



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2016 – 04:11 PM EDT

PDB ID : 5L5G
Title : Plexin A2 full extracellular region, domains 1 to 8 modeled, data to 10 angstrom
Authors : Janssen, B.J.C.; Kong, Y.; Malinauskas, T.; Vangoor, V.R.; Coles, C.H.; Kaufmann, R.; Ni, T.; Gilbert, R.J.C.; Padilla-Parra, S.; Pasterkamp, R.J.; Jones, E.Y.
Deposited on : 2016-05-28
Resolution : 10.00 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

<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	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027939
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)	:	rb-20027939

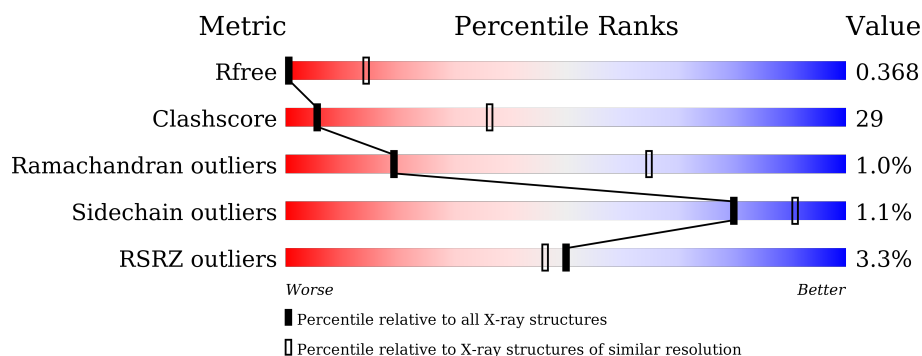
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 10.00 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}	91344	1015 (11.50-3.66)
Clashscore	102246	1065 (15.00-3.70)
Ramachandran outliers	100387	1036 (11.50-3.66)
Sidechain outliers	100360	1006 (11.50-3.66)
RSRZ outliers	91569	1014 (11.50-3.66)

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	1212	<div> <div>5%</div> <div> <div></div> <div>51%</div> <div>23%</div> <div>•</div> <div>25%</div> </div> </div>
1	B	1212	<div> <div>3%</div> <div> <div></div> <div>47%</div> <div>19%</div> <div>•</div> <div>33%</div> </div> </div>
1	C	1212	<div> <div>%</div> <div> <div></div> <div>53%</div> <div>27%</div> <div>•</div> <div>18%</div> </div> </div>
1	D	1212	<div> <div>%</div> <div> <div></div> <div>54%</div> <div>27%</div> <div>•</div> <div>18%</div> </div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 28787 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 Plexin-A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	906	Total	C	N	O	S	0	0	0
			7060	4461	1214	1333	52			
1	B	809	Total	C	N	O	S	0	0	0
			6337	4004	1092	1195	46			
1	C	993	Total	C	N	O	S	0	0	0
			7695	4856	1321	1462	56			
1	D	993	Total	C	N	O	S	0	0	0
			7695	4856	1321	1462	56			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	32	GLU	-	expression tag	UNP P70207
A	1232	GLY	-	expression tag	UNP P70207
A	1233	GLY	-	expression tag	UNP P70207
A	1234	SER	-	expression tag	UNP P70207
A	1235	ARG	-	expression tag	UNP P70207
A	1236	THR	-	expression tag	UNP P70207
A	1237	LYS	-	expression tag	UNP P70207
A	1238	HIS	-	expression tag	UNP P70207
A	1239	HIS	-	expression tag	UNP P70207
A	1240	HIS	-	expression tag	UNP P70207
A	1241	HIS	-	expression tag	UNP P70207
A	1242	HIS	-	expression tag	UNP P70207
A	1243	HIS	-	expression tag	UNP P70207
B	32	GLU	-	expression tag	UNP P70207
B	1232	GLY	-	expression tag	UNP P70207
B	1233	GLY	-	expression tag	UNP P70207
B	1234	SER	-	expression tag	UNP P70207
B	1235	ARG	-	expression tag	UNP P70207
B	1236	THR	-	expression tag	UNP P70207
B	1237	LYS	-	expression tag	UNP P70207
B	1238	HIS	-	expression tag	UNP P70207

