



Full wwPDB NMR Structure Validation Report ⓘ

Mar 25, 2026 – 07:17 AM UTC

PDB ID : 2JX0 / pdb_00002jx0
Title : The paxillin-binding domain (PBD) of G Protein Coupled Receptor (GPCR)-kinase (GRK) interacting protein 1 (GIT1)
Authors : Zhang, Z.; Guibao, C.D.; Simmerman, J.A.; Zheng, J.
Deposited on : 2007-11-01

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

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A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

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	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

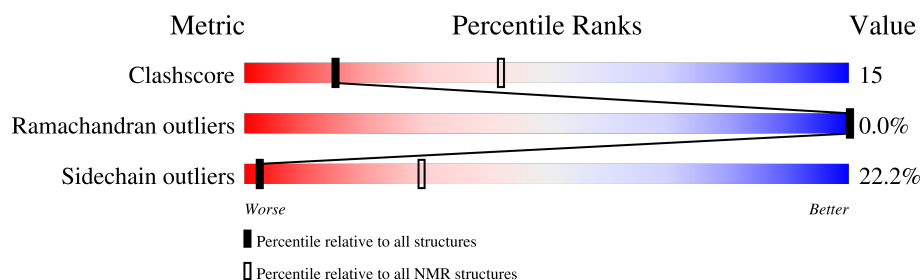
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	135	55% 27% . 12% .

2 Ensemble composition and analysis

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:644-A:729, A:739-A:767 (115)	0.36	1

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 2 single-model clusters were found.

Cluster number	Models
1	1, 3, 4, 6, 7, 9, 10, 13, 16, 18
2	2, 5, 8, 14, 15
3	12, 17, 19
Single-model clusters	11; 20

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2078 atoms, of which 1054 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called ARF GTPase-activating protein GIT1.

Mol	Chain	Residues	Atoms						Trace
1	A	131	Total	C	H	N	O	S	0
			2078	646	1054	178	196	4	

There are 4 discrepancies between the modelled and reference sequences:

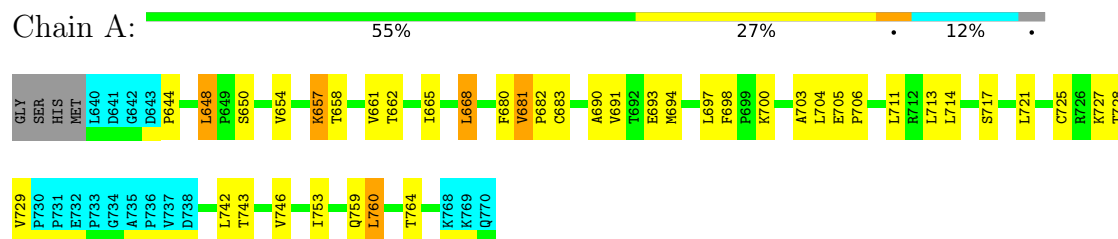
Chain	Residue	Modelled	Actual	Comment	Reference
A	636	GLY	-	expression tag	UNP Q9Z272
A	637	SER	-	expression tag	UNP Q9Z272
A	638	HIS	-	expression tag	UNP Q9Z272
A	639	MET	-	expression tag	UNP Q9Z272

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: ARF GTPase-activating protein GIT1

