



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2018 – 11:47 am GMT

PDB ID : 3S2K  
Title : Structural basis of Wnt signaling inhibition by Dickkopf binding to LRP5/6.  
Authors : Ahn, V.E.; Chu, M.L.-H.; Choi, H.-J.; Tran, D.; Abo, A.; Weis, W.I.  
Deposited on : 2011-05-16  
Resolution : 2.80 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk31020  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk31020

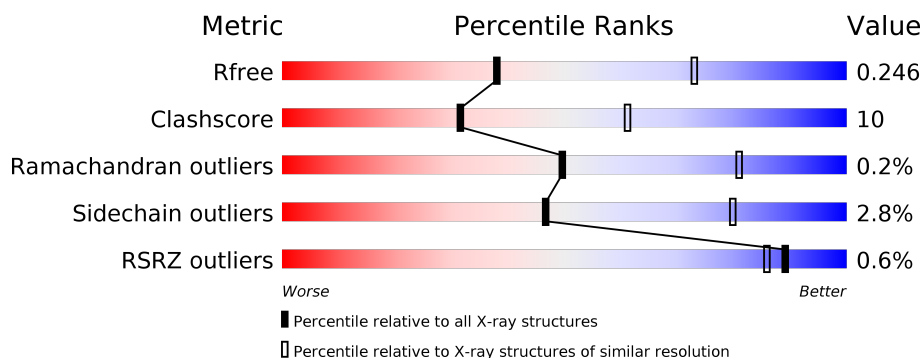
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	111664	2792 (2.80-2.80)
Clashscore	122126	3209 (2.80-2.80)
Ramachandran outliers	120053	3158 (2.80-2.80)
Sidechain outliers	120020	3160 (2.80-2.80)
RSRZ outliers	108989	2726 (2.80-2.80)

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  $\geq 3$ , 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	629	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 23%, green 72%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>72%</span> <span>23%</span> <span>• •</span> </div> </div>
1	B	629	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 21%, green 75%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>75%</span> <span>21%</span> <span>• •</span> </div> </div>
2	C	97	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 62%, yellow 15%, grey 22%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span></span> <span>62%</span> <span>15%</span> <span>•</span> <span>22%</span> </div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10613 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 Low-density lipoprotein receptor-related protein 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	610	Total	C	N	O	S	0	0	0
			4860	3050	860	925	25			
1	B	612	Total	C	N	O	S	0	0	0
			4873	3057	862	929	25			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	628	ALA	-	EXPRESSION TAG	UNP O75581
A	629	ASP	-	EXPRESSION TAG	UNP O75581
A	1062	ILE	VAL	SEE REMARK 999	UNP O75581
A	1247	HIS	-	EXPRESSION TAG	UNP O75581
A	1248	HIS	-	EXPRESSION TAG	UNP O75581
A	1249	HIS	-	EXPRESSION TAG	UNP O75581
A	1250	HIS	-	EXPRESSION TAG	UNP O75581
A	1251	HIS	-	EXPRESSION TAG	UNP O75581
A	1252	HIS	-	EXPRESSION TAG	UNP O75581
A	1253	HIS	-	EXPRESSION TAG	UNP O75581
A	1254	HIS	-	EXPRESSION TAG	UNP O75581
A	1255	HIS	-	EXPRESSION TAG	UNP O75581
A	1256	HIS	-	EXPRESSION TAG	UNP O75581
B	628	ALA	-	EXPRESSION TAG	UNP O75581
B	629	ASP	-	EXPRESSION TAG	UNP O75581
B	1062	ILE	VAL	SEE REMARK 999	UNP O75581
B	1247	HIS	-	EXPRESSION TAG	UNP O75581
B	1248	HIS	-	EXPRESSION TAG	UNP O75581
B	1249	HIS	-	EXPRESSION TAG	UNP O75581
B	1250	HIS	-	EXPRESSION TAG	UNP O75581
B	1251	HIS	-	EXPRESSION TAG	UNP O75581
B	1252	HIS	-	EXPRESSION TAG	UNP O75581
B	1253	HIS	-	EXPRESSION TAG	UNP O75581
B	1254	HIS	-	EXPRESSION TAG	UNP O75581
B	1255	HIS	-	EXPRESSION TAG	UNP O75581

