



wwPDB X-ray Structure Validation Summary Report ⓘ

May 23, 2020 – 09:53 am BST

PDB ID : 5VJQ
Title : Complex between HyHEL10 Fab fragment heavy chain mutant (I29F, S52T, Y53F) and Pekin duck egg lysozyme isoform I (DEL-I)
Authors : Langley, D.B.; Christ, D.
Deposited on : 2017-04-19
Resolution : 1.90 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 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

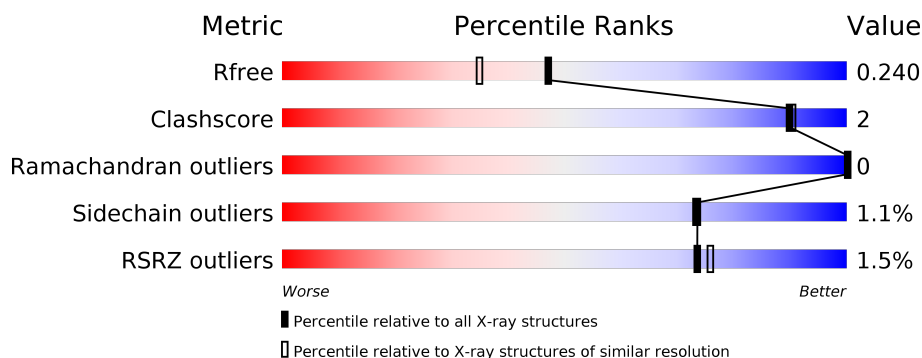
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 $\leq 5\%$. 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	213	<div> <div style="width: 93%;"></div> <div style="width: 5%;"></div> <div style="width: 2%;"></div> </div> <div>93% 5% .</div>
1	C	213	<div> <div style="width: 91%;"></div> <div style="width: 6%;"></div> <div style="width: 3%;"></div> </div> <div>91% 6% .</div>
1	E	213	<div> <div style="width: 93%;"></div> <div style="width: 5%;"></div> <div style="width: 2%;"></div> </div> <div>93% . .</div>
1	G	213	<div> <div style="width: 93%;"></div> <div style="width: 5%;"></div> <div style="width: 2%;"></div> </div> <div>93% . .</div>
2	B	213	<div> <div style="width: 95%;"></div> <div style="width: 5%;"></div> <div style="width: 0%;"></div> </div> <div>95% 5%</div>
2	D	213	<div> <div style="width: 95%;"></div> <div style="width: 5%;"></div> <div style="width: 0%;"></div> </div> <div>95% 5%</div>

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Mol	Chain	Length	Quality of chain
2	F	213	<div><div></div><div>%</div><div>93%</div><div>7%</div></div>
2	H	213	<div><div></div><div>3%</div><div>95%</div><div></div><div>.</div></div>
3	I	129	<div><div></div><div>%</div><div>98%</div><div></div><div>.</div></div>
3	J	129	<div><div></div><div>2%</div><div>95%</div><div>5%</div></div>
3	K	129	<div><div></div><div>11%</div><div>86%</div><div>10%</div><div>.</div><div>.</div></div>
3	L	129	<div><div></div><div>2%</div><div>91%</div><div>7%</div><div>.</div></div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 17903 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 HyHEL10 heavy chain Fab fragment carrying three mutations; I29F, S52T, Y53F.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	S	0	3	0
			1598	1014	255	321	8			
1	C	207	Total	C	N	O	S	0	3	0
			1599	1015	258	318	8			
1	E	207	Total	C	N	O	S	0	0	0
			1576	1002	249	319	6			
1	G	206	Total	C	N	O	S	0	0	0
			1566	996	248	316	6			

- Molecule 2 is a protein called HyHEL10 light chain Fab fragment.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	212	Total	C	N	O	S	0	4	0
			1658	1029	283	338	8			
2	D	213	Total	C	N	O	S	0	1	0
			1636	1016	277	337	6			
2	F	212	Total	C	N	O	S	0	2	0
			1635	1018	277	334	6			
2	H	212	Total	C	N	O	S	0	4	0
			1653	1028	280	339	6			

- Molecule 3 is a protein called Lysozyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	129	Total	C	N	O	S	0	1	0
			998	615	185	188	10			
3	J	129	Total	C	N	O	S	0	1	0
			1002	616	188	188	10			
3	K	125	Total	C	N	O	S	0	3	0
			981	599	189	183	10			
3	L	126	Total	C	N	O	S	0	0	0
			967	593	182	182	10			