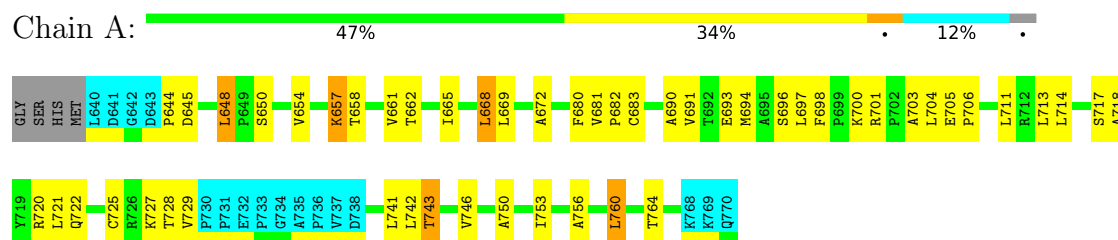


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

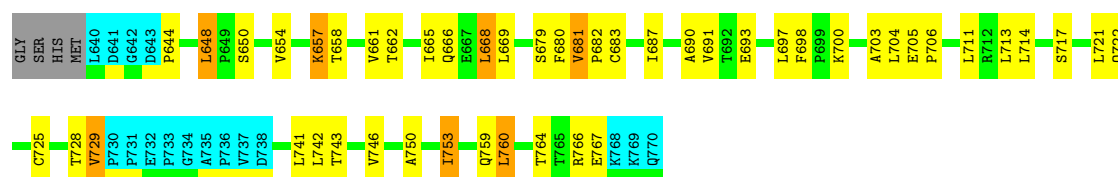
- Molecule 1: ARF GTPase-activating protein GIT1