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1256	HIS	-	EXPRESSION TAG	UNP O75581

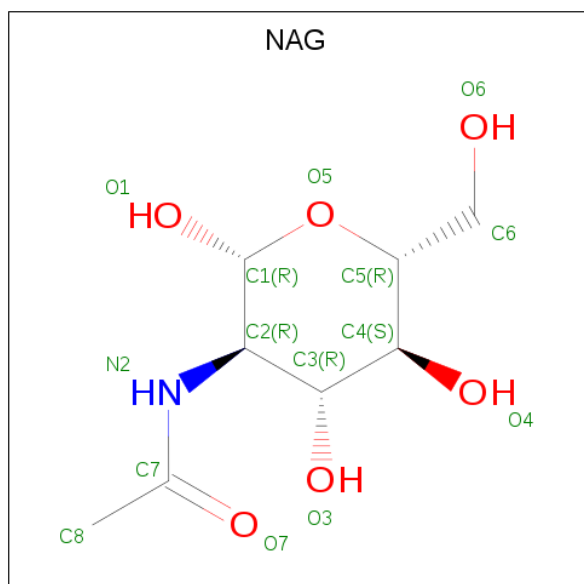
- Molecule 2 is a protein called Dickkopf-related protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	76	Total	C	N	O	S	0	0	0
			596	362	123	101	10			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	175	ALA	-	EXPRESSION TAG	UNP O94907
C	176	ASP	-	EXPRESSION TAG	UNP O94907
C	177	PRO	-	EXPRESSION TAG	UNP O94907
C	267	HIS	-	EXPRESSION TAG	UNP O94907
C	268	HIS	-	EXPRESSION TAG	UNP O94907
C	269	HIS	-	EXPRESSION TAG	UNP O94907
C	270	HIS	-	EXPRESSION TAG	UNP O94907
C	271	HIS	-	EXPRESSION TAG	UNP O94907

- Molecule 3 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is ALPHA-L-FUCOSE (three-letter code: FUC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	6	4		
4	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



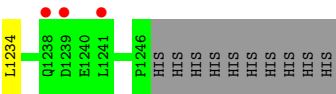
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is water.

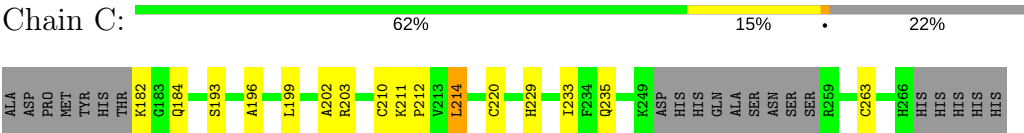
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	22	Total 22	O 22	0	0
6	B	30	Total 30	O 30	0	0
6	C	4	Total 4	O 4	0	0







● Molecule 2: Dickkopf-related protein 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	96.04Å 108.01Å 173.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.82 – 2.80 49.46 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (45.82-2.80) 99.7 (49.46-2.80)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.57 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.7.1 _743	Depositor
R, $R_{free}$	0.194 , 0.251 0.188 , 0.246	Depositor DCC
$R_{free}$ test set	2235 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	60.6	Xtriage
Anisotropy	0.178	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 42.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	10613	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, NAG, FUC

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	0.22	0/4963	0.40	0/6734
1	B	0.23	0/4976	0.42	0/6753
2	C	0.23	0/605	0.40	0/801
All	All	0.23	0/10544	0.41	0/14288

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	4860	0	4735	100	0
1	B	4873	0	4743	91	0
2	C	596	0	589	11	0
3	A	98	0	88	1	0
3	B	98	0	88	2	0
4	A	10	0	10	0	0
4	B	10	0	10	0	0
5	A	6	0	8	1	0
5	B	6	0	8	0	0
6	A	22	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	30	0	0	1	0
6	C	4	0	0	0	0
All	All	10613	0	10279	203	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 10.

All (203) 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:A:715:LEU:HD12	1:A:757:PRO:HB2	1.50	0.92
1:B:773:ILE:HB	1:B:787:VAL:HG13	1.57	0.86
1:B:628:ALA:N	1:B:884:SER:HG	1.76	0.82
1:A:723:ASP:HB3	1:A:726:THR:HG22	1.63	0.80
1:A:1145:LEU:HD12	1:A:1164:GLN:HG3	1.64	0.78
2:C:202:ALA:HB3	2:C:211:LYS:HD2	1.64	0.78
1:A:1206:PRO:HG2	1:A:1220:VAL:HG21	1.64	0.78
1:A:810:LEU:HB3	2:C:229:HIS:CE1	2.22	0.74
1:B:1058:ARG:HH11	1:B:1058:ARG:HG3	1.54	0.72
1:A:679:THR:HG22	1:A:686:ILE:HG12	1.73	0.69
1:A:1032:CYS:SG	1:A:1035:THR:HG22	2.32	0.69
1:A:730:GLU:OE1	1:A:739:ARG:HD3	1.94	0.67
1:A:902:HIS:CD2	1:A:929:CYS:HB2	2.30	0.66
1:B:869:ILE:HG22	1:B:870:GLN:HG2	1.76	0.66
2:C:199:LEU:HD23	2:C:212:PRO:HA	1.78	0.65
1:A:1220:VAL:HG13	1:A:1226:THR:HG22	1.79	0.65
1:A:634:LEU:HD21	1:A:879:ILE:HD11	1.78	0.63
1:A:1057:ASP:HA	1:A:1077:GLN:HG2	1.80	0.63
2:C:196:ALA:HB3	2:C:199:LEU:HD12	1.80	0.62
1:A:710:MET:HG2	1:A:711:ALA:N	2.13	0.62
1:A:1060:ARG:HG3	1:A:1076:LEU:HD12	1.82	0.62
1:B:1032:CYS:SG	1:B:1035:THR:HG22	2.40	0.61
1:A:1005:SER:HB3	1:A:1014:ILE:HB	1.83	0.61
1:A:715:LEU:HD13	1:A:891:ASN:HB2	1.82	0.60
1:A:699:VAL:HG12	1:A:700:VAL:HG23	1.83	0.60
1:A:1055:GLU:O	1:A:1056:GLN:HB3	2.00	0.60
1:A:1153:PHE:CD2	1:A:1154:GLU:HG2	2.36	0.60
1:A:1101:LEU:HD22	1:A:1104:PRO:HG3	1.84	0.59
1:A:771:PRO:HB2	1:A:790:VAL:O	2.02	0.59
1:B:669:PHE:HD2	1:B:880:LEU:HD11	1.67	0.59
1:A:838:LEU:HD12	1:A:846:TYR:O	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:936:LEU:HD21	1:B:1191:ILE:CG1	2.33	0.59
1:B:798:ILE:HG12	1:B:805:LEU:CD2	2.34	0.58
2:C:182:LYS:HE3	2:C:193:SER:O	2.03	0.58
1:A:1192:HIS:ND1	5:A:101:GOL:H12	2.19	0.58
1:A:907:VAL:HB	1:A:908:PRO:HD2	1.85	0.58
1:A:944:ILE:HG21	1:A:979:LEU:HD21	1.84	0.58
1:B:934:THR:HG22	1:B:1196:GLU:H	1.70	0.57
1:A:1160:ILE:HG22	1:A:1167:ILE:HG12	1.85	0.57
1:A:643:ARG:HH21	1:A:655:ALA:HB2	1.70	0.57
1:A:990:ARG:HG2	1:A:1001:THR:HG22	1.85	0.57
1:B:795:GLY:O	1:B:797:THR:HG22	2.04	0.57
1:B:1035:THR:HG23	1:B:1037:VAL:HG22	1.86	0.57
1:B:679:THR:HG22	1:B:686:ILE:HG12	1.87	0.56
1:A:1102:SER:OG	1:A:1122:ASP:HB2	2.06	0.56
1:B:1160:ILE:HD12	1:B:1188:LEU:HB3	1.88	0.56
1:A:814:LEU:HD13	1:A:816:GLU:HG3	1.88	0.56
1:B:629:ASP:OD1	1:B:630:PRO:HD3	2.06	0.56
1:B:747:LEU:HD22	1:B:750:PRO:HG3	1.87	0.56
1:B:715:LEU:HD12	1:B:757:PRO:HB2	1.87	0.56
1:B:1221:LYS:HE3	1:B:1227:ARG:CG	2.37	0.55
