



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:03 AM GMT

PDB ID : 3NXG
Title : JC polyomavirus VP1
Authors : Neu, U.; Stroeh, L.J.; Stehle, T.
Deposited on : 2010-07-13
Resolution : 1.95 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

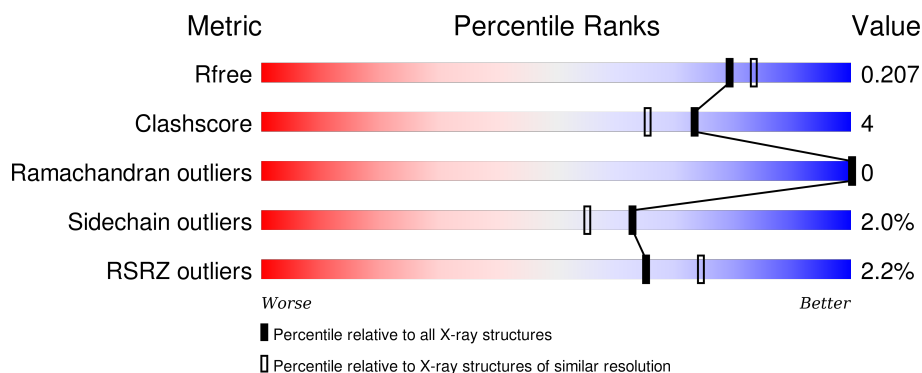
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	91344	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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. 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	272	<div> <div>2%</div> <div>88% 7% • 5%</div> </div>
1	B	272	<div> <div>2%</div> <div>86% 8% • 5%</div> </div>
1	C	272	<div> <div>2%</div> <div>85% 8% • 6%</div> </div>
1	D	272	<div> <div>3%</div> <div>86% 8% • 5%</div> </div>
1	E	272	<div> <div>%</div> <div>88% 7% • 5%</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
2	GOL	A	4	-	-	-	X
2	GOL	B	5	-	-	-	X
2	GOL	C	1	-	-	-	X
2	GOL	D	2	-	-	-	X
3	EDO	A	1	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11187 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 Major capsid protein VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	259	Total	C	N	O	S	0	4	0
			2028	1280	347	390	11			
1	B	258	Total	C	N	O	S	0	5	0
			2032	1285	346	390	11			
1	C	257	Total	C	N	O	S	0	7	0
			2035	1287	349	388	11			
1	D	258	Total	C	N	O	S	0	5	0
			2026	1279	346	390	11			
1	E	259	Total	C	N	O	S	0	2	0
			2029	1279	350	389	11			

There are 20 discrepancies between the modelled and reference sequences:

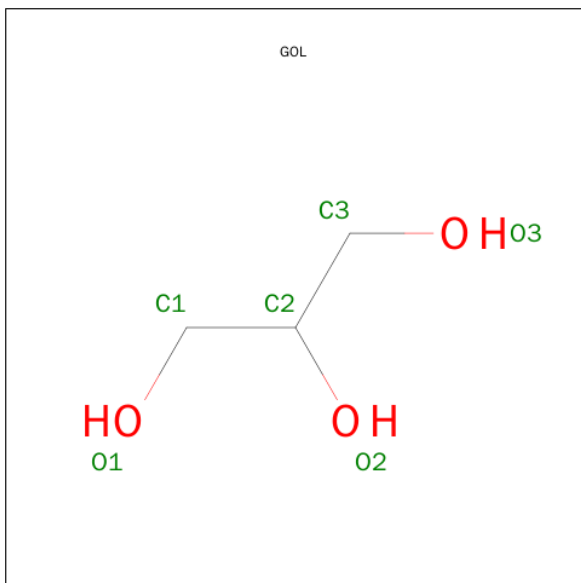
Chain	Residue	Modelled	Actual	Comment	Reference
A	18	GLY	-	EXPRESSION TAG	UNP P03089
A	19	SER	-	EXPRESSION TAG	UNP P03089
A	20	HIS	-	EXPRESSION TAG	UNP P03089
A	21	MET	-	EXPRESSION TAG	UNP P03089
B	18	GLY	-	EXPRESSION TAG	UNP P03089
B	19	SER	-	EXPRESSION TAG	UNP P03089
B	20	HIS	-	EXPRESSION TAG	UNP P03089
B	21	MET	-	EXPRESSION TAG	UNP P03089
C	18	GLY	-	EXPRESSION TAG	UNP P03089
C	19	SER	-	EXPRESSION TAG	UNP P03089
C	20	HIS	-	EXPRESSION TAG	UNP P03089
C	21	MET	-	EXPRESSION TAG	UNP P03089
D	18	GLY	-	EXPRESSION TAG	UNP P03089
D	19	SER	-	EXPRESSION TAG	UNP P03089
D	20	HIS	-	EXPRESSION TAG	UNP P03089
D	21	MET	-	EXPRESSION TAG	UNP P03089
E	18	GLY	-	EXPRESSION TAG	UNP P03089
E	19	SER	-	EXPRESSION TAG	UNP P03089
E	20	HIS	-	EXPRESSION TAG	UNP P03089