4.2.2 Score per residue for model 2

- Molecule 1: ARF GTPase-activating protein GIT1





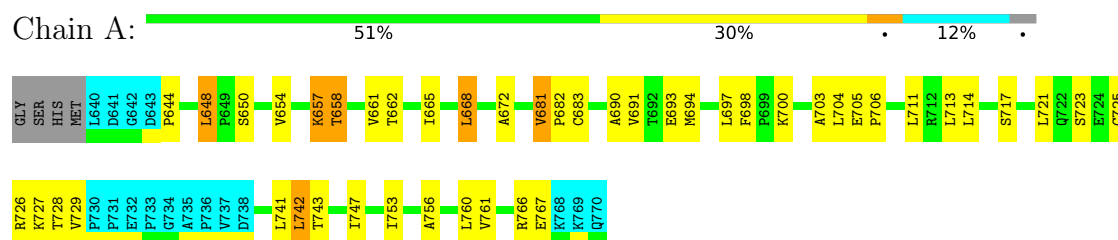
4.2.3 Score per residue for model 3

- Molecule 1: ARF GTPase-activating protein GIT1



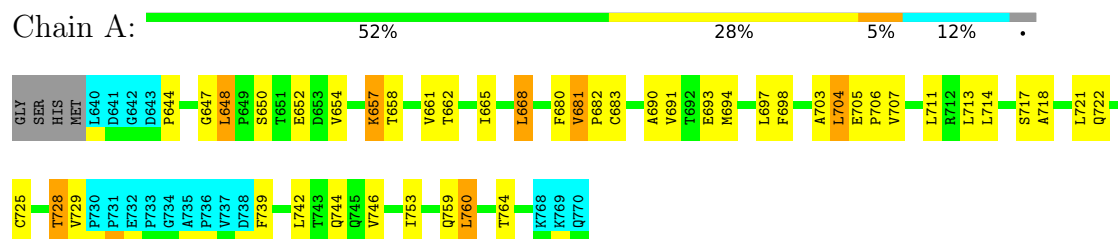
4.2.4 Score per residue for model 4

- Molecule 1: ARF GTPase-activating protein GIT1



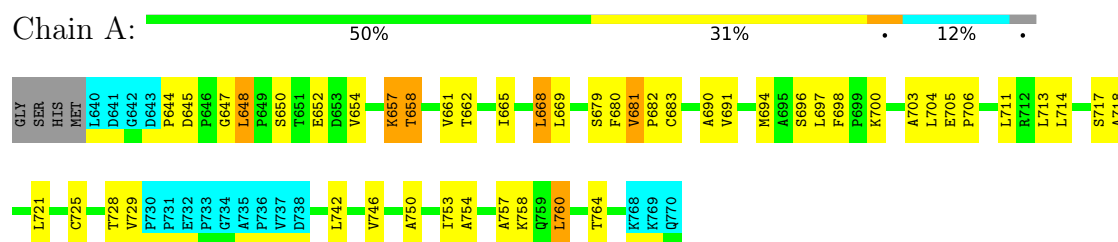
4.2.5 Score per residue for model 5

- Molecule 1: ARF GTPase-activating protein GIT1



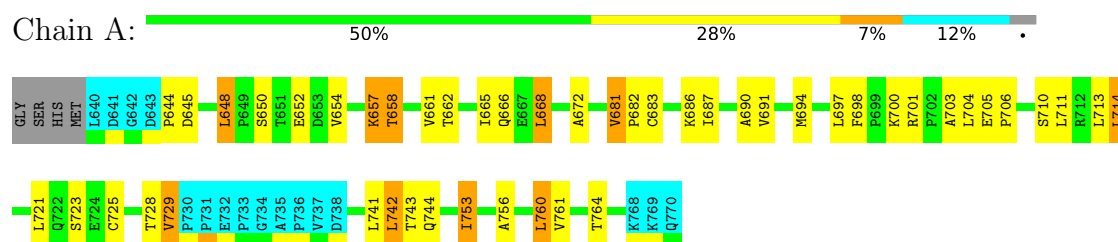
4.2.6 Score per residue for model 6

- Molecule 1: ARF GTPase-activating protein GIT1



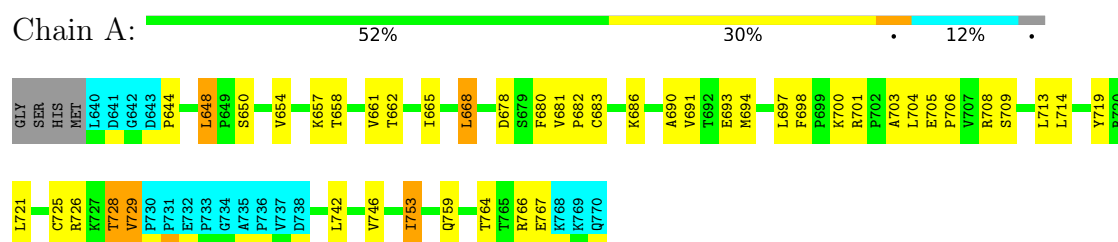
4.2.7 Score per residue for model 7

- Molecule 1: ARF GTPase-activating protein GIT1



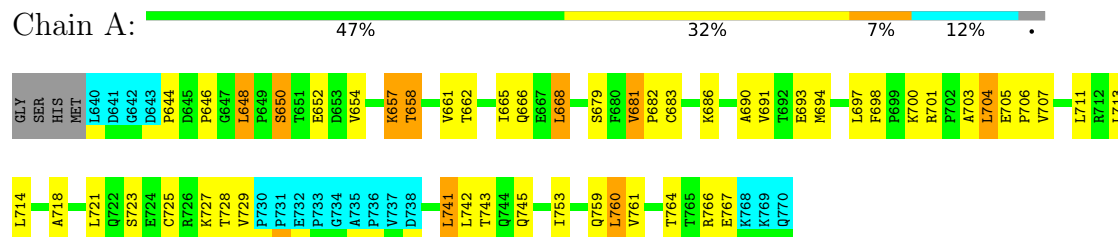
4.2.8 Score per residue for model 8

- Molecule 1: ARF GTPase-activating protein GIT1



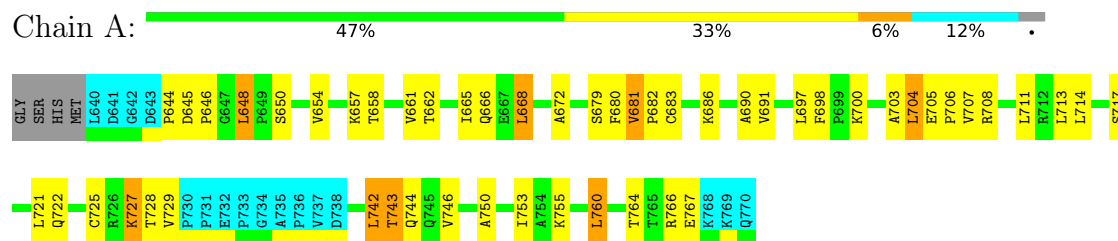
4.2.9 Score per residue for model 9

