



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 31, 2023 – 11:19 AM JST

PDB ID : 5CD8
Title : Crystal structure of the NTD of Drosophila Oskar protein
Authors : Yang, N.; Hu, M.; Yu, Z.; Wang, M.; Lehmann, R.; Xu, R.M.
Deposited on : 2015-07-03
Resolution : 3.00 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

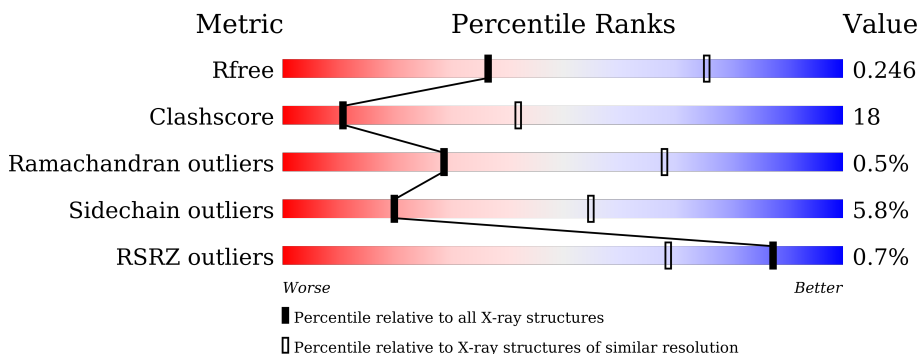
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	93	 47% 34% 18%
1	B	93	 40% 35% 20%
1	C	93	 59% 20% 20%
1	D	93	 3% 51% 24% 22%
1	E	93	 46% 29% 25%
1	F	93	 45% 31% 22%

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 3466 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 Maternal effect protein oskar.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	76	597	374	102	120	1	0	1	0
1	B	74	578	362	100	115	1	0	0	0
1	C	74	578	362	100	115	1	0	0	0
1	D	73	573	359	99	114	1	0	0	0
1	E	70	548	346	93	108	1	0	0	0
1	F	73	573	359	99	114	1	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	148	GLY	-	expression tag	UNP P25158
A	149	SER	-	expression tag	UNP P25158
B	148	GLY	-	expression tag	UNP P25158
B	149	SER	-	expression tag	UNP P25158
C	148	GLY	-	expression tag	UNP P25158
C	149	SER	-	expression tag	UNP P25158
D	148	GLY	-	expression tag	UNP P25158
D	149	SER	-	expression tag	UNP P25158
E	148	GLY	-	expression tag	UNP P25158
E	149	SER	-	expression tag	UNP P25158
F	148	GLY	-	expression tag	UNP P25158
F	149	SER	-	expression tag	UNP P25158

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 3 is water.

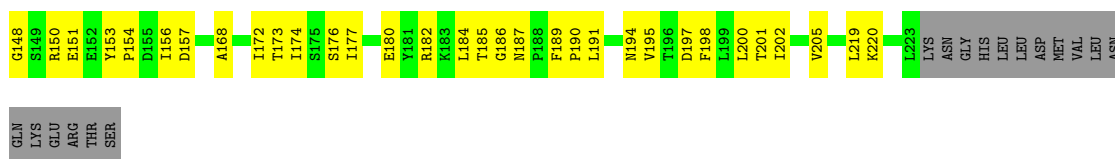
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	5	Total O 5 5	0	0
3	D	1	Total O 1 1	0	0
3	E	1	Total O 1 1	0	0

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.

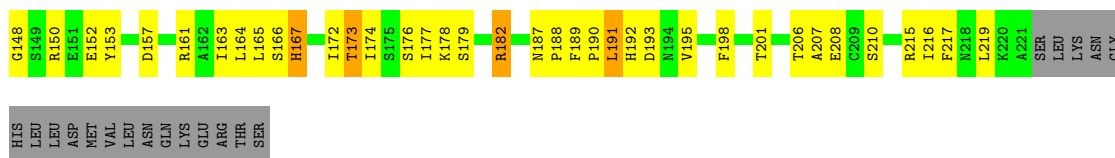
- Molecule 1: Maternal effect protein oskar

Chain A: 



- Molecule 1: Maternal effect protein oskar

Chain B: 