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Chain	Residue	Modelled	Actual	Comment	Reference
E	21	MET	-	EXPRESSION TAG	UNP P03089

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



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

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		



- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	203	Total	O	0	0
			203	203		
4	B	202	Total	O	0	0
			202	202		
4	C	189	Total	O	0	0
			189	189		
4	D	190	Total	O	0	0
			190	190		
4	E	203	Total	O	0	0
			203	203		

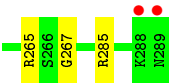
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). 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.

- Chain A:
-
- Sequence logo for Chain A. The y-axis represents information content in bits (0.00 to 0.25). The x-axis shows amino acid positions. A color scale at the top indicates conservation levels: 2% (red), 88% (green), 7% (yellow), and 5% (grey). Red dots above the sequence indicate positions with high conservation (bits > 0.15).
- | Position | Amino Acid | Conservation Level (%) | Information Content (bits) |
|----------|------------|------------------------|----------------------------|
| 1 | GLY | 88% | 0.00 |
| 2 | SER | 88% | 0.00 |
| 3 | HIS | 88% | 0.00 |
| 4 | MET | 88% | 0.00 |
| 5 | GLY | 88% | 0.00 |
| 6 | GLY | 88% | 0.00 |
| 7 | V24 | 88% | 0.15 |
| 8 | L27 | 88% | 0.00 |
| 9 | E28 | 88% | 0.00 |
| 10 | V29 | 88% | 0.00 |
| 11 | K30 | 88% | 0.00 |
| 12 | V33 | 88% | 0.15 |
| 13 | D34 | 88% | 0.15 |
| 14 | S35 | 88% | 0.00 |
| 15 | I36 | 88% | 0.00 |
| 16 | E46 | 88% | 0.00 |
| 17 | E68 | 88% | 0.00 |
| 18 | V91 | 88% | 0.15 |
| 19 | GLU | 88% | 0.00 |
| 20 | ASP | 88% | 0.00 |
| 21 | LEU | 88% | 0.00 |
| 22 | THR | 88% | 0.00 |
| 23 | CYS | 88% | 0.00 |
| 24 | GLY | 88% | 0.00 |
| 25 | ASN | 88% | 0.00 |
| 26 | I99 | 88% | 0.15 |
| 27 | E103 | 88% | 0.00 |
| 28 | V120 | 88% | 0.00 |
| 29 | H128 | 88% | 0.00 |
| 30 | G133 | 88% | 0.00 |
| 31 | Q137 | 88% | 0.00 |
| 32 | G138 | 88% | 0.00 |
| 33 | T139 | 88% | 0.00 |
| 34 | R161 | 88% | 0.00 |
| 35 | P171 | 88% | 0.00 |
| 36 | R182 | 88% | 0.00 |
| 37 | H185 | 88% | 0.00 |
| 38 | C199 | 88% | 0.00 |
| 39 | G218 | 88% | 0.00 |
| 40 | G219 | 88% | 0.00 |
| 41 | G267 | 88% | 0.00 |
| 42 | P285 | 88% | 0.00 |
| 43 | P289 | 88% | 0.15 |