1:A:968:ARG:HG3	1:A:984:SER:OG	2.06	0.55
1:B:939:SER:HB2	1:B:967:VAL:HG21	1.89	0.55
1:B:1014:ILE:HG22	1:B:1016:PRO:HD3	1.89	0.54
1:B:1119:ALA:HB1	1:B:1147:PRO:HB2	1.89	0.54
1:B:1072:TYR:CE1	1:B:1085:ARG:HD3	2.42	0.54
1:A:1215:SER:HB2	1:A:1242:SER:HA	1.88	0.54
1:A:988:MET:HB2	1:A:1003:VAL:O	2.08	0.54
1:B:880:LEU:HD23	1:B:880:LEU:C	2.28	0.54
1:B:646:SER:HB2	1:B:651:ASN:HD22	1.74	0.53
1:A:1002:VAL:HG22	1:A:1003:VAL:HG23	1.90	0.53
1:B:1114:GLY:HA2	1:B:1131:LEU:HD22	1.89	0.53
1:B:744:TRP:CE2	1:B:955:PRO:HD3	2.43	0.53
1:A:1110:ASP:OD1	1:A:1113:LEU:HG	2.09	0.53
1:A:1215:SER:HG	1:A:1216:HIS:CE1	2.27	0.53
1:B:773:ILE:HB	1:B:787:VAL:CG1	2.36	0.53
1:B:703:GLY:HA2	1:B:958:ILE:HD12	1.91	0.53
2:C:214:LEU:HD23	2:C:220:CYS:HB3	1.91	0.53
1:B:1200:GLN:HE22	1:B:1204:GLN:HE21	1.55	0.52
1:B:1125:ARG:HD2	6:B:10:HOH:O	2.09	0.52
1:B:669:PHE:CD2	1:B:880:LEU:HD11	2.45	0.52
1:B:937:LEU:O	1:B:1192:HIS:N	2.39	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:859:ASN:HB3	1:B:862:SER:HB3	1.93	0.51
1:A:986:GLN:HG3	1:A:990:ARG:NH2	2.26	0.51
1:A:726:THR:HG23	1:A:728:ARG:HG3	1.93	0.51
1:A:634:LEU:HD11	1:A:879:ILE:HG12	1.92	0.51
1:A:699:VAL:HG13	1:A:736:GLY:CA	2.41	0.51
1:B:1001:THR:CG2	1:B:1004:VAL:HG22	2.40	0.51
1:A:1029:TYR:OH	1:A:1088:LEU:HB3	2.11	0.50
1:B:1221:LYS:HE3	1:B:1227:ARG:HG2	1.93	0.50
1:A:1182:GLN:HB3	1:A:1185:ILE:HD11	1.94	0.49
1:A:908:PRO:O	1:A:909:VAL:HG12	2.12	0.49
1:A:988:MET:SD	1:A:990:ARG:NE	2.86	0.49
1:A:1040:VAL:HG13	1:A:1048:VAL:HB	1.93	0.49
1:B:722:ALA:HB1	1:B:750:PRO:HB2	1.94	0.49
1:B:1071:MET:HB3	1:B:1088:LEU:HD23	1.95	0.48
1:B:964:LEU:HD22	1:B:967:VAL:HG12	1.95	0.48
1:A:1014:ILE:HG22	1:A:1016:PRO:HD3	1.93	0.48
1:B:1159:TRP:HZ3	1:B:1170:ILE:HG23	1.78	0.48
1:B:751:ARG:HG2	1:B:767:TRP:CZ2	2.48	0.48
1:A:1051:VAL:O	1:A:1090:GLY:HA3	2.13	0.48
1:A:814:LEU:CD1	1:A:816:GLU:HG3	2.43	0.48
1:B:1026:ARG:O	1:B:1043:LEU:HD13	2.14	0.48
1:A:673:ASP:OD2	1:A:675:ARG:HD2	2.14	0.48
1:B:629:ASP:N	1:B:630:PRO:CD	2.77	0.48
1:B:635:LEU:HB2	1:B:880:LEU:HD22	1.95	0.48
1:B:1050:VAL:HG12	1:B:1232:MET:HG3	1.95	0.48
1:A:1030:TRP:CE2	1:A:1039:ASN:HB3	2.49	0.48
1:A:805:LEU:O	1:A:817:SER:HA	2.13	0.47
1:B:1051:VAL:O	1:B:1090:GLY:HA3	2.14	0.47
1:B:936:LEU:HD21	1:B:1191:ILE:HD11	1.95	0.47
1:B:1005:SER:HB2	1:B:1014:ILE:HB	1.96	0.47
1:B:1198:ASN:HB3	1:B:1201:GLU:HB3	1.95	0.47
1:B:699:VAL:HG13	1:B:736:GLY:CA	2.44	0.47