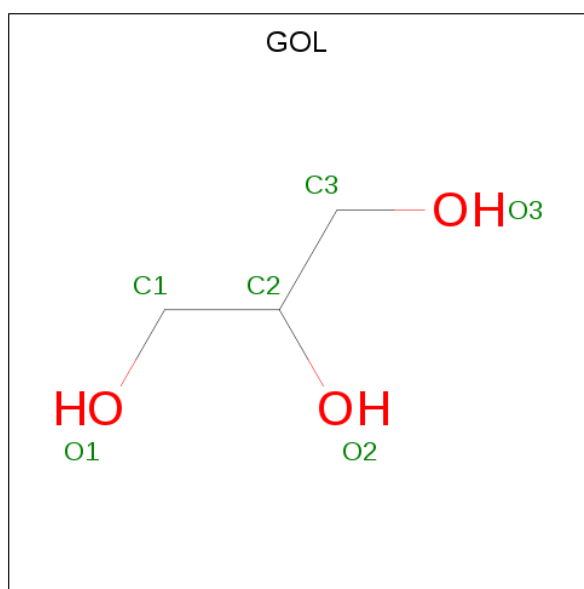
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	37	SER	GLY	conflict	UNP U3J0P1
I	71	GLY	ARG	conflict	UNP U3J0P1
J	37	SER	GLY	conflict	UNP U3J0P1
J	71	GLY	ARG	conflict	UNP U3J0P1
K	37	SER	GLY	conflict	UNP U3J0P1
K	71	GLY	ARG	conflict	UNP U3J0P1
L	37	SER	GLY	conflict	UNP U3J0P1
L	71	GLY	ARG	conflict	UNP U3J0P1

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	H	1	Total Cl 1 1	0	0
4	B	1	Total Cl 1 1	0	0
4	D	1	Total Cl 1 1	0	0
4	F	1	Total Cl 1 1	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	J	1	Total	C	O	0	0
			6	3	3		
5	E	1	Total	C	O	0	0
			6	3	3		
5	H	1	Total	C	O	0	0
			6	3	3		

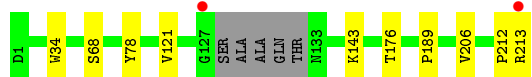
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	108	Total	O	0	0
			108	108		
6	B	159	Total	O	0	0
			159	159		
6	I	51	Total	O	0	0
			51	51		
6	C	104	Total	O	0	0
			104	104		
6	D	130	Total	O	0	0
			130	130		
6	J	71	Total	O	0	0
			71	71		
6	E	74	Total	O	0	0
			74	74		
6	F	92	Total	O	0	0
			92	92		
6	K	39	Total	O	0	0
			39	39		
6	G	71	Total	O	0	0
			71	71		
6	H	65	Total	O	0	0
			65	65		
6	L	30	Total	O	0	0
			30	30		

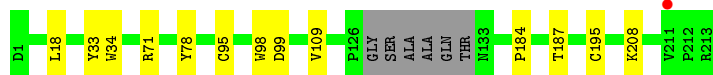
3 Residue-property plots [i](#)

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 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.

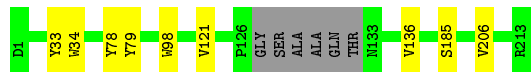
- Molecule 1: HyHEL10 heavy chain Fab fragment carrying three mutations; I29F, S52T, Y53F



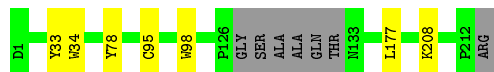
- Molecule 1: HyHEL10 heavy chain Fab fragment carrying three mutations; I29F, S52T, Y53F



- Molecule 1: HyHEL10 heavy chain Fab fragment carrying three mutations; I29F, S52T, Y53F




- Molecule 1: HyHEL10 heavy chain Fab fragment carrying three mutations; I29F, S52T, Y53F



- Molecule 2: HyHEL10 light chain Fab fragment

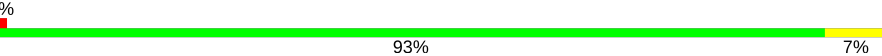


- Molecule 2: HyHEL10 light chain Fab fragment

Chain D:  95% 5%



- Molecule 2: HyHEL10 light chain Fab fragment

Chain F:  93% 7%



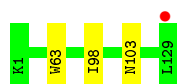
- Molecule 2: HyHEL10 light chain Fab fragment