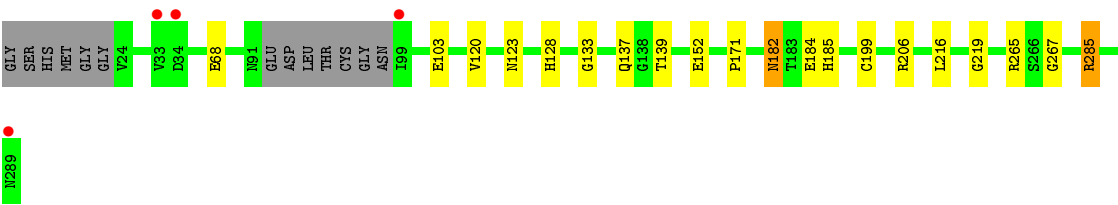
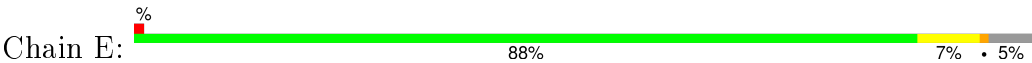
- Chain B:
-
- 2% 86% 8% 5%
- GLY SER HIS MET GLY GLY V24 E25 V33 F42 L43 F46 I61 H91 GLU ASP LEU THR CYS GLY ASN I99 I112 T115 M118 R119 Y120 M123 H128 G133 T139 L157 K163 Q179 M182 T183 E184 C199 L216 T217 G218 G219
- V222 F240 R265 S266 G267 K288 ASN

- Chain C: 
- 
- GLY SER HIS MET GLY GLY VAL E25 K30 K33 D34 S35 I36 C41 F42 E68 I85 L90 ASN GLU ASP LEU THR CYS GLN ASN I99 E103 I112 M118 M119 Y120 H128 G133 Q137 G138 T139 P171 M182 T183 E184 H185 D203 F206 G219 F240 G267 K284 R285 K288 H289

- Chain D:



● Molecule 1: Major capsid protein VP1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	149.57Å 96.02Å 128.55Å 90.00° 110.44° 90.00°	Depositor
Resolution (Å)	19.83 – 1.95 19.83 – 1.95	Depositor EDS
% Data completeness (in resolution range)	96.7 (19.83-1.95) 96.7 (19.83-1.95)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.174 , 0.207 0.175 , 0.207	Depositor DCC
R_{free} test set	6089 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	14.9	Xtriage
Anisotropy	0.183	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 51.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 119850 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11187	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, EDO

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	0.42	1/2085 (0.0%)	0.55	0/2833
1	B	0.41	1/2093 (0.0%)	0.55	0/2843
1	C	0.41	0/2102	0.55	0/2854
1	D	0.41	0/2086	0.55	0/2834
1	E	0.43	1/2080 (0.0%)	0.56	0/2825
All	All	0.42	3/10446 (0.0%)	0.55	0/14189

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	199	CYS	CB-SG	-6.92	1.70	1.82
1	B	199	CYS	CB-SG	-6.45	1.71	1.82
1	A	199	CYS	CB-SG	-6.23	1.71	1.82

There are no bond angle outliers.

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	2028	0	1983	15	0
1	B	2032	0	1993	21	0
1	C	2035	0	2001	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2026	0	1986	19	0
1	E	2029	0	1987	16	0
2	A	6	0	8	0	0
2	B	6	0	8	0	0
2	C	6	0	8	0	0
2	D	6	0	8	0	0
2	E	6	0	8	0	0
3	A	8	0	12	0	0
3	C	4	0	6	0	0
3	D	4	0	6	0	0
3	E	4	0	6	0	0
4	A	203	0	0	1	0
4	B	202	0	0	3	0
4	C	189	0	0	2	0
4	D	190	0	0	2	0
4	E	203	0	0	2	0
All	All	11187	0	10020	82	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 4.

All (82) 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:120:VAL:CG2	1:D:133:GLY:O	2.35	0.74
1:E:139:THR:HG23	4:E:315:HOH:O	1.89	0.72
1:A:120:VAL:CG2	1:A:133:GLY:O	2.39	0.70
1:C:128:HIS:HE1	1:D:267:GLY:O	1.76	0.69
1:B:42[B]:PHE:CD1	1:B:112:ILE:HD13	2.29	0.68
1:D:128:HIS:HE1	1:E:267:GLY:O	1.76	0.68
1:E:120:VAL:CG2	1:E:133:GLY:O	2.43	0.67
1:D:120:VAL:HG23	1:D:133:GLY:O	1.96	0.66
1:A:267:GLY:O	1:E:128:HIS:HE1	1.79	0.65
1:B:120:VAL:HG22	1:B:133:GLY:O	1.97	0.65
1:D:123:ASN:ND2	1:D:265:ARG:HG3	2.14	0.63
1:C:203:ASP:OD2	1:C:206[B]:ARG:HD3	1.98	0.63
1:A:120:VAL:HG23	1:A:133:GLY:O	1.99	0.62
1:C:139:THR:HG23	4:C:298:HOH:O	1.99	0.61
1:B:42[B]:PHE:HD1	1:B:112:ILE:CD1	2.12	0.61
1:C:42[B]:PHE:CD1	1:C:112:ILE:HD13	2.36	0.61
1:A:139:THR:HB	1:A:218:GLY:HA2	1.82	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:128:HIS:HE1	1:C:267:GLY:O	1.87	0.57
1:D:103:GLU:OE1	1:D:285:ARG:HD2	2.05	0.56
1:D:139:THR:HG23	4:D:403:HOH:O	2.05	0.56
1:E:120:VAL:HG22	1:E:133:GLY:O	2.06	0.55
1:C:42[B]:PHE:HD1	1:C:112:ILE:CD1	2.20	0.55
1:C:118:MET:HE2	1:D:216:LEU:CD1	2.36	0.55
1:C:182:ASN:HD22	1:C:182:ASN:C	2.10	0.55
1:D:182:ASN:C	1:D:182:ASN:HD22	2.10	0.55
1:C:120:VAL:HG22	1:C:133:GLY:O	2.08	0.54
1:C:68:GLU:HG3	4:C:323:HOH:O	2.08	0.53
1:E:182:ASN:HD22	1:E:182:ASN:C	2.11	0.53
1:A:137:GLN:NE2	1:B:219:GLY:HA2	2.24	0.53
1:B:42[B]:PHE:CD1	1:B:112:ILE:CD1	2.90	0.52
1:B:139:THR:HG23	4:B:316:HOH:O	2.11	0.51
1:B:163:LYS:HE3	4:B:808:HOH:O	2.10	0.51
1:A:46:GLU:HG3	4:A:335:HOH:O	2.09	0.51
1:A:128:HIS:HE1	1:B:267:GLY:O	1.94	0.51
1:E:103:GLU:OE1	1:E:285:ARG:HD2	2.11	0.50
1:E:139:THR:HG22	1:E:219:GLY:H	1.75	0.50
1:B:182:ASN:C	1:B:182:ASN:HD22	2.15	0.50
1:B:123:ASN:ND2	1:B:265:ARG:HD3	2.27	0.49
1:B:123:ASN:HD22	1:B:265:ARG:HD3	1.78	0.48
1:D:157:LEU:O	1:D:179:GLN:HA	2.14	0.48
1:D:139:THR:HB	1:D:218:GLY:HA2	1.95	0.48
1:A:182:ASN:HD22	1:A:182:ASN:C	2.16	0.48
1:B:42[B]:PHE:HD1	1:B:112:ILE:HD11	1.77	0.47
1:E:152:GLU:OE2	1:E:206[B]:ARG:HD2	2.15	0.46
1:A:103:GLU:OE1	1:A:285:ARG:HD2	2.16	0.46
1:A:68[B]:GLU:HG3	1:A:161:ARG:NH1	2.31	0.46
1:E:123:ASN:ND2	1:E:265:ARG:HG3	2.31	0.46
1:B:120:VAL:O	1:B:120:VAL:HG13	2.16	0.46