1:A:635:LEU:HB2	1:A:880:LEU:HD23	1.95	0.47
1:B:857:ARG:HG2	1:B:869:ILE:HD11	1.96	0.47
1:A:1159:TRP:HZ3	1:A:1170:ILE:HG23	1.79	0.47
1:B:1233:HIS:CE1	1:B:1234:LEU:HG	2.50	0.47
1:B:1027:TYR:CE1	1:B:1042:ARG:HG2	2.50	0.47
1:B:1160:ILE:HG22	1:B:1167:ILE:HG12	1.95	0.47
1:A:986:GLN:HG3	1:A:990:ARG:HH22	1.80	0.47
1:A:721:TRP:CE2	1:A:730:GLU:HB2	2.49	0.47
1:B:748:ASP:OD2	1:B:768:GLY:HA3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1004:VAL:HG12	1:A:1005:SER:N	2.29	0.46
1:A:634:LEU:O	1:A:644:ARG:HA	2.16	0.46
1:B:1058:ARG:HG3	1:B:1058:ARG:NH1	2.25	0.46
1:A:1206:PRO:HG2	1:A:1220:VAL:CG2	2.42	0.46
1:A:1157:LEU:HD23	1:A:1170:ILE:HD11	1.96	0.46
2:C:214:LEU:HB3	2:C:263:CYS:SG	2.56	0.46
1:A:1004:VAL:HG12	1:A:1005:SER:H	1.81	0.46
1:A:1025:SER:O	1:A:1026:ARG:HB2	2.16	0.46
2:C:184:GLN:O	2:C:210:CYS:HB2	2.16	0.46
1:B:1206:PRO:HB2	1:B:1226:THR:HG21	1.97	0.46
3:B:2865:NAG:O7	3:B:2865:NAG:H3	2.15	0.46
1:A:931:ALA:HB1	1:A:932:PRO:HD2	1.98	0.45
1:B:1001:THR:HG21	1:B:1004:VAL:HG22	1.98	0.45
1:B:1062:ILE:HG13	1:B:1063:VAL:N	2.32	0.45
1:B:850:TRP:CH2	2:C:233:ILE:HD13	2.51	0.45
1:B:959:LEU:HA	1:B:960:PRO:HD3	1.80	0.45
1:A:1159:TRP:CZ3	1:A:1170:ILE:HG23	2.52	0.45
1:A:939:SER:HB2	1:A:967:VAL:HG21	1.99	0.45
1:B:1017:TYR:CE2	1:B:1060:ARG:HB3	2.51	0.45
1:B:1102:SER:HB3	1:B:1122:ASP:HB2	1.97	0.45
1:B:699:VAL:HG12	1:B:700:VAL:HG23	1.97	0.45
1:A:1060:ARG:HG3	1:A:1076:LEU:CD1	2.46	0.45
1:B:686:ILE:HG21	1:B:719:LEU:HD21	1.98	0.45
1:B:843:ASP:OD1	1:B:843:ASP:N	2.49	0.45
1:A:1245:GLU:HA	1:A:1246:PRO:HD3	1.86	0.45
1:B:991:LYS:O	1:B:999:GLY:HA2	2.17	0.45
3:B:2859:NAG:O7	3:B:2859:NAG:H3	2.16	0.45
1:A:1038:ILE:HD12	1:A:1052:LEU:HD13	1.99	0.44
1:A:839:THR:HG22	1:A:846:TYR:HB2	1.98	0.44
1:A:1057:ASP:HB2	1:A:1075:ASN:HD21	1.81	0.44
1:A:775:ARG:HG2	1:A:776:ALA:N	2.32	0.44
1:A:963:SER:HA	1:A:965:ARG:NH1	2.32	0.44
1:B:832:LEU:CB	1:B:835:PRO:HG3	2.47	0.44
1:A:1205:HIS:CE1	1:A:1207:CYS:HB3	2.53	0.44
1:B:739:ARG:HG3	1:B:740:GLN:N	2.31	0.44
1:B:787:VAL:HA	1:B:788:PRO:HD3	1.65	0.44
1:A:751:ARG:HG3	1:A:767:TRP:CD1	2.53	0.44
1:A:891:ASN:HD21	1:A:906:ALA:HB2	1.83	0.44
1:A:934:THR:HG22	1:A:1153:PHE:CZ	2.53	0.43
1:A:813:ASN:OD1	1:A:835:PRO:HD2	2.18	0.43
1:A:744:TRP:CE2	1:A:955:PRO:HD3	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:681:ILE:HG22	1:B:707:PRO:HD2	1.99	0.43
1:B:814:LEU:HD13	1:B:816:GLU:HG3	2.00	0.43
1:A:1157:LEU:O	1:A:1169:LYS:HA	2.18	0.43
1:B:628:ALA:HB1	1:B:630:PRO:HD2	1.99	0.43
1:A:1077:GLN:HB2	1:A:1080:SER:O	2.19	0.43
1:A:978:GLN:OE1	1:A:991:LYS:HE2	2.18	0.43
1:B:1064:VAL:C	1:B:1066:PRO:HD3	2.38	0.43
1:A:939:SER:HB3	1:A:970:ILE:HD13	2.00	0.43
1:B:1206:PRO:HB2	1:B:1226:THR:CG2	2.48	0.43
1:B:901:SER:CB	1:B:928:THR:HA	2.49	0.43
1:A:1150:LEU:HD23	1:A:1159:TRP:HB3	1.99	0.43
1:B:847:TRP:HH2	1:B:866:ARG:HD2	1.84	0.43
2:C:203:ARG:HG2	2:C:235:GLN:OE1	2.18	0.43
3:A:3039:NAG:O7	3:A:3039:NAG:H3	2.18	0.43
1:B:1030:TRP:CE2	1:B:1039:ASN:HB3	2.54	0.43
1:B:859:ASN:CB	1:B:862:SER:HB3	2.49	0.42
1:A:1027:TYR:HE1	1:A:1029:TYR:HE2	1.66	0.42
1:B:684:LYS:NZ	1:B:705:ASP:O	2.50	0.42
1:A:1055:GLU:O	1:A:1056:GLN:CB	2.67	0.42
1:A:798:ILE:HG23	1:A:820:MET:CE	2.49	0.42
1:A:848:THR:HG22	1:A:855:ILE:HG12	2.00	0.42
1:B:1161:ASP:HB3	1:B:1164:GLN:HB2	2.02	0.42
1:B:1166:MET:HE3	1:B:1166:MET:HB2	1.94	0.42
1:B:1072:TYR:CZ	1:B:1085:ARG:HD3	2.55	0.42
1:B:1035:THR:O	1:B:1037:VAL:HG13	2.19	0.42
1:B:805:LEU:O	1:B:817:SER:HA	2.20	0.42
1:A:936:LEU:HD23	1:A:1193:ALA:HA	2.01	0.42
1:B:1066:PRO:HA	1:B:1088:LEU:HD11	2.02	0.42
1:B:635:LEU:HB2	1:B:880:LEU:CD2	2.50	0.42
1:A:1144:ILE:CG2	1:A:1147:PRO:HG3	2.50	0.41
1:B:991:LYS:HE3	1:B:1000:PHE:HB3	2.01	0.41
1:B:1041:THR:HG22	1:B:1042:ARG:O	2.20	0.41
1:A:1156:TRP:CH2	1:A:1176:GLU:HB3	2.55	0.41
1:A:786:LEU:HD12	1:A:786:LEU:HA	1.94	0.41
1:B:1036:ASN:ND2	1:B:1058:ARG:HG2	2.35	0.41
1:A:979:LEU:O	1:A:991:LYS:HA	2.21	0.41
1:A:656:ILE:HA	1:A:657:PRO:HD3	1.91	0.41
1:A:935:PHE:HB3	1:A:948:VAL:HG12	2.02	0.41
1:A:710:MET:CG	1:A:711:ALA:N	2.82	0.41
1:A:1025:SER:HB3	1:A:1027:TYR:CE2	2.56	0.41
1:A:636:PHE:CE2	1:A:643:ARG:HB2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:919:HIS:HB2	1:A:946:ARG:HH21	1.86	0.41
1:B:838:LEU:HD12	1:B:846:TYR:O	2.21	0.40
1:B:763:TYR:CE1	1:B:775:ARG:HG3	2.56	0.40
1:A:762:MET:HB3	1:A:778:MET:HG2	2.03	0.40
1:A:991:LYS:NZ	1:A:998:GLN:O	2.51	0.40
1:B:1002:VAL:HG22	1:B:1003:VAL:HG23	2.02	0.40
2:C:199:LEU:HD23	2:C:212:PRO:CA	2.47	0.40
1:A:959:LEU:HA	1:A:960:PRO:HD3	1.77	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	606/629 (96%)	553 (91%)	51 (8%)	2 (0%)	43	75
1	B	608/629 (97%)	565 (93%)	42 (7%)	1 (0%)	49	81
2	C	72/97 (74%)	67 (93%)	5 (7%)	0	100	100
All	All	1286/1355 (95%)	1185 (92%)	98 (8%)	3 (0%)	49	81

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	909	VAL
1	A	1056	GLN
1	B	657	PRO

### 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	532/550 (97%)	518 (97%)	14 (3%)	49	81
1	B	533/550 (97%)	516 (97%)	17 (3%)	42	76
2	C	66/85 (78%)	65 (98%)	1 (2%)	67	91
All	All	1131/1185 (95%)	1099 (97%)	32 (3%)	47	80

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	726	THR
1	A	734	LEU
1	A	820	MET
1	A	880	LEU
1	A	909	VAL
1	A	949	ILE
1	A	968	ARG
1	A	991	LYS
1	A	1002	VAL
1	A	1027	TYR
1	A	1082	LYS
1	A	1125	ARG
1	A	1140	GLU
1	A	1197	LEU
1	B	634	LEU
1	B	683	LEU
1	B	739	ARG
1	B	787	VAL
1	B	797	THR
1	B	814	LEU
1	B	880	LEU
1	B	1002	VAL
1	B	1004	VAL
1	B	1026	ARG
1	B	1040	VAL
1	B	1062	ILE
1	B	1096	LEU
1	B	1125	ARG
1	B	1128	SER
1	B	1131	LEU

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Mol	Chain	Res	Type
1	B	1197	LEU
2	C	214	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1204	GLN
2	C	229	HIS

### 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 ⓘ

18 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	$\# Z  > 2$
5	GOL	A	101	-	5,5,5	0.36	0	5,5,5	0.27	0
3	NAG	A	2692	1,3,4	14,14,15	0.51	0	17,19,21	0.80	1 (5%)
3	NAG	A	2693	3	14,14,15	0.50	0	17,19,21	0.69	0
4	FUC	A	2694	3	9,10,11	0.67	0	13,14,16	0.63	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	A	2859	1	14,14,15	0.52	0	17,19,21	0.90	1 (5%)
3	NAG	A	2865	1	14,14,15	0.46	0	17,19,21	0.84	1 (5%)
3	NAG	A	2926	1	14,14,15	0.46	0	17,19,21	0.77	1 (5%)
3	NAG	A	3039	1,3	14,14,15	0.47	0	17,19,21	1.20	2 (11%)
3	NAG	A	3040	3	14,14,15	0.49	0	17,19,21	0.71	0
5	GOL	B	102	-	5,5,5	0.38	0	5,5,5	0.20	0
3	NAG	B	2692	1,3,4	14,14,15	0.49	0	17,19,21	0.78	1 (5%)
3	NAG	B	2693	3	14,14,15	0.48	0	17,19,21	0.75	0
4	FUC	B	2694	3	9,10,11	0.63	0	13,14,16	0.63	0
3	NAG	B	2859	1	14,14,15	0.48	0	17,19,21	0.90	0
3	NAG	B	2865	1	14,14,15	0.45	0	17,19,21	0.95	0
3	NAG	B	2926	1	14,14,15	0.47	0	17,19,21	0.72	1 (5%)
3	NAG	B	3039	1,3	14,14,15	0.49	0	17,19,21	1.32	2 (11%)
3	NAG	B	3040	3	14,14,15	0.47	0	17,19,21	0.76	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	A	101	-	-	0/4/4/4	0/0/0/0
3	NAG	A	2692	1,3,4	-	0/6/23/26	0/1/1/1
3	NAG	A	2693	3	-	0/6/23/26	0/1/1/1
4	FUC	A	2694	3	-	0/0/17/20	0/1/1/1
3	NAG	A	2859	1	-	0/6/23/26	0/1/1/1
3	NAG	A	2865	1	-	0/6/23/26	0/1/1/1
3	NAG	A	2926	1	-	0/6/23/26	0/1/1/1
3	NAG	A	3039	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	3040	3	-	0/6/23/26	0/1/1/1
5	GOL	B	102	-	-	0/4/4/4	0/0/0/0
3	NAG	B	2692	1,3,4	-	0/6/23/26	0/1/1/1
3	NAG	B	2693	3	-	0/6/23/26	0/1/1/1
4	FUC	B	2694	3	-	0/0/17/20	0/1/1/1
3	NAG	B	2859	1	-	0/6/23/26	0/1/1/1
3	NAG	B	2865	1	-	0/6/23/26	0/1/1/1
3	NAG	B	2926	1	-	0/6/23/26	0/1/1/1
3	NAG	B	3039	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	3040	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	3039	NAG	O5-C1-C2	-2.31	108.34	111.52
3	B	3039	NAG	O5-C1-C2	-2.18	108.51	111.52
3	A	2926	NAG	C1-O5-C5	2.02	114.96	112.19
3	B	2926	NAG	C1-O5-C5	2.07	115.03	112.19
3	A	2865	NAG	C1-O5-C5	2.21	115.22	112.19
3	A	2692	NAG	O5-C5-C6	2.26	110.73	107.15
3	B	2692	NAG	O5-C5-C6	2.50	111.10	107.15
3	A	3039	NAG	C1-O5-C5	2.61	115.78	112.19
3	A	2859	NAG	C1-O5-C5	3.10	116.46	112.19
3	B	3039	NAG	C1-O5-C5	3.14	116.51	112.19

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	101	GOL	1	0
3	A	3039	NAG	1	0
3	B	2859	NAG	1	0
3	B	2865	NAG	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	610/629 (96%)	-0.29	4 (0%) 87 83	38, 61, 102, 132	0
1	B	612/629 (97%)	-0.34	4 (0%) 87 83	31, 51, 89, 125	0
2	C	76/97 (78%)	-0.36	0 100 100	35, 56, 93, 106	0
All	All	1298/1355 (95%)	-0.32	8 (0%) 89 86	31, 56, 97, 132	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1078	GLU	3.4
1	B	1238	GLN	3.0
1	B	1241	LEU	2.6
1	A	1079	ARG	2.5
1	B	1239	ASP	2.5
1	A	1005	SER	2.4
1	A	1000	PHE	2.4
1	B	1005	SER	2.2

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	NAG	B	2693	14/15	0.68	0.31	110,138,145,145	0
3	NAG	B	2926	14/15	0.76	0.17	80,98,117,119	0
5	GOL	A	101	6/6	0.79	0.28	97,103,106,107	0
3	NAG	B	2865	14/15	0.82	0.32	88,121,132,135	0
5	GOL	B	102	6/6	0.84	0.20	71,77,84,88	0
3	NAG	A	2693	14/15	0.84	0.27	145,150,158,160	0
3	NAG	A	3040	14/15	0.85	0.42	94,129,143,149	0
3	NAG	A	2865	14/15	0.85	0.26	61,97,103,104	0
3	NAG	A	2926	14/15	0.87	0.17	93,101,105,106	0
3	NAG	A	3039	14/15	0.87	0.21	70,89,106,113	0
4	FUC	B	2694	10/11	0.88	0.21	93,105,124,129	0
4	FUC	A	2694	10/11	0.88	0.23	127,135,140,144	0
3	NAG	B	2859	14/15	0.90	0.25	64,86,102,107	0
3	NAG	B	3040	14/15	0.90	0.31	67,95,102,102	0
3	NAG	B	3039	14/15	0.90	0.22	62,81,99,100	0
3	NAG	A	2859	14/15	0.91	0.26	76,88,92,93	0
3	NAG	A	2692	14/15	0.92	0.16	80,94,109,132	0
3	NAG	B	2692	14/15	0.95	0.17	61,85,98,118	0

## 6.5 Other polymers

There are no such residues in this entry.