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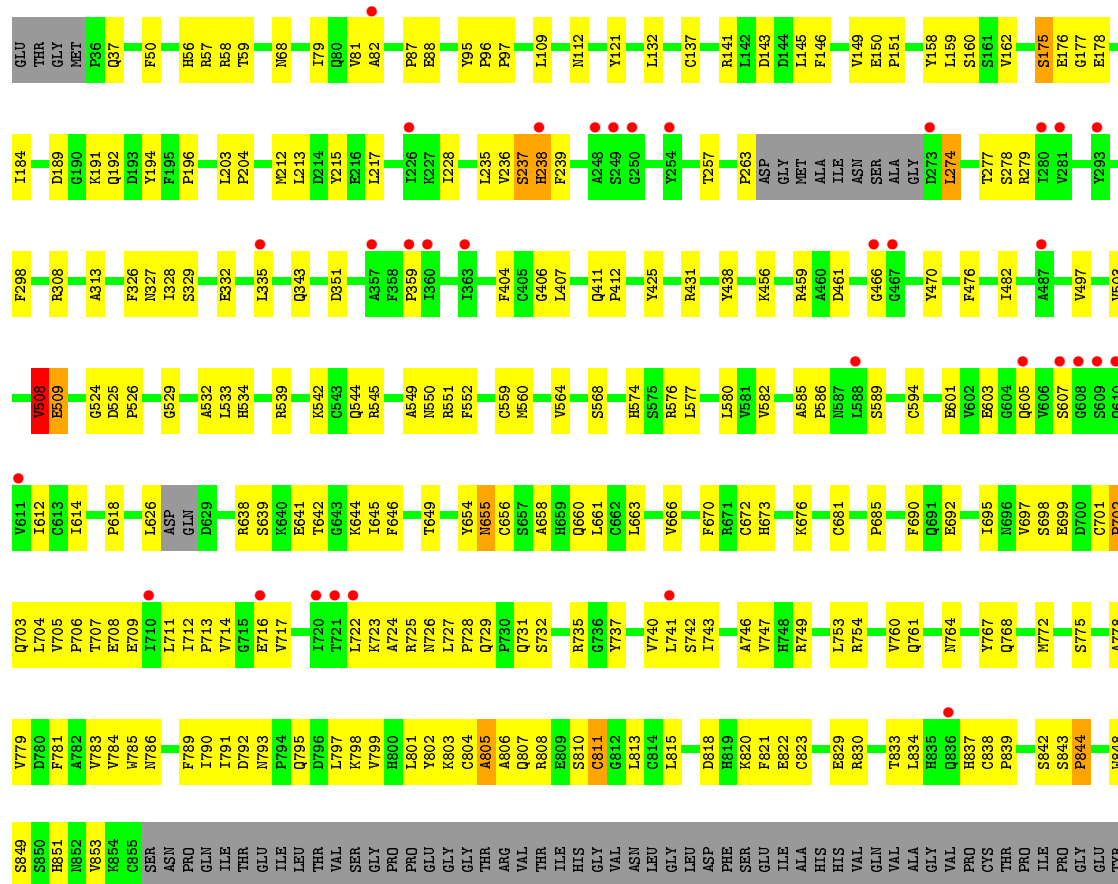
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Chain	Residue	Modelled	Actual	Comment	Reference
B	1239	HIS	-	expression tag	UNP P70207
B	1240	HIS	-	expression tag	UNP P70207
B	1241	HIS	-	expression tag	UNP P70207
B	1242	HIS	-	expression tag	UNP P70207
B	1243	HIS	-	expression tag	UNP P70207
C	32	GLU	-	expression tag	UNP P70207
C	1232	GLY	-	expression tag	UNP P70207
C	1233	GLY	-	expression tag	UNP P70207
C	1234	SER	-	expression tag	UNP P70207
C	1235	ARG	-	expression tag	UNP P70207
C	1236	THR	-	expression tag	UNP P70207
C	1237	LYS	-	expression tag	UNP P70207
C	1238	HIS	-	expression tag	UNP P70207
C	1239	HIS	-	expression tag	UNP P70207
C	1240	HIS	-	expression tag	UNP P70207
C	1241	HIS	-	expression tag	UNP P70207
C	1242	HIS	-	expression tag	UNP P70207
C	1243	HIS	-	expression tag	UNP P70207
D	32	GLU	-	expression tag	UNP P70207
D	1232	GLY	-	expression tag	UNP P70207
D	1233	GLY	-	expression tag	UNP P70207
D	1234	SER	-	expression tag	UNP P70207
D	1235	ARG	-	expression tag	UNP P70207
D	1236	THR	-	expression tag	UNP P70207
D	1237	LYS	-	expression tag	UNP P70207
D	1238	HIS	-	expression tag	UNP P70207
D	1239	HIS	-	expression tag	UNP P70207
D	1240	HIS	-	expression tag	UNP P70207
D	1241	HIS	-	expression tag	UNP P70207
D	1242	HIS	-	expression tag	UNP P70207
D	1243	HIS	-	expression tag	UNP P70207