1:C:128:HIS:HD2	4:D:1105:HOH:O	1.99	0.45
1:D:68[A]:GLU:HG2	1:D:161:ARG:NH1	2.31	0.45
1:D:30:LYS:HE3	1:D:100:LEU:HD21	1.99	0.45
1:B:46:GLU:HG3	4:B:467:HOH:O	2.17	0.45
1:D:182:ASN:HD22	1:D:184:GLU:H	1.66	0.44
1:D:182:ASN:HB3	1:D:185:HIS:CD2	2.52	0.44
1:C:182:ASN:HD22	1:C:184:GLU:H	1.63	0.44
1:C:41:CYS:SG	1:C:85:ILE:HD11	2.58	0.44
1:A:219:GLY:HA2	1:E:137:GLN:HE21	1.82	0.44
1:A:219:GLY:HA2	1:E:137:GLN:NE2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:LEU:HB3	1:A:28:GLU:H	1.71	0.44
1:C:139:THR:HG22	1:C:219:GLY:H	1.83	0.44
1:C:118:MET:HE2	1:D:216:LEU:HD12	2.00	0.43
1:C:90:LEU:HD21	1:C:284:LYS:HE2	2.00	0.43
1:C:103:GLU:OE1	1:C:285:ARG:HD2	2.19	0.43
1:B:139:THR:HB	1:B:218:GLY:HA2	2.01	0.43
1:C:42[B]:PHE:CD1	1:C:112:ILE:CD1	2.97	0.43
1:C:182:ASN:ND2	1:C:184:GLU:H	2.16	0.43
1:C:42[B]:PHE:HD1	1:C:112:ILE:HD11	1.83	0.42
1:B:115:THR:HB	1:B:118:MET:HE3	2.02	0.42
1:D:118:MET:HE2	1:E:216:LEU:CD1	2.50	0.42
1:B:43:LEU:HA	1:B:43:LEU:HD12	1.93	0.42
1:E:68:GLU:HG3	4:E:340:HOH:O	2.19	0.41
1:C:137:GLN:HE21	1:D:219:GLY:HA2	1.85	0.41
1:A:171:PRO:HB3	1:A:185:HIS:CG	2.55	0.41
1:B:157:LEU:O	1:B:179:GLN:HA	2.21	0.41
1:C:68:GLU:H	1:C:68:GLU:HG3	1.61	0.41
1:A:120:VAL:HG13	1:B:61:ILE:HG21	2.03	0.41
1:D:182:ASN:ND2	1:D:184:GLU:H	2.18	0.41
1:B:182:ASN:HD22	1:B:184:GLU:H	1.69	0.41
1:C:171:PRO:HB3	1:C:185:HIS:CG	2.56	0.40
1:C:120:VAL:HG13	1:C:120:VAL:O	2.21	0.40
1:E:171:PRO:HB3	1:E:185:HIS:CG	2.57	0.40
1:E:182:ASN:HD22	1:E:184:GLU:H	1.70	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	259/272 (95%)	252 (97%)	7 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	259/272 (95%)	251 (97%)	8 (3%)	0	100	100
1	C	260/272 (96%)	250 (96%)	10 (4%)	0	100	100
1	D	259/272 (95%)	252 (97%)	7 (3%)	0	100	100
1	E	257/272 (94%)	248 (96%)	9 (4%)	0	100	100
All	All	1294/1360 (95%)	1253 (97%)	41 (3%)	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	A	228/237 (96%)	223 (98%)	5 (2%)	60	51
1	B	230/237 (97%)	225 (98%)	5 (2%)	60	51
1	C	230/237 (97%)	223 (97%)	7 (3%)	48	36
1	D	229/237 (97%)	226 (99%)	3 (1%)	76	72
1	E	228/237 (96%)	226 (99%)	2 (1%)	84	83
All	All	1145/1185 (97%)	1123 (98%)	22 (2%)	63	58