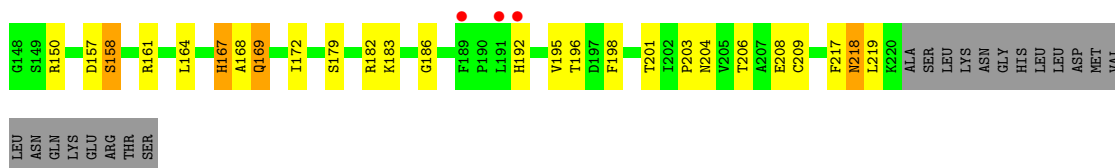
- Molecule 1: Maternal effect protein oskar

Chain C: 



- Molecule 1: Maternal effect protein oskar

Chain D: 



- Molecule 1: Maternal effect protein oskar

Chain E:  46% 29% 25%

GLY	SER	ARG	GLU	E152	Y153	S158	E159	L164	A168	I172	T173	S176	I177	E180	Y181	R182	T185	G186	M187	P188	F189	P190	L191	D197	N204	C209	S210	E211	K214	R215	I216	F217	N218	L219	K220	A221	SER	LEU	LYS	ASN	GLY	HIS	LEU	LEU	ASP	MET	VAL	LEU
-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

ASN	GLN	LYS	GLU	THR	SER
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- Molecule 1: Maternal effect protein oskar

Chain F:  45% 31% 22%

G148	S149	R150	E151	E152	Y153	I156	D157	R161	L165	S166	H167	A168	Q169	I172	T173	I174	S175	S176	I177	R182	P190	V195	F198	L199	L200	T201	I202	P203	N204	S210	K214	R215	I216	F217	R218	L219	K220	ALA	SER	LEU	LYS	ASN	GLY	HIS	LEU	LEU	ASP	MET	VAL
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

LEU	ASN	GLN	LYS	GLU	THR	SER
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4 Data and refinement statistics i

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	66.95Å 66.95Å 112.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.43 – 3.00 40.43 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (40.43-3.00) 99.8 (40.43-3.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.82 (at 3.01Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.189 , 0.242 0.186 , 0.246	Depositor DCC
R_{free} test set	539 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	79.8	Xtrriage
Anisotropy	0.677	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 81.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.037 for -h,-k,l 0.235 for h,-h-k,-l 0.056 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3466	wwPDB-VP
Average B, all atoms (Å ²)	111.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.02% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.37	0/610	0.55	0/826
1	B	0.34	0/588	0.57	0/796
1	C	0.29	0/588	0.44	0/796
1	D	0.27	0/583	0.47	0/789
1	E	0.28	0/558	0.50	0/757
1	F	0.28	0/583	0.47	0/789
All	All	0.31	0/3510	0.50	0/4753

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	597	0	593	24	0
1	B	578	0	573	30	0
1	C	578	0	573	16	0
1	D	573	0	568	21	1
1	E	548	0	546	17	1
1	F	573	0	568	29	0
2	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	6	0	8	1	0
3	A	5	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
All	All	3466	0	3437	126	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 18.

