	PG4	E	302	-	-	5/10/10/10	-
3	GOL	A	1102	-	-	1/4/4/4	-
3	GOL	J	1202	-	-	0/4/4/4	-
3	GOL	G	203	-	-	4/4/4/4	-
3	GOL	G	202	-	-	1/4/4/4	-
3	GOL	D	301	-	-	0/4/4/4	-
3	GOL	B	301	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	1104	-	-	0/4/4/4	-
3	GOL	J	1203	-	-	0/4/4/4	-
3	GOL	E	303	-	-	0/4/4/4	-
3	GOL	D	302	-	-	0/4/4/4	-
3	GOL	E	301	-	-	2/4/4/4	-
3	GOL	H	201	-	-	4/4/4/4	-
3	GOL	A	1103	-	-	0/4/4/4	-
3	GOL	A	1101	-	-	2/4/4/4	-
3	GOL	I	202	-	-	2/4/4/4	-
3	GOL	C	301	-	-	2/4/4/4	-
3	GOL	F	202	-	-	0/4/4/4	-
3	GOL	I	201	-	-	2/4/4/4	-
3	GOL	G	201	-	-	2/4/4/4	-
3	GOL	H	202	-	-	2/4/4/4	-
3	GOL	H	203	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1101	GOL	C1-C2-C3-O3
3	C	301	GOL	C1-C2-C3-O3
3	E	301	GOL	O1-C1-C2-C3
3	F	201	GOL	C1-C2-C3-O3
3	G	201	GOL	C1-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	301	GOL	2	0
3	E	301	GOL	4	0
3	A	1101	GOL	1	0
3	G	201	GOL	1	0

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	A	264/273 (96%)	-0.23	8 (3%) 52 48	18, 37, 72, 97	2 (0%)
1	B	264/273 (96%)	-0.16	10 (3%) 44 39	19, 40, 80, 106	2 (0%)
1	C	263/273 (96%)	-0.13	5 (1%) 66 62	20, 40, 73, 101	1 (0%)
1	D	263/273 (96%)	-0.20	4 (1%) 72 68	21, 39, 71, 98	1 (0%)
1	E	266/273 (97%)	-0.30	1 (0%) 88 86	18, 37, 67, 93	1 (0%)
2	F	124/131 (94%)	0.26	4 (3%) 50 46	33, 49, 84, 93	0
2	G	124/131 (94%)	0.12	5 (4%) 42 38	30, 47, 75, 93	0
2	H	124/131 (94%)	0.00	1 (0%) 82 80	33, 46, 67, 83	0
2	I	124/131 (94%)	0.35	4 (3%) 50 46	35, 52, 79, 106	0
2	J	124/131 (94%)	0.32	2 (1%) 70 67	31, 52, 82, 96	0
All	All	1940/2020 (96%)	-0.07	44 (2%) 61 57	18, 41, 78, 106	7 (0%)

The worst 5 of 44 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	123	SER	4.1
2	I	123	SER	3.7
1	B	39	THR	3.4
2	J	123	SER	3.2
1	A	40	GLY	3.2

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 [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
3	GOL	F	202	6/6	0.74	0.20	73,83,84,84	3
3	GOL	H	202	6/6	0.77	0.20	74,76,84,94	3
3	GOL	J	1202	6/6	0.77	0.17	68,81,85,89	3
3	GOL	A	1104	6/6	0.82	0.20	63,66,72,77	3
3	GOL	D	302	6/6	0.85	0.17	57,68,77,81	3
3	GOL	B	301	6/6	0.85	0.15	56,68,69,70	3
3	GOL	B	302	6/6	0.86	0.17	61,63,70,80	3
3	GOL	J	1203	6/6	0.86	0.20	77,86,89,92	3
3	GOL	E	301	6/6	0.87	0.19	61,70,80,80	3
3	GOL	E	303	6/6	0.87	0.16	59,62,70,75	3
4	PG4	E	302	13/13	0.87	0.17	54,68,71,79	2
3	GOL	H	201	6/6	0.88	0.19	53,65,67,67	3
3	GOL	A	1103	6/6	0.89	0.13	50,62,69,74	3
3	GOL	I	201	6/6	0.90	0.19	63,74,86,86	3
3	GOL	I	202	6/6	0.90	0.11	69,79,80,82	3
3	GOL	G	203	6/6	0.90	0.25	64,79,87,93	3
3	GOL	C	301	6/6	0.90	0.17	66,67,73,75	3
3	GOL	G	202	6/6	0.90	0.14	61,68,74,74	3
3	GOL	J	1201	6/6	0.91	0.20	66,78,80,81	3
3	GOL	A	1101	6/6	0.91	0.16	55,61,68,77	3
3	GOL	F	201	6/6	0.91	0.15	62,67,72,74	3
3	GOL	D	301	6/6	0.91	0.13	58,61,66,70	3
3	GOL	G	201	6/6	0.92	0.14	62,69,73,75	3
3	GOL	H	203	6/6	0.92	0.14	71,79,82,85	3
3	GOL	A	1102	6/6	0.93	0.10	50,53,56,57	3

6.5 Other polymers [i](#)

There are no such residues in this entry.