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	LEU
1	A	30	LYS
1	A	36	ILE
1	A	139	THR
1	A	182	ASN
1	B	120	VAL
1	B	139	THR
1	B	182	ASN
1	B	216	LEU
1	B	222	VAL

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Mol	Chain	Res	Type
1	C	30	LYS
1	C	34	ASP
1	C	36	ILE
1	C	68	GLU
1	C	120	VAL
1	C	139	THR
1	C	182	ASN
1	D	36	ILE
1	D	139	THR
1	D	182	ASN
1	E	182	ASN
1	E	285	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	ASN
1	A	125	GLN
1	A	128	HIS
1	A	137	GLN
1	A	173	ASN
1	A	182	ASN
1	B	123	ASN
1	B	125	GLN
1	B	128	HIS
1	B	137	GLN
1	B	182	ASN
1	C	123	ASN
1	C	125	GLN
1	C	128	HIS
1	C	137	GLN
1	C	173	ASN
1	C	182	ASN
1	D	123	ASN
1	D	125	GLN
1	D	128	HIS
1	D	137	GLN
1	D	182	ASN
1	E	123	ASN
1	E	125	GLN
1	E	128	HIS
1	E	137	GLN

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Mol	Chain	Res	Type
1	E	182	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

10 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	EDO	A	1	-	3,3,3	0.43	0	2,2,2	0.49	0
3	EDO	A	290	-	3,3,3	0.49	0	2,2,2	0.43	0
2	GOL	A	4	-	5,5,5	0.38	0	5,5,5	0.30	0
2	GOL	B	5	-	5,5,5	0.36	0	5,5,5	0.38	0
2	GOL	C	1	-	5,5,5	0.32	0	5,5,5	0.30	0
3	EDO	C	290	-	3,3,3	0.43	0	2,2,2	0.51	0
3	EDO	D	1	-	3,3,3	0.45	0	2,2,2	0.50	0
2	GOL	D	2	-	5,5,5	0.32	0	5,5,5	0.33	0
3	EDO	E	1	-	3,3,3	0.47	0	2,2,2	0.36	0
2	GOL	E	3	-	5,5,5	0.36	0	5,5,5	0.34	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	EDO	A	1	-	-	0/1/1/1	0/0/0/0
3	EDO	A	290	-	-	0/1/1/1	0/0/0/0
2	GOL	A	4	-	-	0/4/4/4	0/0/0/0
2	GOL	B	5	-	-	0/4/4/4	0/0/0/0
2	GOL	C	1	-	-	0/4/4/4	0/0/0/0
3	EDO	C	290	-	-	0/1/1/1	0/0/0/0
3	EDO	D	1	-	-	0/1/1/1	0/0/0/0
2	GOL	D	2	-	-	0/4/4/4	0/0/0/0
3	EDO	E	1	-	-	0/1/1/1	0/0/0/0
2	GOL	E	3	-	-	0/4/4/4	0/0/0/0

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 ⓘ

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	259/272 (95%)	-0.36	6 (2%) 64 73	8, 14, 27, 45	0
1	B	258/272 (94%)	-0.30	6 (2%) 64 73	8, 14, 30, 44	0
1	C	257/272 (94%)	-0.31	6 (2%) 64 73	8, 14, 29, 48	0
1	D	258/272 (94%)	-0.31	7 (2%) 58 68	7, 14, 28, 50	0
1	E	259/272 (95%)	-0.38	4 (1%) 76 84	7, 13, 27, 46	0
All	All	1291/1360 (94%)	-0.33	29 (2%) 65 74	7, 14, 28, 50	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	33	VAL	8.3
1	E	33	VAL	6.1
1	C	33	VAL	6.0
1	B	33	VAL	6.0
1	A	33	VAL	5.8
1	E	289	ASN	4.5
1	B	91	ASN	3.4
1	A	24	VAL	3.3
1	C	289	ASN	3.3
1	B	24	VAL	3.2
1	B	240	PHE	3.1
1	C	288	LYS	3.1
1	D	240	PHE	3.1
1	D	289	ASN	2.9
1	A	289	ASN	2.7
1	C	34	ASP	2.7
1	D	24	VAL	2.7
1	D	99	ILE	2.6
1	E	99	ILE	2.6
1	C	99	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	288	LYS	2.4
1	B	25	GLU	2.3
1	A	99	ILE	2.2
1	E	34	ASP	2.2
1	D	89	ASN	2.1
1	B	288	LYS	2.1
1	A	91	ASN	2.1
1	C	240	PHE	2.1
1	A	34	ASP	2.1

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	EDO	A	1	4/4	0.91	0.14	10.80	35,36,36,38	0
2	GOL	D	2	6/6	0.83	0.19	6.91	30,33,37,41	0
2	GOL	B	5	6/6	0.86	0.16	5.38	30,31,35,38	0
2	GOL	A	4	6/6	0.85	0.17	4.65	35,37,39,41	0
2	GOL	C	1	6/6	0.82	0.19	4.37	33,35,38,41	0
2	GOL	E	3	6/6	0.92	0.13	1.76	29,30,31,33	0
3	EDO	C	290	4/4	0.92	0.09	0.83	35,35,35,36	0
3	EDO	D	1	4/4	0.92	0.09	0.74	32,33,34,35	0
3	EDO	E	1	4/4	0.81	0.14	-	40,41,41,41	0
3	EDO	A	290	4/4	0.76	0.19	-	44,45,45,45	0

6.5 Other polymers

There are no such residues in this entry.