All (126) 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:218:ASN:HD22	1:D:219:LEU:H	1.23	0.83
1:F:210:SER:HB2	1:F:216:ILE:HD11	1.64	0.80
1:B:167:HIS:CD2	1:B:172:ILE:HD12	2.21	0.75
1:A:189:PHE:HE2	1:A:191:LEU:HB2	1.52	0.74
1:F:166:SER:HB2	1:F:167:HIS:ND1	2.02	0.74
1:E:197:ASP:OD1	1:F:215:ARG:NH1	2.22	0.73
1:E:211:GLU:HA	1:F:203:PRO:HB3	1.71	0.71
1:F:153:TYR:CE2	1:F:190:PRO:HB3	2.26	0.71
1:B:172:ILE:HG12	1:B:177:ILE:HG13	1.71	0.71
1:F:150:ARG:NH2	1:F:201:THR:HG22	2.06	0.69
1:E:189:PHE:HE2	1:E:191:LEU:HB2	1.61	0.66
1:A:173:THR:O	1:A:177:ILE:HG13	1.96	0.65
1:A:189:PHE:CE2	1:A:191:LEU:HB2	2.32	0.64
1:B:182:ARG:HA	1:B:187:ASN:O	1.98	0.64
1:A:184:LEU:HD23	1:A:185:THR:CG2	2.30	0.62
1:B:210:SER:HB3	1:B:216:ILE:HD12	1.80	0.62
1:F:210:SER:HB3	1:F:214:LYS:HB2	1.80	0.62
1:E:210:SER:OG	1:E:214:LYS:HB3	2.00	0.61
1:A:172:ILE:HD13	1:A:177:ILE:HG12	1.82	0.61
1:F:172:ILE:HG12	1:F:176:SER:HB3	1.82	0.60
1:F:195:VAL:O	1:F:199:LEU:HG	2.02	0.60
1:A:176:SER:O	1:A:180:GLU:HG2	2.02	0.60
1:C:210:SER:HB3	1:C:216:ILE:HD11	1.84	0.60
1:F:174:ILE:HG12	1:F:217:PHE:CE1	2.37	0.59
1:B:191:LEU:HD13	1:B:195:VAL:HA	1.84	0.58
1:E:172:ILE:HD13	1:E:177:ILE:HG13	1.85	0.58
1:D:182:ARG:HD2	1:D:186:GLY:O	2.03	0.57
1:A:168:ALA:HB2	1:A:219:LEU:HD12	1.85	0.57
1:D:150:ARG:HH22	1:D:201:THR:HG21	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:198:PHE:O	1:D:201:THR:HB	2.04	0.57
1:D:150:ARG:NH2	1:D:201:THR:HG21	2.20	0.57
1:F:153:TYR:CZ	1:F:190:PRO:HB3	2.41	0.56
1:B:178:LYS:HG2	1:B:189:PHE:HB3	1.88	0.56
1:B:152:GLU:OE2	1:C:192:HIS:HB3	2.06	0.56
1:B:182:ARG:NH2	1:B:188:PRO:HB3	2.21	0.56
1:E:182:ARG:HA	1:E:187:ASN:O	2.04	0.56
1:F:167:HIS:CD2	1:F:172:ILE:HD12	2.40	0.56
1:A:150:ARG:HH12	1:A:201:THR:HB	1.70	0.55
1:D:196:THR:HG23	1:D:217:PHE:CZ	2.41	0.55
1:F:157:ASP:HB3	1:F:161:ARG:NH1	2.21	0.55
1:F:161:ARG:O	1:F:165:LEU:HG	2.06	0.55
1:E:176:SER:O	1:E:180:GLU:HG2	2.08	0.54
1:A:184:LEU:HD23	1:A:185:THR:HG22	1.89	0.54
1:D:158:SER:HB3	1:D:161:ARG:HH11	1.73	0.54
1:C:208:GLU:HB2	1:D:206:THR:HG22	1.89	0.53
1:B:206:THR:O	1:B:217:PHE:HA	2.09	0.53
1:C:153:TYR:O	1:C:156:ILE:HG22	2.09	0.53
1:E:214:LYS:HD2	1:E:216:ILE:HD11	1.89	0.53
1:A:148:GLY:O	1:A:151:GLU:HG2	2.09	0.53
1:A:182:ARG:HA	1:A:187:ASN:O	2.08	0.53
1:F:150:ARG:HH22	1:F:201:THR:HG22	1.71	0.52
1:B:150:ARG:HH12	1:B:201:THR:HG21	1.74	0.52
1:F:174:ILE:HG23	1:F:195:VAL:HG11	1.92	0.51
1:B:174:ILE:CD1	1:B:217:PHE:HE1	2.24	0.51
1:E:172:ILE:HG12	1:E:176:SER:HB3	1.92	0.51
1:E:189:PHE:CE2	1:E:191:LEU:HB2	2.42	0.51
1:F:174:ILE:O	1:F:177:ILE:HB	2.10	0.51
1:D:167:HIS:CD2	1:D:172:ILE:HD12	2.46	0.51
1:E:218:ASN:OD1	1:E:219:LEU:N	2.40	0.51
1:A:153:TYR:O	1:A:156:ILE:HG22	2.11	0.51
1:A:184:LEU:HD23	1:A:185:THR:HG23	1.93	0.51
1:C:210:SER:HB3	1:C:216:ILE:CD1	2.42	0.50