- Molecule 1: ARF GTPase-activating protein GIT1



4.2.10 Score per residue for model 10

- Molecule 1: ARF GTPase-activating protein GIT1



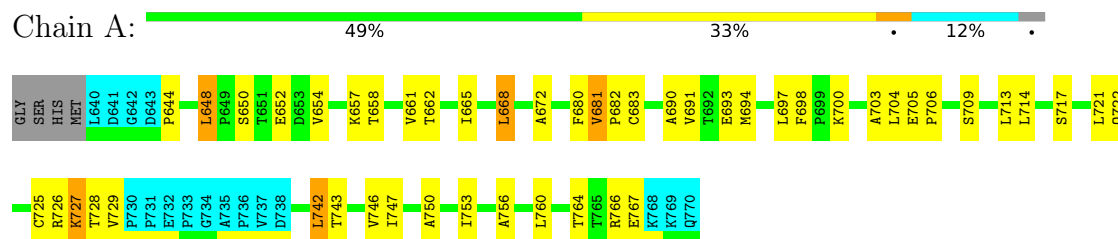
4.2.11 Score per residue for model 11

- Molecule 1: ARF GTPase-activating protein GIT1



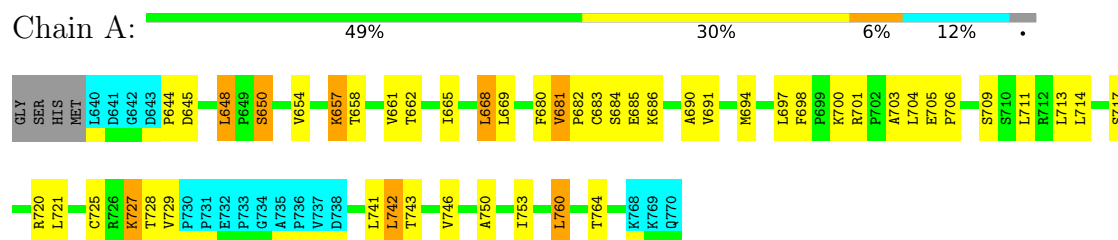
4.2.12 Score per residue for model 12

- Molecule 1: ARF GTPase-activating protein GIT1



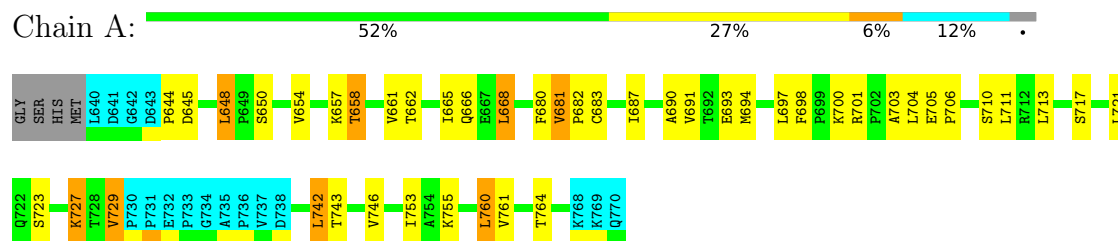
4.2.13 Score per residue for model 13

- Molecule 1: ARF GTPase-activating protein GIT1



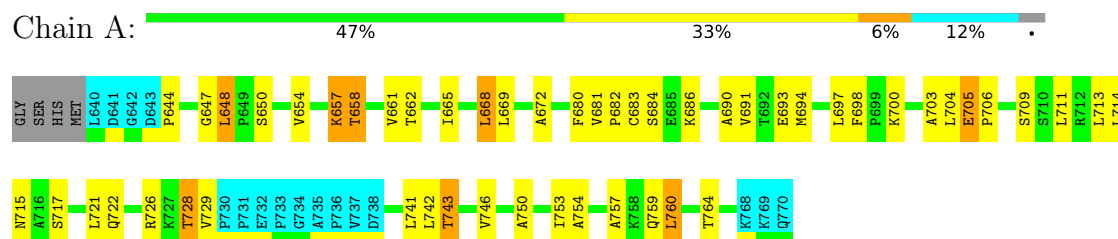
4.2.18 Score per residue for model 18

- Molecule 1: ARF GTPase-activating protein GIT1



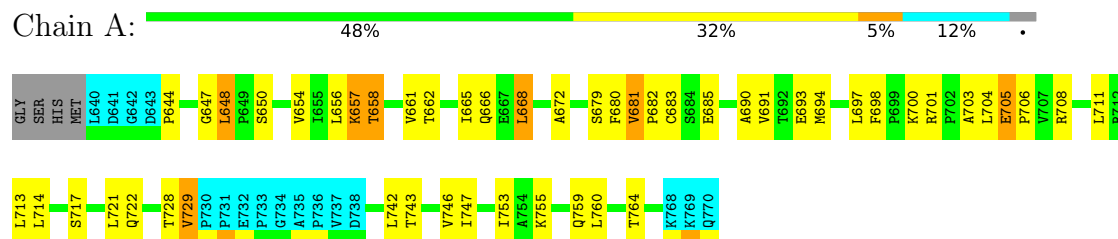
4.2.19 Score per residue for model 19

- Molecule 1: ARF GTPase-activating protein GIT1



4.2.20 Score per residue for model 20

- Molecule 1: ARF GTPase-activating protein GIT1