Chain H:  95% 3%



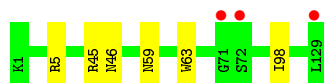
- Molecule 3: Lysozyme

Chain I:  98% 2%




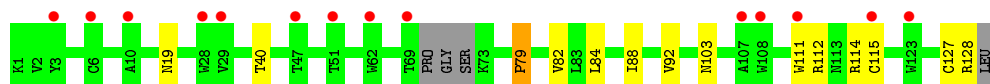
- Molecule 3: Lysozyme

Chain J:  95% 5%




- Molecule 3: Lysozyme

Chain K:  86% 11% 10%



- Molecule 3: Lysozyme

Chain L:  91% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.65Å 132.66Å 199.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.32 – 1.90 49.32 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.8 (49.32-1.90) 97.8 (49.32-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.193 , 0.235 0.199 , 0.240	Depositor DCC
R_{free} test set	9009 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	24.4	Xtriage
Anisotropy	0.147	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17903	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.84% 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, CL

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	0.63	0/1643	0.79	0/2258
1	C	0.63	0/1644	0.80	0/2259
1	E	0.60	0/1621	0.75	0/2230
1	G	0.59	0/1611	0.74	0/2214
2	B	0.66	0/1696	0.81	0/2303
2	D	0.67	0/1674	0.80	1/2278 (0.0%)
2	F	0.59	0/1673	0.75	0/2275
2	H	0.61	0/1690	0.77	0/2298
3	I	0.56	0/1019	0.70	0/1383
3	J	0.62	0/1023	0.83	3/1387 (0.2%)
3	K	0.68	0/998	0.79	0/1349
3	L	0.53	0/984	0.74	1/1332 (0.1%)
All	All	0.62	0/17276	0.77	5/23566 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	45	ARG	NE-CZ-NH1	6.75	123.67	120.30
3	J	45	ARG	NE-CZ-NH2	-6.33	117.13	120.30
2	D	170	ASP	CB-CG-OD1	5.18	122.96	118.30
3	L	66	ASP	CB-CG-OD1	5.11	122.90	118.30
3	J	5	ARG	NE-CZ-NH1	5.08	122.84	120.30

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	1598	0	1513	7	0
1	C	1599	0	1520	9	0
1	E	1576	0	1495	5	0
1	G	1566	0	1487	4	0
2	B	1658	0	1562	4	0
2	D	1636	0	1526	4	0
2	F	1635	0	1530	6	0
2	H	1653	0	1549	4	0
3	I	998	0	936	1	0
3	J	1002	0	940	2	0
3	K	981	0	909	8	0
3	L	967	0	906	5	0
4	B	1	0	0	0	0
4	D	1	0	0	0	0
4	F	1	0	0	0	0
4	H	1	0	0	0	0
5	C	18	0	24	4	0
5	E	6	0	8	0	0
5	H	6	0	8	1	0
5	J	6	0	8	0	0
6	A	108	0	0	2	0
6	B	159	0	0	0	0
6	C	104	0	0	1	0
6	D	130	0	0	1	0
6	E	74	0	0	0	0
6	F	92	0	0	0	0
6	G	71	0	0	0	0
6	H	65	0	0	0	0
6	I	51	0	0	0	0
6	J	71	0	0	0	0
6	K	39	0	0	0	0
6	L	30	0	0	0	0
All	All	17903	0	15921	59	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 2.

The worst 5 of 59 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)
3:K:40:THR:HG22	3:K:88[A]:ILE:HD11	1.54	0.88
3:K:88[A]:ILE:O	3:K:88[A]:ILE:HG22	1.84	0.77
1:A:143:LYS:HG2	1:A:176[A]:THR:HG22	1.77	0.66
1:G:98:TRP:O	5:H:302:GOL:H2	1.96	0.65
1:C:99:ASP:HA	5:C:302:GOL:H31	1.78	0.65

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	207/213 (97%)	205 (99%)	2 (1%)	0	100	100
1	C	206/213 (97%)	204 (99%)	2 (1%)	0	100	100
1	E	203/213 (95%)	201 (99%)	2 (1%)	0	100	100
1	G	202/213 (95%)	198 (98%)	4 (2%)	0	100	100
2	B	214/213 (100%)	210 (98%)	4 (2%)	0	100	100
2	D	212/213 (100%)	209 (99%)	3 (1%)	0	100	100
2	F	212/213 (100%)	208 (98%)	4 (2%)	0	100	100
2	H	214/213 (100%)	206 (96%)	8 (4%)	0	100	100
3	I	128/129 (99%)	127 (99%)	1 (1%)	0	100	100
3	J	128/129 (99%)	127 (99%)	1 (1%)	0	100	100
3	K	124/129 (96%)	120 (97%)	4 (3%)	0	100	100
3	L	122/129 (95%)	122 (100%)	0	0	100	100
All	All	2172/2220 (98%)	2137 (98%)	35 (2%)	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	184/190 (97%)	182 (99%)	2 (1%)	73	73
1	C	184/190 (97%)	184 (100%)	0	100	100
1	E	182/190 (96%)	182 (100%)	0	100	100
1	G	180/190 (95%)	178 (99%)	2 (1%)	73	73
2	B	190/191 (100%)	188 (99%)	2 (1%)	73	73
2	D	185/191 (97%)	183 (99%)	2 (1%)	73	73
2	F	184/191 (96%)	181 (98%)	3 (2%)	62	60
2	H	186/191 (97%)	181 (97%)	5 (3%)	44	38
3	I	103/106 (97%)	102 (99%)	1 (1%)	76	76
3	J	103/106 (97%)	103 (100%)	0	100	100
3	K	98/106 (92%)	93 (95%)	5 (5%)	24	14
3	L	99/106 (93%)	99 (100%)	0	100	100
All	All	1878/1948 (96%)	1856 (99%)	22 (1%)	73	70

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	191	SER
3	K	103	ASN
2	H	105[A]	GLU
3	K	19	ASN
3	K	79	PRO

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

Mol	Chain	Res	Type
1	C	171	GLN

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 ⓘ

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	GOL	J	201	-	5,5,5	0.30	0	5,5,5	0.70	0
5	GOL	C	303	-	5,5,5	0.28	0	5,5,5	0.62	0
5	GOL	C	302	-	5,5,5	0.74	0	5,5,5	1.06	0
5	GOL	E	301	-	5,5,5	0.20	0	5,5,5	0.42	0
5	GOL	C	301	-	5,5,5	0.25	0	5,5,5	0.57	0
5	GOL	H	302	-	5,5,5	0.45	0	5,5,5	0.73	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
5	GOL	J	201	-	-	2/4/4/4	-
5	GOL	C	303	-	-	1/4/4/4	-
5	GOL	C	302	-	-	4/4/4/4	-
5	GOL	E	301	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	C	301	-	-	0/4/4/4	-
5	GOL	H	302	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	302	GOL	C1-C2-C3-O3
5	C	302	GOL	O2-C2-C3-O3
5	E	301	GOL	C1-C2-C3-O3
5	H	302	GOL	C1-C2-C3-O3
5	C	302	GOL	O1-C1-C2-C3

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	303	GOL	1	0
5	C	302	GOL	3	0
5	H	302	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 [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	208/213 (97%)	0.01	2 (0%) 82 84	15, 26, 42, 50	0
1	C	207/213 (97%)	-0.02	1 (0%) 91 92	14, 26, 40, 48	0
1	E	207/213 (97%)	-0.01	0 100 100	19, 29, 42, 50	0
1	G	206/213 (96%)	0.04	0 100 100	17, 32, 50, 61	0
2	B	212/213 (99%)	-0.09	0 100 100	15, 22, 33, 44	0
2	D	213/213 (100%)	-0.02	0 100 100	15, 24, 39, 46	0
2	F	212/213 (99%)	0.13	2 (0%) 84 85	17, 28, 50, 56	0
2	H	212/213 (99%)	0.28	6 (2%) 53 56	19, 32, 49, 70	0
3	I	129/129 (100%)	-0.14	1 (0%) 86 87	17, 31, 44, 53	0
3	J	129/129 (100%)	-0.15	3 (2%) 60 63	16, 25, 39, 59	0
3	K	125/129 (96%)	0.84	14 (11%) 5 6	24, 35, 51, 62	0
3	L	126/129 (97%)	0.06	3 (2%) 59 62	22, 37, 54, 65	0
All	All	2186/2220 (98%)	0.07	32 (1%) 73 76	14, 28, 47, 70	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	I	129	LEU	5.6
3	L	129	LEU	4.1
3	K	29	VAL	3.7
3	J	71	GLY	3.4
3	K	108	TRP	3.3

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. 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(\AA^2)	Q<0.9
5	GOL	C	302	6/6	0.83	0.24	29,30,32,33	0
5	GOL	E	301	6/6	0.85	0.26	44,51,54,59	0
5	GOL	H	302	6/6	0.86	0.19	35,37,38,38	0
5	GOL	C	303	6/6	0.87	0.22	41,44,45,49	0
5	GOL	J	201	6/6	0.87	0.26	44,49,51,53	0
5	GOL	C	301	6/6	0.89	0.20	38,44,45,48	0
4	CL	H	301	1/1	0.98	0.10	29,29,29,29	0
4	CL	D	301	1/1	0.99	0.08	22,22,22,22	0
4	CL	F	301	1/1	0.99	0.07	24,24,24,24	0
4	CL	B	301	1/1	1.00	0.07	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.