1:C:150:ARG:HH22	1:C:201:THR:HG22	1.77	0.50
1:F:167:HIS:ND1	1:F:167:HIS:N	2.59	0.49
1:C:176:SER:O	1:C:180:GLU:HG2	2.12	0.49
1:D:157:ASP:HB3	1:D:161:ARG:NH2	2.28	0.49
1:D:218:ASN:ND2	1:D:219:LEU:H	2.03	0.49
1:A:200:LEU:HD13	1:B:215:ARG:HD3	1.96	0.48
1:B:198:PHE:O	1:B:201:THR:HB	2.14	0.47
1:D:150:ARG:HH12	1:D:201:THR:HG22	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:VAL:O	1:A:198:PHE:HB3	2.14	0.47
1:D:183:LYS:O	1:D:183:LYS:HG2	2.13	0.47
1:F:157:ASP:O	1:F:161:ARG:HG3	2.14	0.47
1:B:193:ASP:OD2	1:F:151:GLU:HA	2.15	0.47
1:E:204:ASN:HA	1:E:220:LYS:HE3	1.97	0.47
1:D:150:ARG:NH2	1:D:198:PHE:CE1	2.83	0.47
1:B:173:THR:O	1:B:177:ILE:HG13	2.15	0.46
1:B:207:ALA:O	1:B:208:GLU:HB3	2.16	0.46
1:A:185:THR:OG1	1:A:187:ASN:HB2	2.16	0.46
1:C:156:ILE:HA	1:C:159:GLU:OE1	2.17	0.45
1:B:163:ILE:O	1:B:166:SER:HB3	2.16	0.45
1:B:157:ASP:O	1:B:161:ARG:HG3	2.16	0.45
1:C:201:THR:HG22	1:C:201:THR:O	2.16	0.45
1:B:165:LEU:HD12	1:B:165:LEU:HA	1.68	0.45
1:B:174:ILE:HD11	1:B:217:PHE:HE1	1.82	0.45
1:C:150:ARG:NH2	1:C:201:THR:HG22	2.32	0.45
1:E:153:TYR:CE2	1:E:190:PRO:HB2	2.52	0.45
1:C:156:ILE:HG23	1:C:157:ASP:N	2.32	0.45
1:A:197[B]:ASP:OD1	1:B:215:ARG:NH2	2.47	0.44
1:A:153:TYR:HA	1:A:154:PRO:HD3	1.84	0.44
1:B:152:GLU:CD	1:C:192:HIS:HB3	2.38	0.44
1:F:203:PRO:O	1:F:204:ASN:HB2	2.18	0.44
1:A:156:ILE:HG23	1:A:157:ASP:N	2.33	0.43
1:D:158:SER:HB3	1:D:161:ARG:NH1	2.33	0.43
1:F:166:SER:HB2	1:F:167:HIS:CE1	2.52	0.43
1:B:153:TYR:HE1	1:B:190:PRO:HB3	1.83	0.43
1:A:172:ILE:HD13	1:A:177:ILE:CG1	2.47	0.43
1:D:203:PRO:O	1:D:204:ASN:HB2	2.18	0.43
1:F:173:THR:O	1:F:177:ILE:HG13	2.18	0.43
1:C:206:THR:HG22	1:D:208:GLU:HB2	2.00	0.43
1:B:172:ILE:HD11	1:B:176:SER:C	2.38	0.43
1:D:196:THR:HG23	1:D:217:PHE:HZ	1.81	0.43
1:E:159:GLU:OE2	1:E:185:THR:HG21	2.19	0.43
1:A:182:ARG:O	1:A:186:GLY:N	2.52	0.42
1:C:218:ASN:OD1	1:C:219:LEU:N	2.43	0.42
1:E:164:LEU:O	1:E:168:ALA:N	2.52	0.42
1:A:156:ILE:HD13	1:A:190:PRO:HG3	2.01	0.42
1:F:215:ARG:HG2	1:F:217:PHE:CE1	2.55	0.42
1:C:173:THR:O	1:C:177:ILE:HG13	2.21	0.41
1:F:156:ILE:HG23	1:F:157:ASP:N	2.36	0.41
1:A:202:ILE:HB	1:A:205:VAL:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:GLY:O	2:D:301:GOL:H11	2.21	0.41
1:B:161:ARG:O	1:B:165:LEU:HB2	2.21	0.41
1:B:207:ALA:HA	1:B:216:ILE:O	2.20	0.41
1:E:209:CYS:HB2	1:F:200:LEU:O	2.21	0.41
1:A:197[B]:ASP:OD1	1:B:215:ARG:NH1	2.54	0.41
1:B:174:ILE:HG23	1:B:195:VAL:HG11	2.02	0.41
1:D:150:ARG:NH2	1:D:198:PHE:HE1	2.19	0.41
1:F:198:PHE:CZ	1:F:202:ILE:HD11	2.56	0.41
1:B:164:LEU:O	1:B:167:HIS:N	2.54	0.41
1:D:164:LEU:O	1:D:168:ALA:N	2.54	0.40
1:E:189:PHE:HA	1:E:190:PRO:HD2	1.89	0.40
1:F:172:ILE:HG12	1:F:173:THR:N	2.37	0.40
1:C:157:ASP:O	1:C:161:ARG:HG3	2.21	0.40
1:D:150:ARG:CZ	1:D:198:PHE:CE1	3.05	0.40
1:F:182:ARG:HD2	1:F:182:ARG:HA	1.55	0.40