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CYANA	refinement	2.0

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	908	943	943	28±3
All	All	18160	18860	18860	555

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 15.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:654:VAL:HG11	1:A:764:THR:HG21	0.96	1.38	11	14
1:A:648:LEU:HD13	1:A:654:VAL:HG21	0.76	1.57	8	10
1:A:672:ALA:HB1	1:A:743:THR:HG23	0.76	1.57	19	9
1:A:661:VAL:HG22	1:A:690:ALA:HB1	0.71	1.62	3	20
1:A:680:PHE:CD2	1:A:746:VAL:HG11	0.65	2.27	10	15
1:A:657:LYS:O	1:A:661:VAL:HG23	0.64	1.92	13	20
1:A:648:LEU:CD1	1:A:654:VAL:HG21	0.64	2.22	4	10
1:A:680:PHE:CE2	1:A:746:VAL:HG11	0.64	2.26	6	12
1:A:691:VAL:HG21	1:A:718:ALA:HB2	0.63	1.71	5	4
1:A:713:LEU:HD13	1:A:756:ALA:HB1	0.62	1.69	4	5
1:A:725:CYS:O	1:A:728:THR:HG23	0.62	1.95	2	15
1:A:650:SER:O	1:A:654:VAL:HG23	0.61	1.96	18	20
1:A:727:LYS:O	1:A:742:LEU:HD21	0.61	1.96	16	5
1:A:705:GLU:N	1:A:706:PRO:HD2	0.61	2.11	10	20