HIS
HIS

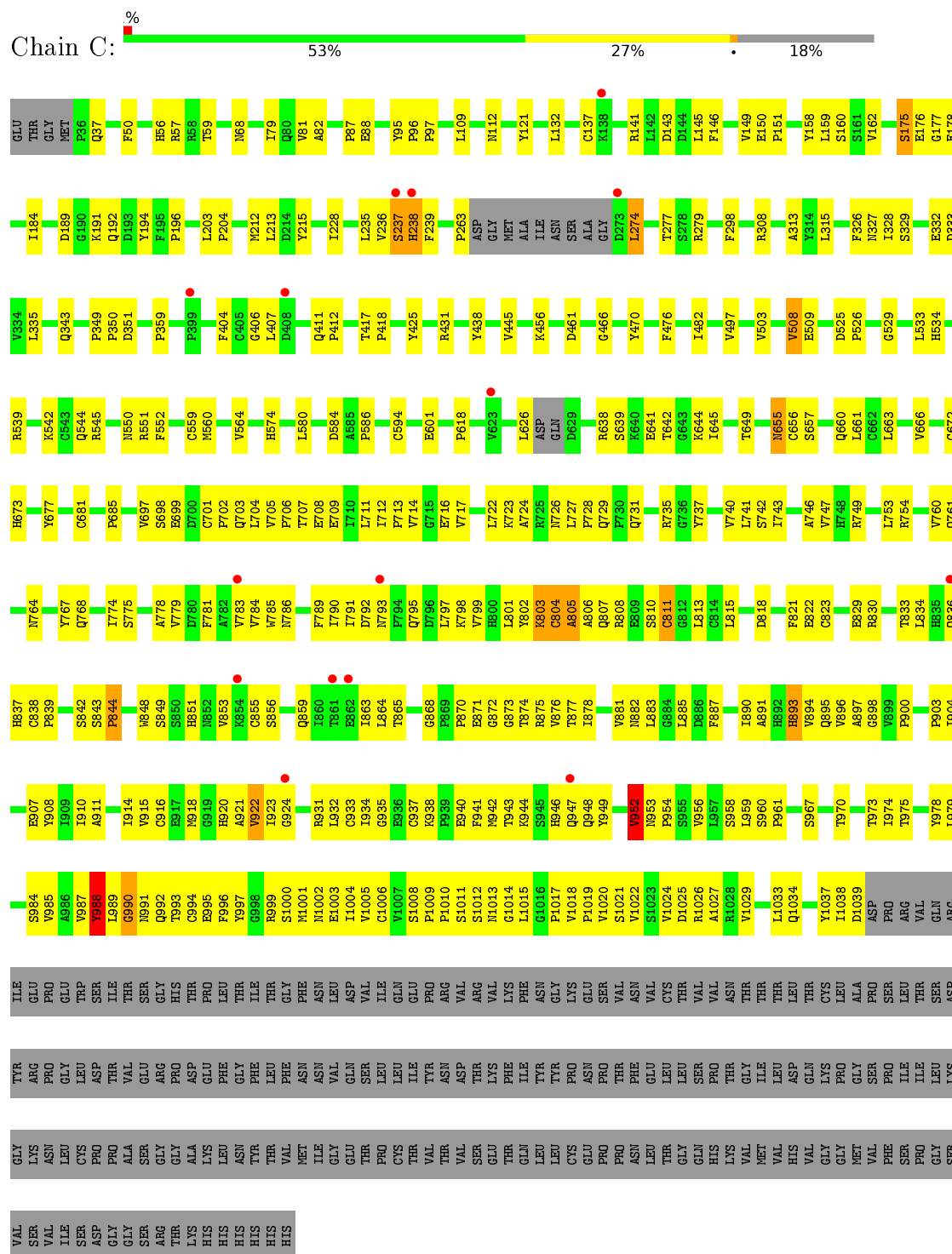
- Molecule 1: Plexin-A2

Chain B: 



GLN
HIS
LYS
VAL
MET
VAL
HIS
VAL
GLY
GLY
MET
VAL
PHE
SER
PRO
GLY
GLY
VAL
SER
VAL
ILE
SER
ASP
GLY
GLY
SER
ARG
THR
LYS
HIS
HIS
HIS
HIS

• Molecule 1: Plexin-A2



GLY	SER	LEU	SER	GLN	T975	P903	E829	V747	Q660	G529	S329	E176	GLU
VAL	ASP	LYS	TYR	ARG	Y978	P904	R830	H748	L661	L533	S332	G177	THR
VAL	ARG	GLY	ARG	ILE	Y979		R830	R749	G662	D833	D333	E178	MET
ILE	PRO	ASN	PRO	PRO	G980	E907	T833	L753	L663	H534	V334	I184	P36
SER	LEU	GLY	GLY	TRP	A981	Y908	L834	R754	V666	B539	L335	Q37	
ASP	SER	CYS	LEU										
PRO	ASP	PRO	ASP		S984	I910	H837	V760	F670	K542	Q343	D189	F50
GLY	THR	PRO	THR	ILE	V985	A911	C838	Q761	H671	C543		G190	
ALA	VAL	ALA	VAL	THR	A986		P839	Q544	H673	D544	D851	K191	H56
SER	GLU	SER	GLU	SER	V987	I914		N764	H673	H545		Q192	R57
THR	ARG	GLY	ARG	GLY	V915	G916	S842	Y767	C681	N550	P359	F194	R58
GLY	PRO	GLY	PRO	HIS	C916	E917	S843	Q768	H682	R551	F404	F195	T59
LYS	ASP	ALA	ASP	THR	G990	M918	P844		H683	F552	C405	P196	
HIS	GLU	LYS	GLU	PRO	Q992	N918	W848	S775	D684		G406	L203	
HIS	LEU	ASN	GLY	LEU	T993	H920	S849	A782	P685	C559	L407	P204	
HIS	THR	TYR	THR	ILE	C994	A921	S850	D780	P685	N560			
HIS	LEU	THR	LEU	THR	E995	W922	H851	V779	V697	V564	Q411	N212	Q90
HIS	PHE	VAL	PHE	GLY	F996	I923	H852	D780	S698		P412	L213	V81
	ASN	ILE	ASN	PHE	Y997	G924	H853	A782	E699	S570		D214	A82
	ASN	ILE	ASN	ASN	G998		K854	V783	C701		Y425	Y215	H83
	VAL	GLY	VAL	LEU	R999	R931	C855	W784	D700	H574	R431	I228	P87
	GLN	GLU	GLN	ASP	S1000	L932	Q859	Q703	C701				E88
	VAL	THR	SER	VAL	M1001	C933		L704	Q703	L580	Y438	L285	Y95
	LEU	PRO	LEU	ILE	I934	I934		N786	L704	V581	V439	V236	P96
	GLN	CYS	LEU	GLN	G935	G935	T863	F789	V705	V582	Y440	S237	P97
	ILE	THR	ILE	GLU	E936	E936	L864	W790	F706			H238	
	VAL	VAL	VAL	PRO	I1004	C937	T865	I791	T707	A585	Y443	F239	L109
	THR	THR	THR	ARG	V1005	K938		E708	E708		S444		
	VAL	VAL	VAL	ASN	C1006		G868	D792	E709	P586	V445		
	ASP	VAL	ASP	VAL	V1007	P939	P869	N793	T710			P283	N112
	THR	SER	THR	ARG	E940	E940	P870	F794	L711	C594		ASP	
	LYS	GLU	LYS	VAL	F941	F941	E871	D796	F713		K456	GLY	Y121
	THR	THR	THR	PHE	N942	N942		D796	P713	B601	R459	MET	
	ILE	GLN	ILE	PHE	T943	T943	T874	L797	V714		I460	ALA	L132
	TYR	LEU	TYR	ASN	K944	K944	R875	K798	G715	G605	D461	ILE	
	GLY	LEU	TYR	ASN	S945	S945	R876	V799	E716			ASN	G137
	LYS	CYS	PRO	LYS	H946	H946	T877	H900	W717	P618	G466	SER	
	ASN	GLU	ASN	GLU	Q947	Q947	T878	L801		K619		ALA	R141
	PRO	PRO	PRO	SER	Q948	Q948		Y802	L722	L626	Y470	GLY	D143
	THR	THR	THR	VAL	Y949	Y949	V881	K803	K723	ASP		D273	
	VAL	VAL	VAL	VAL			N882	C804	A724	GLN	F476	L274	D144
	GLY	CYS	CYS	CYS	N953	N953	L883	A805					L145
	THR	THR	THR	THR	P954	P954	G884	A806	L727	D629	I482	T277	F146
	LEU	LEU	LEU	LEU	P955	P955	L885	Q807	Q728	H630		S278	I147
	SER	VAL	VAL	VAL	V956	V956	D886	R808	Q729		V497	R279	L148
	PRO	VAL	VAL	VAL	F957	F957	F887	E809		R638			V149
	ASN	ASN	ASN	ASN	L957	L957		S810	S732	S639	F298		E150
	THR	THR	THR	THR	S958	S958	T890	C811		V640	V503		P151
	ILE	THR	THR	THR	L959	L959	A891	G812	R735	B641		R308	
	LEU	THR	LEU	LEU	S960	S960	H892	L813	G736	W642	V608	L309	Y158
	ASP	ASP	ASP	LEU	P961	P961	H893	C814	Y737	D643	E509		L159
	GLN	VAL	GLN	THR			H894	C815		K644		A313	S160
	LYS	GLY	LYS	CYS	S967	S967	V894	L815	V740	I645	S523	Y314	S161
	PRO	GLY	GLY	GLY	G968	G968	D895	D818	L741	G524	G524	L315	V162
	THR	VAL	VAL	ALA	D1039	D1039	V896		S742		D525		
	PRO	PHE	VAL	PRO	T970	T970	A897	F821	I743	W649	P526	F326	G166
	SER	PHE	PHE	SER	G969	G969	G898	E822		N655	H527	N327	
	ILE	THR	THR	ILE	T973	T973	W899		A746		C528	I328	S175
	ILE	PRO	PRO	THR	I974	I974	P900	C823					

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	238.40 Å 238.40 Å 642.18 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	63.05 – 10.00 63.05 – 10.00	Depositor EDS
% Data completeness (in resolution range)	92.5 (63.05-10.00) 92.6 (63.05-10.00)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.335 , 0.370 0.327 , 0.368	Depositor DCC
R_{free} test set	520 reflections (4.69%)	DCC
Wilson B-factor (Å ²)	(Not available)	Xtriage
Anisotropy	(Not available)	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 306.7	EDS
L-test for twinning ¹	$\langle L \rangle =$ (Not available), $\langle L^2 \rangle =$ (Not available)	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.70	EDS
Total number of atoms	28787	wwPDB-VP
Average B, all atoms (Å ²)	236.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: (*Not available*)

¹Theoretical 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

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	0.68	4/7230 (0.1%)	0.74	8/9821 (0.1%)
1	B	0.64	3/6488 (0.0%)	0.89	7/8804 (0.1%)
1	C	0.65	7/7878 (0.1%)	0.94	13/10705 (0.1%)
1	D	0.68	8/7879 (0.1%)	1.02	23/10708 (0.2%)
All	All	0.66	22/29475 (0.1%)	0.91	51/40038 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	1
1	C	0	4
1	D	0	4
All	All	0	11

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	702	PRO	C-N	26.25	1.94	1.34
1	A	508	VAL	C-N	-24.18	0.78	1.34
1	A	702	PRO	C-N	24.13	1.89	1.34
1	D	655	ASN	C-N	-16.53	0.96	1.34
1	B	655	ASN	C-N	16.05	1.71	1.34

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	702	PRO	O-C-N	-44.19	51.99	122.70
1	C	988	TYR	CB-CG-CD1	-34.32	100.41	121.00
1	D	988	TYR	CB-CG-CD1	-34.12	100.53	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	508	VAL	O-C-N	-33.23	69.54	122.70
1	C	803	LYS	O-C-N	-31.50	72.31	122.70

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	701	CYS	Mainchain
1	A	855	CYS	Mainchain
1	B	508	VAL	Mainchain
1	C	508	VAL	Mainchain
1	C	803	LYS	Mainchain

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	7060	0	6854	430	8
1	B	6337	0	6141	353	6
1	C	7695	0	7466	460	5
1	D	7695	0	7468	492	3
All	All	28787	0	27929	1661	11

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 29.

The worst 5 of 1661 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:463:PRO:HG2	1:B:612:ILE:CG2	1.25	1.55
1:A:407:LEU:CD2	1:C:944:LYS:HD2	1.03	1.48
1:D:533:LEU:CD1	1:D:642:THR:HG23	1.41	1.48
1:A:407:LEU:CD2	1:C:944:LYS:CD	1.93	1.43
1:A:702:PRO:O	1:A:703:GLN:CG	1.65	1.41

The worst 5 of 11 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:A:731:GLN:OE1	1:C:146:PHE:CD1[3_455]	1.56	0.64
1:B:407:LEU:CD2	1:D:944:LYS:CD[2_564]	1.79	0.41
1:A:731:GLN:NE2	1:C:146:PHE:CE1[3_455]	1.87	0.33
1:A:766:SER:OG	1:B:839:PRO:CA[5_665]	1.98	0.22
1:A:839:PRO:CG	1:B:768:GLN:OE1[5_665]	2.02	0.18

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	896/1212 (74%)	861 (96%)	26 (3%)	9 (1%)	19	65
1	B	797/1212 (66%)	771 (97%)	19 (2%)	7 (1%)	21	67
1	C	981/1212 (81%)	937 (96%)	35 (4%)	9 (1%)	21	67
1	D	983/1212 (81%)	942 (96%)	31 (3%)	10 (1%)	19	65
All	All	3657/4848 (75%)	3511 (96%)	111 (3%)	35 (1%)	19	65

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	702	PRO
1	A	851	HIS
1	B	508	VAL
1	B	509	GLU
1	B	851	HIS

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	796/1064 (75%)	787 (99%)	9 (1%)	80	91
1	B	714/1064 (67%)	706 (99%)	8 (1%)	80	91
1	C	870/1064 (82%)	860 (99%)	10 (1%)	80	91
1	D	870/1064 (82%)	860 (99%)	10 (1%)	80	91
All	All	3250/4256 (76%)	3213 (99%)	37 (1%)	80	91

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	811	CYS
1	C	298	PHE
1	D	811	CYS
1	C	237	SER
1	C	238	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	726	ASN
1	C	837	HIS
1	D	953	ASN
1	C	761	GLN
1	C	807	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 [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	6
1	A	6
1	C	6
1	D	5

The worst 5 of 23 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	855:CYS	C	856:SER	N	5.61
1	C	702:PRO	C	703:GLN	N	3.75
1	D	702:PRO	C	703:GLN	N	3.35
1	C	559:CYS	C	560:MET	N	2.82
1	C	855:CYS	C	856:SER	N	2.48

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	906/1212 (74%)	0.08	63 (6%) 19 22	153, 176, 433, 433	0
1	B	809/1212 (66%)	-0.09	33 (4%) 41 39	147, 209, 350, 350	0
1	C	993/1212 (81%)	-0.28	15 (1%) 76 70	200, 270, 340, 340	0
1	D	993/1212 (81%)	-0.28	10 (1%) 84 79	184, 270, 345, 345	0
All	All	3701/4848 (76%)	-0.15	121 (3%) 50 46	147, 228, 345, 433	0

The worst 5 of 121 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	707	THR	9.9
1	A	708	GLU	8.1
1	B	721	THR	6.4
1	A	709	GLU	6.1
1	A	710	ILE	6.0

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 carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.