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:D:169:GLN:NE2	1:E:152:GLU:OE1[2_434]	2.09	0.11

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	75/93 (81%)	70 (93%)	5 (7%)	0	100	100
1	B	72/93 (77%)	68 (94%)	4 (6%)	0	100	100
1	C	72/93 (77%)	66 (92%)	6 (8%)	0	100	100
1	D	71/93 (76%)	66 (93%)	4 (6%)	1 (1%)	11	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	68/93 (73%)	64 (94%)	4 (6%)	0	100	100
1	F	71/93 (76%)	65 (92%)	5 (7%)	1 (1%)	11	43
All	All	429/558 (77%)	399 (93%)	28 (6%)	2 (0%)	29	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	169	GLN
1	F	169	GLN

5.3.2 Protein sidechains [i](#)

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	69/84 (82%)	66 (96%)	3 (4%)	29	66
1	B	66/84 (79%)	59 (89%)	7 (11%)	6	26
1	C	66/84 (79%)	65 (98%)	1 (2%)	65	87
1	D	66/84 (79%)	59 (89%)	7 (11%)	6	26
1	E	63/84 (75%)	61 (97%)	2 (3%)	39	74
1	F	66/84 (79%)	63 (96%)	3 (4%)	27	64
All	All	396/504 (79%)	373 (94%)	23 (6%)	20	55

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	174	ILE
1	A	194	ASN
1	A	220	LYS
1	B	167	HIS
1	B	173	THR
1	B	179	SER
1	B	182	ARG
1	B	191	LEU

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Mol	Chain	Res	Type
1	B	192	HIS
1	B	219	LEU
1	C	209	CYS
1	D	158	SER
1	D	167	HIS
1	D	179	SER
1	D	192	HIS
1	D	195	VAL
1	D	209	CYS
1	D	218	ASN
1	E	158	SER
1	E	173	THR
1	F	167	HIS
1	F	182	ARG
1	F	219	LEU

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

Mol	Chain	Res	Type
1	D	218	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	A	301	-	5,5,5	0.36	0	5,5,5	0.24	0
2	GOL	D	301	-	5,5,5	0.36	0	5,5,5	0.24	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	301	-	-	2/4/4/4	-
2	GOL	D	301	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	GOL	O1-C1-C2-C3
2	D	301	GOL	O1-C1-C2-C3
2	A	301	GOL	O1-C1-C2-O2
2	D	301	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	301	GOL	1	0

5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [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	76/93 (81%)	-0.22	0	100	100	52, 85, 125, 153	0
1	B	74/93 (79%)	-0.21	0	100	100	57, 83, 147, 168	0
1	C	74/93 (79%)	-0.10	0	100	100	80, 121, 163, 173	3 (4%)
1	D	73/93 (78%)	0.00	3 (4%)	37	14	75, 118, 163, 186	0
1	E	70/93 (75%)	-0.07	0	100	100	88, 116, 160, 182	0
1	F	73/93 (78%)	-0.09	0	100	100	82, 119, 180, 207	2 (2%)
All	All	440/558 (78%)	-0.12	3 (0%)	87	69	52, 108, 163, 207	5 (1%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	191	LEU	3.8
1	D	192	HIS	2.7
1	D	189	PHE	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 monosaccharides 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(Å ²)	Q<0.9
2	GOL	D	301	6/6	0.83	0.16	141,142,143,143	0
2	GOL	A	301	6/6	0.88	0.15	103,108,108,108	0

6.5 Other polymers [i](#)

There are no such residues in this entry.