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:648:LEU:HD23	1:A:698:PHE:CE2	0.60	2.31	1	2
1:A:710:SER:OG	1:A:760:LEU:HD23	0.60	1.96	11	2
1:A:728:THR:HG22	1:A:742:LEU:CD1	0.60	2.27	16	2
1:A:729:VAL:HG23	1:A:742:LEU:HD22	0.60	1.74	14	1
1:A:668:LEU:HD22	1:A:683:CYS:HB3	0.59	1.73	20	20
1:A:680:PHE:HB2	1:A:728:THR:HG21	0.59	1.73	19	3
1:A:760:LEU:O	1:A:764:THR:HG23	0.58	1.97	2	14
1:A:658:THR:OG1	1:A:694:MET:HE1	0.58	1.98	20	1
1:A:691:VAL:HG13	1:A:714:LEU:HG	0.58	1.75	9	19
1:A:646:PRO:O	1:A:704:LEU:HD13	0.58	1.98	9	3
1:A:672:ALA:HB1	1:A:743:THR:CG2	0.58	2.28	19	4
1:A:713:LEU:HD12	1:A:714:LEU:N	0.57	2.14	16	19
1:A:648:LEU:HD22	1:A:654:VAL:HG21	0.57	1.76	1	5
1:A:668:LEU:HD22	1:A:683:CYS:CB	0.57	2.29	12	20
1:A:648:LEU:HD11	1:A:764:THR:HG22	0.56	1.78	11	7
1:A:729:VAL:HG11	1:A:739:PHE:HB3	0.55	1.79	5	1
1:A:648:LEU:HD22	1:A:698:PHE:CE2	0.55	2.36	20	6
1:A:648:LEU:HD23	1:A:698:PHE:CE1	0.54	2.37	12	3
1:A:760:LEU:HD12	1:A:761:VAL:N	0.54	2.17	4	1
1:A:644:PRO:HB2	1:A:703:ALA:HB2	0.54	1.80	3	20
1:A:680:PHE:CB	1:A:728:THR:HG21	0.54	2.33	19	2
1:A:711:LEU:HD23	1:A:711:LEU:O	0.54	2.03	19	1
1:A:728:THR:HG22	1:A:742:LEU:HD11	0.53	1.80	16	1
1:A:648:LEU:HD22	1:A:698:PHE:CZ	0.53	2.39	14	6
1:A:681:VAL:N	1:A:682:PRO:HD2	0.52	2.20	11	20
1:A:728:THR:HA	1:A:742:LEU:HD21	0.52	1.81	14	1
1:A:661:VAL:HG22	1:A:690:ALA:CB	0.52	2.33	17	14
1:A:648:LEU:HD22	1:A:654:VAL:CG2	0.51	2.36	15	4
1:A:662:THR:HA	1:A:665:ILE:HD12	0.51	1.82	9	20
1:A:648:LEU:HD12	1:A:698:PHE:CE2	0.51	2.40	9	5
1:A:647:GLY:C	1:A:648:LEU:HD13	0.51	2.29	19	3
1:A:727:LYS:O	1:A:742:LEU:HD11	0.51	2.06	9	2
1:A:648:LEU:HD11	1:A:764:THR:CG2	0.51	2.36	8	3
1:A:647:GLY:C	1:A:648:LEU:HD23	0.51	2.31	20	4
1:A:705:GLU:N	1:A:706:PRO:CD	0.50	2.75	20	20
1:A:743:THR:HG22	1:A:747:ILE:CD1	0.50	2.36	17	4
1:A:729:VAL:HG22	1:A:729:VAL:O	0.49	2.08	5	1
1:A:687:ILE:O	1:A:691:VAL:HG23	0.49	2.08	18	5
1:A:657:LYS:CB	1:A:694:MET:HE3	0.49	2.37	14	2
1:A:658:THR:HG22	1:A:757:ALA:HB1	0.49	1.83	6	2
1:A:665:ILE:HG23	1:A:750:ALA:HB1	0.49	1.83	12	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:713:LEU:HD13	1:A:756:ALA:CB	0.48	2.37	16	2
1:A:645:ASP:O	1:A:703:ALA:HB3	0.48	2.09	11	8
1:A:658:THR:HG21	1:A:761:VAL:CG2	0.48	2.38	4	1
1:A:661:VAL:CG2	1:A:690:ALA:HB1	0.47	2.36	9	13
1:A:713:LEU:CD1	1:A:756:ALA:HB1	0.47	2.39	7	4
1:A:669:LEU:HD21	1:A:750:ALA:HB3	0.47	1.86	19	5
1:A:658:THR:HG21	1:A:761:VAL:HB	0.47	1.85	18	5
1:A:669:LEU:HD21	1:A:750:ALA:CB	0.47	2.40	1	7
1:A:657:LYS:HB3	1:A:694:MET:HE3	0.47	1.85	14	1
1:A:648:LEU:HD22	1:A:698:PHE:CE1	0.46	2.45	18	3
1:A:760:LEU:O	1:A:760:LEU:HD13	0.46	2.10	7	3
1:A:729:VAL:O	1:A:729:VAL:HG13	0.46	2.11	9	2
1:A:741:LEU:HD12	1:A:745:GLN:HE21	0.45	1.71	9	1
1:A:743:THR:HG22	1:A:747:ILE:HD11	0.45	1.88	12	3
1:A:665:ILE:HD11	1:A:753:ILE:CD1	0.44	2.43	7	3
1:A:729:VAL:O	1:A:729:VAL:HG22	0.44	2.12	9	1
1:A:654:VAL:CG1	1:A:764:THR:HG21	0.44	2.26	11	1
1:A:714:LEU:HD22	1:A:760:LEU:HD22	0.44	1.89	4	1
1:A:714:LEU:HD13	1:A:760:LEU:CD1	0.44	2.43	5	1
1:A:710:SER:HB3	1:A:760:LEU:HD23	0.44	1.89	16	1
1:A:760:LEU:HD23	1:A:760:LEU:O	0.43	2.13	12	1
1:A:656:LEU:HD12	1:A:657:LYS:N	0.43	2.28	20	2
1:A:646:PRO:O	1:A:704:LEU:HD12	0.43	2.13	15	1
1:A:648:LEU:HD23	1:A:698:PHE:CZ	0.43	2.49	1	2
1:A:704:LEU:HD23	1:A:707:VAL:HG23	0.43	1.91	9	4
1:A:714:LEU:HD13	1:A:760:LEU:HD13	0.42	1.91	5	1
1:A:729:VAL:HG11	1:A:739:PHE:CB	0.42	2.44	5	1
1:A:710:SER:HA	1:A:713:LEU:HD21	0.42	1.90	18	1
1:A:665:ILE:HD13	1:A:754:ALA:HB2	0.41	1.92	19	3
1:A:760:LEU:HD12	1:A:760:LEU:C	0.41	2.40	4	1
1:A:728:THR:HG22	1:A:742:LEU:HD12	0.41	1.93	7	1
1:A:681:VAL:N	1:A:682:PRO:CD	0.41	2.83	17	9
1:A:691:VAL:HG13	1:A:714:LEU:CG	0.41	2.46	15	2
1:A:653:ASP:HA	1:A:656:LEU:HD21	0.40	1.94	14	1
1:A:697:LEU:HD12	1:A:697:LEU:C	0.40	2.42	16	1
1:A:656:LEU:C	1:A:656:LEU:HD12	0.40	2.42	17	1

6.3 Torsion angles [i](#)

6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	115/135 (85%)	110±1 (95±1%)	5±1 (5±1%)	0±0 (0±0%)	100	100
All	All	2300/2700 (85%)	2194 (95%)	105 (5%)	1 (0%)	100	100

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	728	THR	1

6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	103/119 (87%)	80±2 (78±2%)	23±2 (22±2%)	2	29
All	All	2060/2380 (87%)	1602 (78%)	458 (22%)	2	29

All 51 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	648	LEU	20
1	A	658	THR	20
1	A	668	LEU	20
1	A	697	LEU	20
1	A	704	LEU	20
1	A	721	LEU	20
1	A	753	ILE	20
1	A	700	LYS	19
1	A	742	LEU	19
1	A	694	MET	17

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Mol	Chain	Res	Type	Models (Total)
1	A	711	LEU	16
1	A	657	LYS	15
1	A	693	GLU	15
1	A	760	LEU	15
1	A	717	SER	14
1	A	681	VAL	14
1	A	759	GLN	11
1	A	722	GLN	10
1	A	743	THR	10
1	A	741	LEU	9
1	A	666	GLN	9
1	A	729	VAL	9
1	A	766	ARG	8
1	A	767	GLU	8
1	A	686	LYS	8
1	A	701	ARG	7
1	A	723	SER	7
1	A	727	LYS	6
1	A	726	ARG	6
1	A	755	LYS	6
1	A	728	THR	6
1	A	679	SER	5
1	A	652	GLU	5
1	A	744	GLN	5
1	A	708	ARG	5
1	A	709	SER	4
1	A	720	ARG	3
1	A	758	LYS	3
1	A	715	ASN	3
1	A	684	SER	3
1	A	705	GLU	3
1	A	696	SER	2
1	A	678	ASP	2
1	A	719	TYR	2
1	A	650	SER	2
1	A	685	GLU	2
1	A	667	GLU	1
1	A	712	ARG	1
1	A	714	LEU	1
1	A	752	ASP	1
1	A	740	GLN	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided