



Full wwPDB NMR Structure Validation Report ⓘ

Nov 16, 2017 – 05:49 PM EST

PDB ID : 2K04
Title : Structure of SDF1 in complex with the CXCR4 N-terminus containing no sulfotyrosines
Authors : Volkman, B.F.; Veldkamp, C.T.; Peterson, F.C.
Deposited on : unknown

This is a Full wwPDB NMR Structure Validation 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/NMRValidationReportHelp>

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:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20030345
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

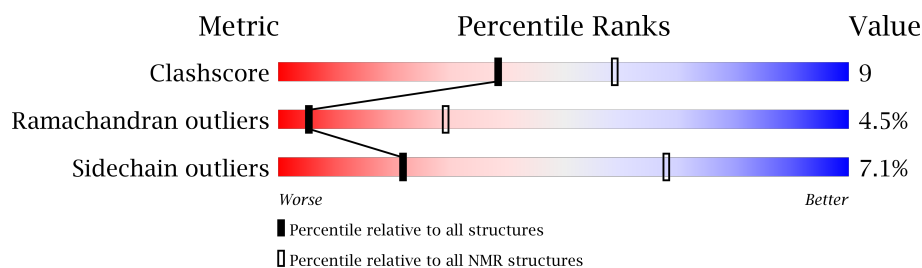
1 Overall quality at a glance

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	70	
1	C	70	
2	B	40	
2	D	40	

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 19 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:9-A:68, B:106-B:111, B:121-B:127, C:209-C:268, D:306-D:311, D:321-D:327 (146)	0.83	19

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 4 clusters. No single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3411 atoms, of which 1688 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Stromal cell-derived factor 1.

Mol	Chain	Residues	Atoms						Trace
1	A	68	Total	C	H	N	O	S	0
			1136	353	579	106	92	6	
1	C	68	Total	C	H	N	O	S	0
			1136	353	579	106	92	6	

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP P48061
A	0	MET	-	EXPRESSION TAG	UNP P48061
A	36	CYS	LEU	ENGINEERED	UNP P48061
A	65	CYS	ALA	ENGINEERED	UNP P48061
C	199	GLY	-	EXPRESSION TAG	UNP P48061
C	200	MET	-	EXPRESSION TAG	UNP P48061
C	236	CYS	LEU	ENGINEERED	UNP P48061
C	265	CYS	ALA	ENGINEERED	UNP P48061

- Molecule 2 is a protein called C-X-C chemokine receptor type 4.

Mol	Chain	Residues	Atoms						Trace
2	B	38	Total	C	H	N	O	S	0
			569	185	265	47	69	3	
2	D	38	Total	C	H	N	O	S	0
			570	185	265	47	70	3	

There are 6 discrepancies between the modelled and reference sequences:

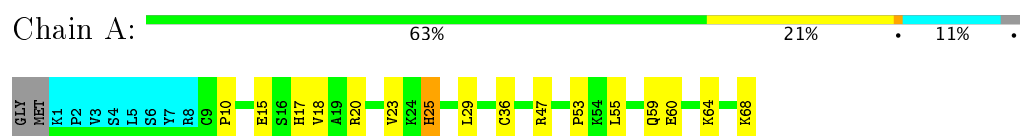
Chain	Residue	Modelled	Actual	Comment	Reference
B	99	GLY	-	EXPRESSION TAG	UNP P61073
B	100	SER	-	EXPRESSION TAG	UNP P61073
B	128	ALA	CYS	ENGINEERED	UNP P61073
D	299	GLY	-	EXPRESSION TAG	UNP P61073
D	300	SER	-	EXPRESSION TAG	UNP P61073
D	328	ALA	CYS	ENGINEERED	UNP P61073

4 Residue-property plots [i](#)

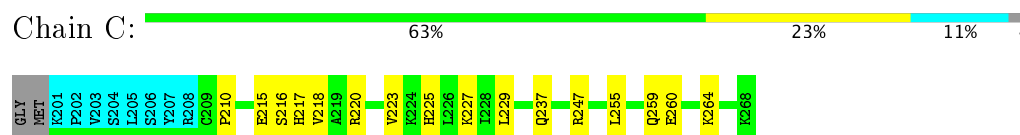
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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.

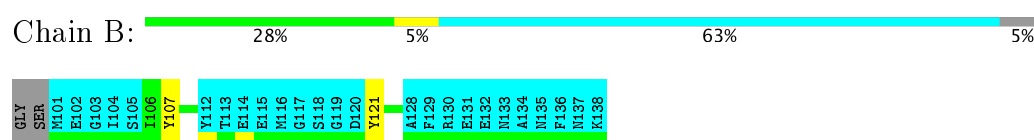
- Molecule 1: Stromal cell-derived factor 1



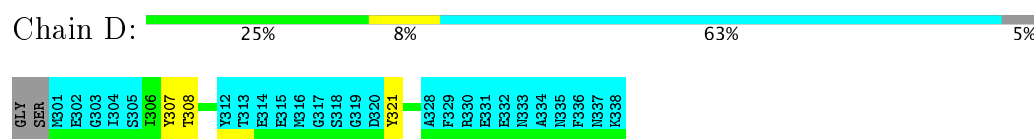
- Molecule 1: Stromal cell-derived factor 1



- Molecule 2: C-X-C chemokine receptor type 4



- Molecule 2: C-X-C chemokine receptor type 4

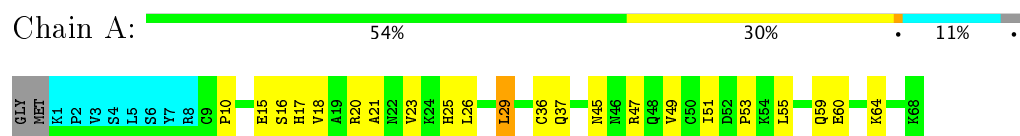


4.2 Scores per residue for each member of the ensemble

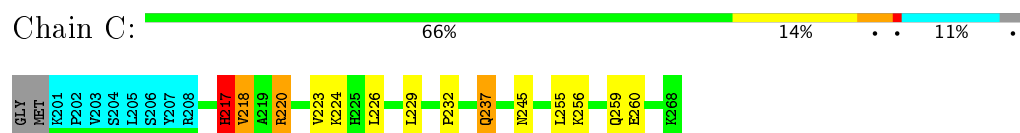
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

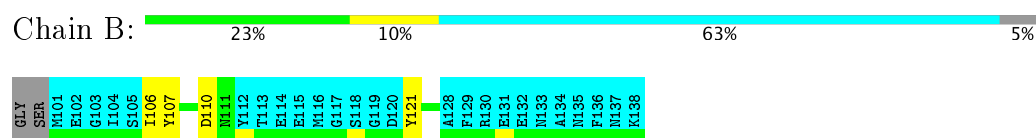
- Molecule 1: Stromal cell-derived factor 1



- Molecule 1: Stromal cell-derived factor 1



- Molecule 2: C-X-C chemokine receptor type 4

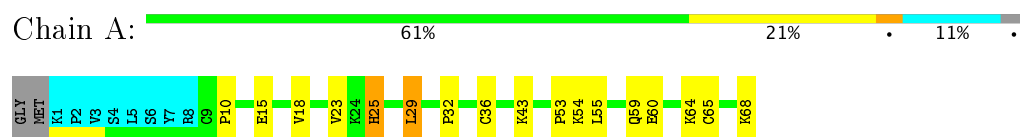


- Molecule 2: C-X-C chemokine receptor type 4



4.2.2 Score per residue for model 2

- Molecule 1: Stromal cell-derived factor 1



- Molecule 1: Stromal cell-derived factor 1



- Molecule 2: C-X-C chemokine receptor type 4





- Molecule 2: C-X-C chemokine receptor type 4

Chain D: 23% 10% 63% 5%



4.2.3 Score per residue for model 3

- Molecule 1: Stromal cell-derived factor 1

Chain A: 61% 24% 11%



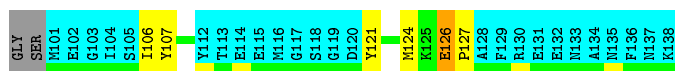
- Molecule 1: Stromal cell-derived factor 1

Chain C: 53% 27% 6% 11%



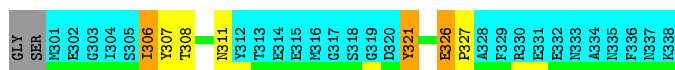
- Molecule 2: C-X-C chemokine receptor type 4

Chain B: 18% 13% 63% 5%



- Molecule 2: C-X-C chemokine receptor type 4

Chain D: 15% 10% 8% 63% 5%



4.2.4 Score per residue for model 4

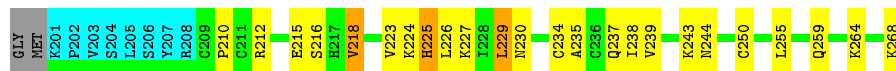
- Molecule 1: Stromal cell-derived factor 1

Chain A: 57% 24% 11%



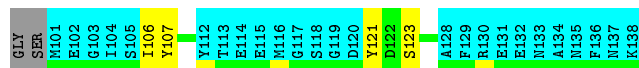
- Molecule 1: Stromal cell-derived factor 1

Chain C: 



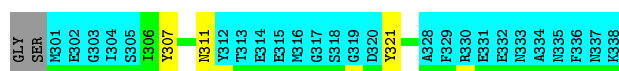
- Molecule 2: C-X-C chemokine receptor type 4

Chain B: 



- Molecule 2: C-X-C chemokine receptor type 4

Chain D: 



4.2.5 Score per residue for model 5

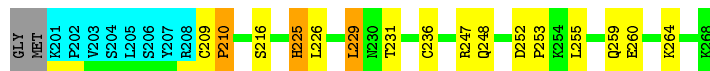
- Molecule 1: Stromal cell-derived factor 1

Chain A: 



- Molecule 1: Stromal cell-derived factor 1

Chain C: 



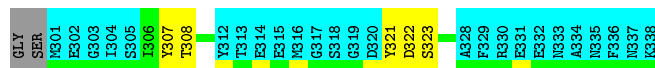
- Molecule 2: C-X-C chemokine receptor type 4

Chain B: 



- Molecule 2: C-X-C chemokine receptor type 4

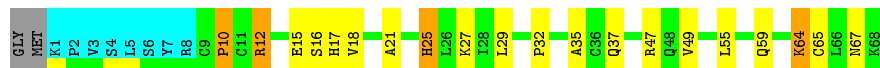
Chain D: 



4.2.6 Score per residue for model 6

- Molecule 1: Stromal cell-derived factor 1

Chain A: 57% 23% 6% 11% .



- Molecule 1: Stromal cell-derived factor 1

Chain C: 59% 23% . 11% .



- Molecule 2: C-X-C chemokine receptor type 4

Chain B: 23% 10% 63% 5%



- Molecule 2: C-X-C chemokine receptor type 4

Chain D: 13% 13% 5% . 63% 5%



4.2.7 Score per residue for model 7

- Molecule 1: Stromal cell-derived factor 1

Chain A: 49% 29% 9% 11% .



- Molecule 1: Stromal cell-derived factor 1

Chain C: 66% 17% . 11% .

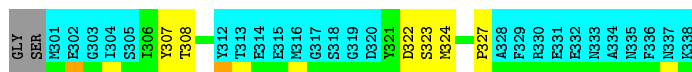


- Molecule 2: C-X-C chemokine receptor type 4

Chain B: 23% 10% 63% 5%

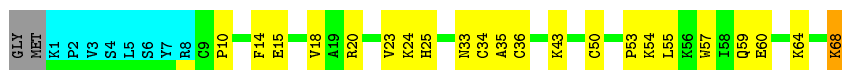


- Molecule 2: C-X-C chemokine receptor type 4



4.2.8 Score per residue for model 8

- Molecule 1: Stromal cell-derived factor 1



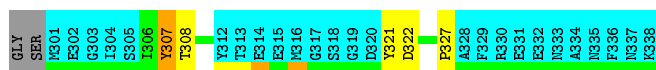
- Molecule 1: Stromal cell-derived factor 1



- Molecule 2: C-X-C chemokine receptor type 4



- Molecule 2: C-X-C chemokine receptor type 4



4.2.9 Score per residue for model 9

- Molecule 1: Stromal cell-derived factor 1



- Molecule 1: Stromal cell-derived factor 1

Chain C: 



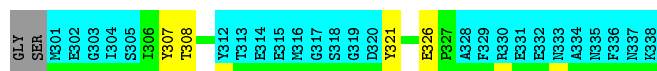
- Molecule 2: C-X-C chemokine receptor type 4

Chain B: 



- Molecule 2: C-X-C chemokine receptor type 4

Chain D: 



4.2.10 Score per residue for model 10

- Molecule 1: Stromal cell-derived factor 1

Chain A: 



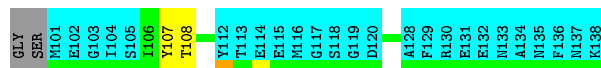
- Molecule 1: Stromal cell-derived factor 1

Chain C: 



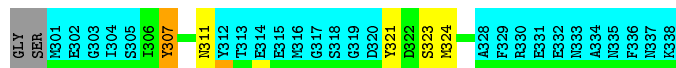
- Molecule 2: C-X-C chemokine receptor type 4

Chain B: 



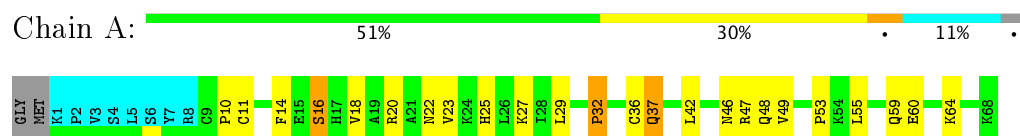
- Molecule 2: C-X-C chemokine receptor type 4

Chain D: 

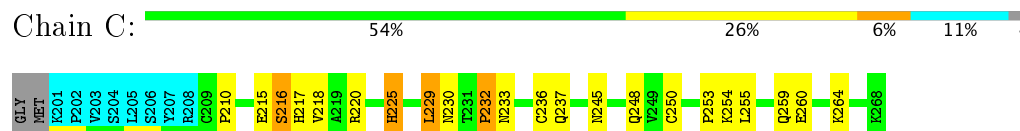


4.2.11 Score per residue for model 11

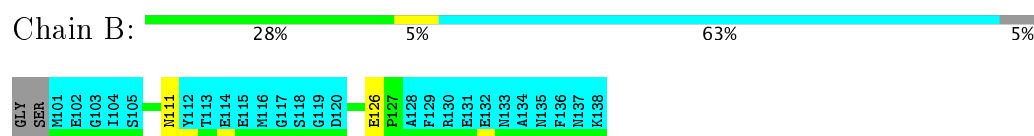
- Molecule 1: Stromal cell-derived factor 1



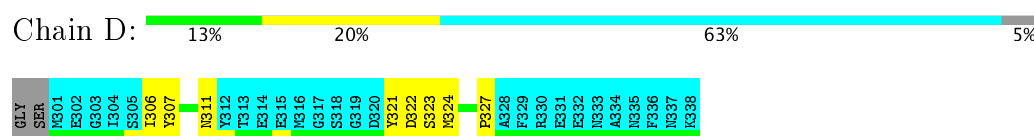
- Molecule 1: Stromal cell-derived factor 1



- Molecule 2: C-X-C chemokine receptor type 4

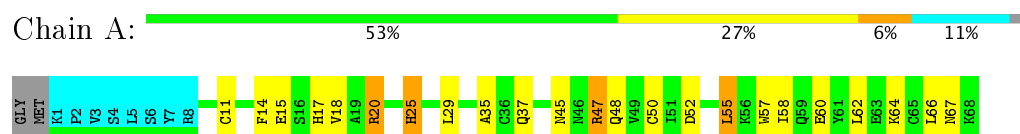


- Molecule 2: C-X-C chemokine receptor type 4

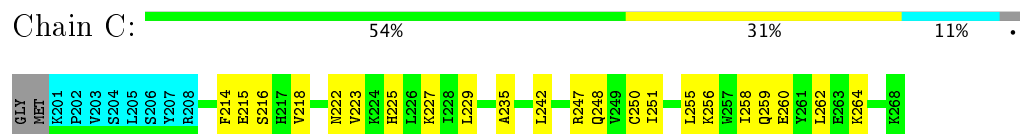


4.2.12 Score per residue for model 12

- Molecule 1: Stromal cell-derived factor 1

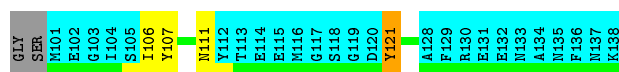


- Molecule 1: Stromal cell-derived factor 1



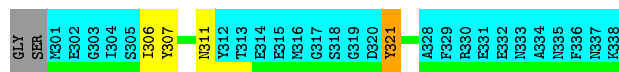
- Molecule 2: C-X-C chemokine receptor type 4





- Molecule 2: C-X-C chemokine receptor type 4

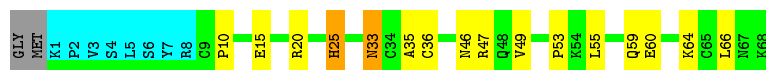
Chain D: 23% 8% 63% 5%



4.2.13 Score per residue for model 13

- Molecule 1: Stromal cell-derived factor 1

Chain A: 63% 20% 11%



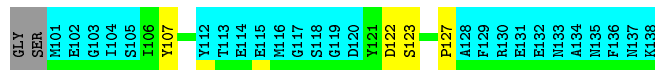
- Molecule 1: Stromal cell-derived factor 1

Chain C: 50% 33% 11%



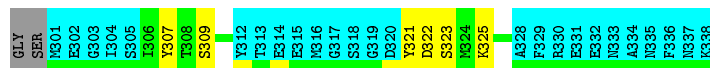
- Molecule 2: C-X-C chemokine receptor type 4

Chain B: 23% 10% 63% 5%



- Molecule 2: C-X-C chemokine receptor type 4

Chain D: 18% 15% 63% 5%



4.2.14 Score per residue for model 14

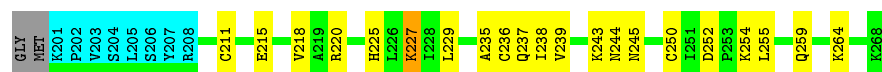
- Molecule 1: Stromal cell-derived factor 1

Chain A: 54% 27% 11%



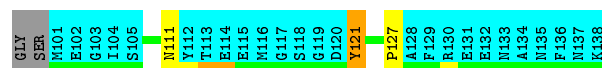
- Molecule 1: Stromal cell-derived factor 1

Chain C: 



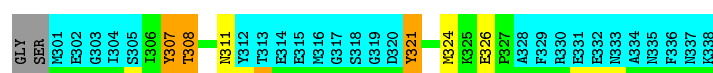
- Molecule 2: C-X-C chemokine receptor type 4

Chain B: 



- Molecule 2: C-X-C chemokine receptor type 4

Chain D: 



4.2.15 Score per residue for model 15

- Molecule 1: Stromal cell-derived factor 1

Chain A: 



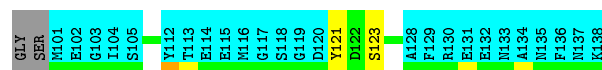
- Molecule 1: Stromal cell-derived factor 1

Chain C: 



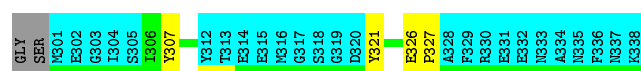
- Molecule 2: C-X-C chemokine receptor type 4

Chain B: 



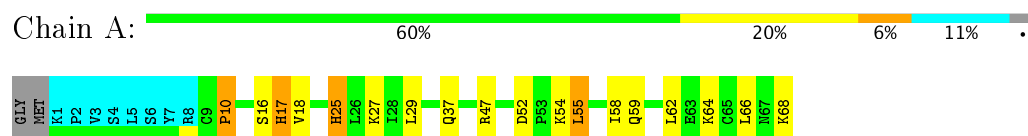
- Molecule 2: C-X-C chemokine receptor type 4

Chain D: 

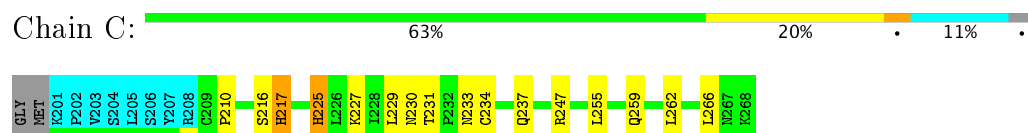


4.2.16 Score per residue for model 16

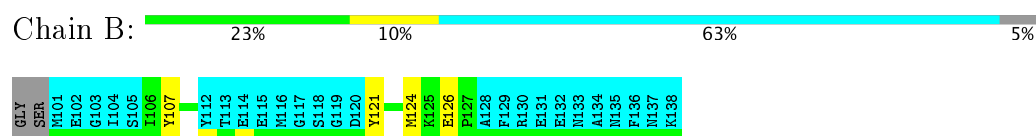
- Molecule 1: Stromal cell-derived factor 1



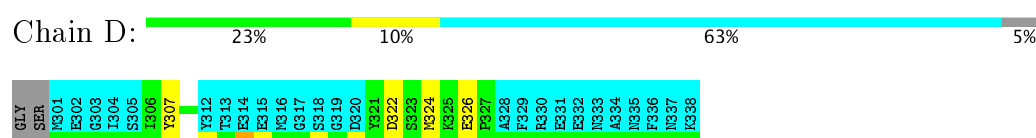
- Molecule 1: Stromal cell-derived factor 1



- Molecule 2: C-X-C chemokine receptor type 4

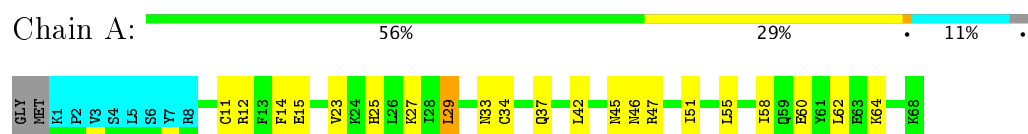


- Molecule 2: C-X-C chemokine receptor type 4

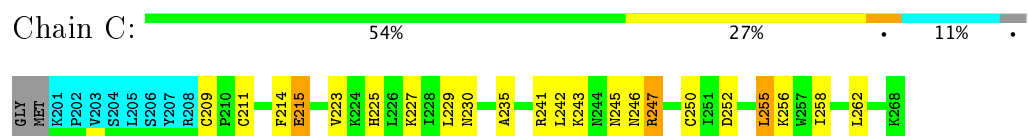


4.2.17 Score per residue for model 17

- Molecule 1: Stromal cell-derived factor 1



- Molecule 1: Stromal cell-derived factor 1



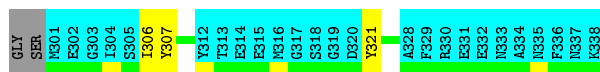
- Molecule 2: C-X-C chemokine receptor type 4





- Molecule 2: C-X-C chemokine receptor type 4

Chain D: 25% 8% 63% 5%



4.2.18 Score per residue for model 18

- Molecule 1: Stromal cell-derived factor 1

Chain A: 53% 30% 11%



- Molecule 1: Stromal cell-derived factor 1

Chain C: 56% 24% 6% 11%



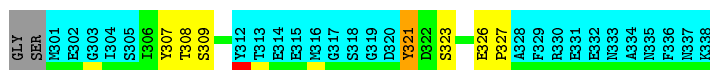
- Molecule 2: C-X-C chemokine receptor type 4

Chain B: 23% 8% 63% 5%



- Molecule 2: C-X-C chemokine receptor type 4

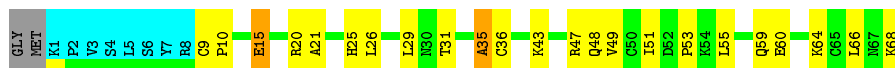
Chain D: 15% 15% 63% 5%



4.2.19 Score per residue for model 19 (medoid)

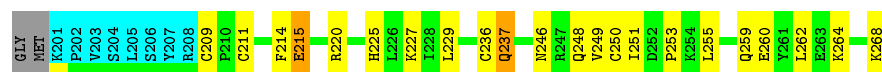
- Molecule 1: Stromal cell-derived factor 1

Chain A: 53% 30% 11%



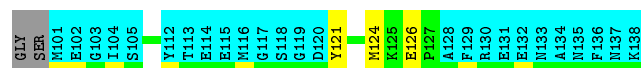
- Molecule 1: Stromal cell-derived factor 1

Chain C: 



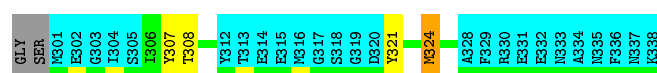
- Molecule 2: C-X-C chemokine receptor type 4

Chain B: 



- Molecule 2: C-X-C chemokine receptor type 4

Chain D: 



4.2.20 Score per residue for model 20

- Molecule 1: Stromal cell-derived factor 1

Chain A: 



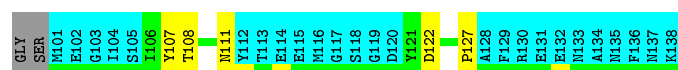
- Molecule 1: Stromal cell-derived factor 1

Chain C: 



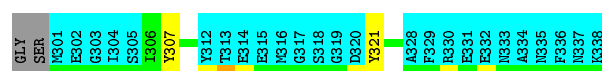
- Molecule 2: C-X-C chemokine receptor type 4

Chain B: 



- Molecule 2: C-X-C chemokine receptor type 4

Chain D: 



5 Refinement protocol and experimental data overview

The models were refined using the following method: *AUTOMATED METHODS WERE USED FOR BACKBONE CHEMICAL SHIFT ASSIGNMENT AND ITERATIVE NOE REFINEMENT. FINAL STRUCTURES WERE OBTAINED BY MOLECULAR DYNAMICS IN EXPLICIT SOLVENT..*

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function.*

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

Software name	Classification	Version
Xplor-NIH	refinement	2.9.3

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality

6.1 Standard geometry

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

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	Planarity
1	C	0.0±0.0	0.1±0.2
All	All	0	1

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	C	220	ARG	Sidechain	1

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	491	507	505	11±3
1	C	491	507	505	11±2
2	B	108	95	95	3±1
2	D	108	95	95	4±1
All	All	23960	24080	24000	437

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 9.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:23:VAL:O	2:D:307:TYR:HB3	0.68	1.89	4	8
1:A:11:CYS:SG	1:A:14:PHE:HB3	0.66	2.31	11	3
1:C:216:SER:O	2:D:321:TYR:HB3	0.65	1.92	5	2
1:C:220:ARG:HB3	1:C:257:TRP:CE3	0.64	2.27	18	1
1:A:60:GLU:O	1:A:64:LYS:HG2	0.64	1.92	5	11
1:A:18:VAL:HG11	1:A:51:ILE:HD12	0.64	1.70	18	5
1:C:215:GLU:HG2	1:C:250:CYS:O	0.64	1.92	17	1
1:C:255:LEU:O	1:C:259:GLN:HG2	0.62	1.95	10	18
1:A:36:CYS:O	1:A:53:PRO:HG3	0.61	1.95	19	11
2:B:107:TYR:HB3	1:C:223:VAL:O	0.61	1.95	4	11
1:A:66:LEU:HB2	1:C:259:GLN:NE2	0.61	2.10	12	3
1:C:264:LYS:O	1:C:268:LYS:HG2	0.60	1.97	2	2
1:C:260:GLU:O	1:C:264:LYS:HG2	0.60	1.97	12	12
1:A:15:GLU:HG3	2:B:121:TYR:CD2	0.59	2.32	19	1
2:B:107:TYR:O	1:C:224:LYS:HA	0.59	1.97	8	1
1:A:20:ARG:HB3	1:A:57:TRP:CE3	0.59	2.33	15	2
1:C:215:GLU:HG3	1:C:218:VAL:N	0.58	2.14	12	1
1:A:64:LYS:O	1:A:68:LYS:HG3	0.58	1.99	4	6
1:C:264:LYS:O	1:C:268:LYS:HG3	0.58	1.97	4	2
1:C:236:CYS:O	1:C:253:PRO:HG3	0.58	1.99	11	6
1:A:15:GLU:HB3	1:A:18:VAL:HG23	0.58	1.75	14	2
1:A:15:GLU:HB3	2:B:121:TYR:HB2	0.57	1.76	15	1
1:A:15:GLU:HG2	1:A:17:HIS:H	0.57	1.60	14	2
1:A:12:ARG:HA	1:A:12:ARG:NE	0.57	2.14	6	1
1:C:259:GLN:NE2	2:D:327:PRO:HB3	0.57	2.15	6	1
1:A:47:ARG:HD2	1:A:47:ARG:N	0.56	2.15	1	1
1:C:259:GLN:OE1	2:D:327:PRO:HG3	0.56	2.00	7	1
1:A:16:SER:O	1:A:55:LEU:HD21	0.56	2.00	10	1
1:C:231:THR:OG1	1:C:234:CYS:HB2	0.56	2.00	20	3
1:A:55:LEU:O	1:A:59:GLN:HG2	0.56	2.01	18	14
1:C:215:GLU:HG3	2:D:321:TYR:CD2	0.56	2.35	19	1
1:A:18:VAL:HA	2:B:121:TYR:CE1	0.55	2.36	2	1
1:A:54:LYS:O	2:B:127:PRO:HD3	0.55	2.01	20	2
1:C:214:PHE:HA	1:C:250:CYS:O	0.55	2.02	12	3
1:C:218:VAL:HG11	1:C:251:ILE:HD12	0.55	1.76	9	6
1:A:16:SER:O	1:A:55:LEU:HD11	0.55	2.02	9	4
1:A:24:LYS:HA	2:D:308:THR:OG1	0.54	2.02	14	1
1:A:20:ARG:HA	1:A:23:VAL:HG12	0.54	1.79	11	4
1:A:13:PHE:O	1:A:50:CYS:HB2	0.54	2.02	18	1
1:C:252:ASP:OD2	1:C:254:LYS:HB2	0.53	2.03	6	4
1:A:15:GLU:HG3	1:A:18:VAL:N	0.53	2.18	8	1
1:A:15:GLU:HA	2:B:121:TYR:HB2	0.53	1.81	4	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:216:SER:O	1:C:255:LEU:HD21	0.53	2.03	20	5
1:C:216:SER:HB2	2:D:323:SER:O	0.53	2.03	10	2
1:C:218:VAL:HG22	2:D:321:TYR:CD1	0.53	2.39	11	1
1:A:11:CYS:HB2	1:A:37:GLN:OE1	0.53	2.03	12	2
1:A:66:LEU:HD12	1:A:66:LEU:O	0.53	2.04	13	1
1:A:25:HIS:HA	2:D:307:TYR:CE2	0.53	2.38	20	1
1:C:211:CYS:SG	1:C:237:GLN:HB3	0.53	2.43	14	1
1:A:16:SER:O	2:B:121:TYR:HB3	0.53	2.03	6	3
1:C:215:GLU:CD	2:D:321:TYR:HB2	0.53	2.24	9	2
1:A:52:ASP:O	1:A:55:LEU:HB2	0.53	2.04	14	2
1:A:25:HIS:HA	2:D:307:TYR:CZ	0.53	2.39	16	4
1:A:59:GLN:NE2	1:C:266:LEU:HB2	0.52	2.20	9	2
1:C:215:GLU:HA	2:D:321:TYR:HB2	0.52	1.81	20	3
1:C:256:LYS:O	1:C:260:GLU:HG2	0.52	2.03	1	1
1:C:218:VAL:HA	2:D:321:TYR:CE1	0.52	2.39	2	2
1:C:237:GLN:HE21	1:C:237:GLN:N	0.52	2.02	6	1
2:B:107:TYR:OH	1:C:226:LEU:HG	0.52	2.04	20	1
1:C:230:ASN:O	2:D:306:ILE:HG21	0.51	2.05	11	2
1:A:26:LEU:HD13	2:D:307:TYR:CE1	0.51	2.39	1	2
1:A:47:ARG:CZ	1:A:49:VAL:HG12	0.51	2.35	18	1
1:A:17:HIS:H	1:A:55:LEU:HD21	0.51	1.64	1	2
1:A:9:CYS:SG	1:A:10:PRO:HD2	0.51	2.45	20	2
1:A:31:THR:OG1	1:A:34:CYS:HB2	0.51	2.06	10	1
1:C:216:SER:O	1:C:255:LEU:HD11	0.51	2.06	11	2
1:A:29:LEU:O	1:A:37:GLN:HB2	0.51	2.06	4	2
1:C:229:LEU:HA	2:D:307:TYR:OH	0.51	2.05	5	2
1:C:217:HIS:HD2	2:D:323:SER:O	0.51	1.89	11	1
1:C:254:LYS:HB3	2:D:327:PRO:HD3	0.50	1.83	6	3
1:A:21:ALA:HA	2:D:308:THR:OG1	0.50	2.07	6	2
2:D:325:LYS:HA	2:D:325:LYS:HE2	0.50	1.83	13	1
2:B:107:TYR:CE1	1:C:226:LEU:HD13	0.50	2.42	18	2
1:A:66:LEU:HB3	1:C:262:LEU:HD12	0.50	1.83	16	4
1:C:239:VAL:HG22	1:C:250:CYS:SG	0.50	2.47	14	2
1:A:64:LYS:O	1:A:68:LYS:HB3	0.50	2.07	14	1
1:A:26:LEU:HG	2:D:307:TYR:OH	0.50	2.06	20	1
1:A:30:ASN:O	2:B:106:ILE:HB	0.50	2.06	4	1
1:A:37:GLN:HA	1:A:37:GLN:HE21	0.50	1.67	11	1
1:A:54:LYS:HA	1:A:59:GLN:NE2	0.49	2.22	2	3
1:C:229:LEU:HD12	1:C:229:LEU:O	0.49	2.07	16	1
1:C:215:GLU:HG2	1:C:249:VAL:HB	0.49	1.84	19	1
1:C:229:LEU:O	1:C:237:GLN:HB2	0.49	2.08	11	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:59:GLN:OE1	2:B:127:PRO:HG3	0.49	2.06	7	4
1:A:15:GLU:HG3	2:B:121:TYR:HB2	0.49	1.85	2	1
1:C:226:LEU:HG	1:C:238:ILE:CG2	0.49	2.38	4	1
1:A:29:LEU:HD12	1:A:29:LEU:O	0.49	2.08	16	1
1:C:215:GLU:HB3	1:C:218:VAL:HG23	0.49	1.85	14	3
1:A:25:HIS:CE1	1:C:227:LYS:HD2	0.49	2.43	18	1
1:A:14:PHE:HA	1:A:50:CYS:O	0.48	2.07	14	3
1:A:15:GLU:HG3	1:A:49:VAL:HB	0.48	1.85	4	2
1:A:14:PHE:CD1	1:A:52:ASP:HB2	0.48	2.43	3	2
1:A:15:GLU:OE1	1:A:49:VAL:HB	0.48	2.09	19	2
1:A:47:ARG:NH1	1:A:49:VAL:HG12	0.48	2.23	11	2
1:A:25:HIS:HB2	1:C:228:ILE:O	0.48	2.08	7	2
1:C:247:ARG:N	1:C:247:ARG:HD2	0.48	2.24	5	2
1:A:27:LYS:HD2	1:C:225:HIS:CD2	0.48	2.44	11	3
1:A:47:ARG:N	1:A:47:ARG:HD3	0.48	2.24	9	1
1:C:229:LEU:O	1:C:237:GLN:HB3	0.48	2.09	3	2
1:A:28:ILE:O	1:C:225:HIS:HB2	0.48	2.08	3	1
1:C:220:ARG:HA	1:C:223:VAL:HG12	0.48	1.85	15	1
2:B:126:GLU:OE2	2:B:127:PRO:HD2	0.47	2.09	3	1
1:C:218:VAL:HA	2:D:321:TYR:CE2	0.47	2.44	3	1
1:A:10:PRO:HG3	1:A:29:LEU:CD1	0.47	2.39	5	1
1:C:216:SER:OG	2:D:324:MET:HB3	0.47	2.09	2	1
1:A:54:LYS:NZ	1:A:54:LYS:HB2	0.47	2.25	7	1
1:C:211:CYS:SG	1:C:214:PHE:HB3	0.47	2.49	17	1
1:A:15:GLU:HB2	2:B:121:TYR:CD2	0.47	2.45	8	1
1:C:216:SER:OG	2:D:324:MET:HA	0.47	2.10	10	1
1:C:259:GLN:OE1	2:D:327:PRO:HB3	0.47	2.09	18	1
1:C:229:LEU:O	1:C:229:LEU:HD12	0.47	2.10	3	1
1:A:15:GLU:HG2	1:A:50:CYS:O	0.47	2.10	4	1
1:C:234:CYS:HB2	1:C:237:GLN:OE1	0.46	2.11	6	1
1:A:60:GLU:O	1:A:64:LYS:HD2	0.46	2.10	14	1
2:B:107:TYR:CZ	1:C:225:HIS:HA	0.46	2.45	13	3
1:C:227:LYS:O	1:C:238:ILE:HA	0.46	2.10	10	3
2:D:306:ILE:HG22	2:D:307:TYR:H	0.46	1.71	3	2
1:C:252:ASP:O	1:C:255:LEU:HB2	0.46	2.11	8	2
1:A:58:ILE:O	1:A:62:LEU:HG	0.46	2.11	17	3
1:A:52:ASP:OD2	1:A:54:LYS:HB2	0.46	2.10	4	2
1:C:247:ARG:CZ	1:C:249:VAL:HG12	0.46	2.41	2	1
1:C:234:CYS:SG	1:C:237:GLN:NE2	0.46	2.88	4	1
1:C:268:LYS:NZ	1:C:268:LYS:HB3	0.46	2.26	18	1
1:C:211:CYS:SG	1:C:237:GLN:HG3	0.46	2.50	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:66:LEU:HB2	1:C:259:GLN:OE1	0.46	2.11	13	1
1:A:22:ASN:HA	1:A:43:LYS:NZ	0.46	2.25	18	1
1:A:21:ALA:HA	2:D:307:TYR:O	0.46	2.10	19	1
1:A:16:SER:OG	2:B:124:MET:HB3	0.46	2.10	3	1
1:C:215:GLU:HB2	1:C:250:CYS:O	0.46	2.10	11	3
1:C:247:ARG:HD3	1:C:247:ARG:N	0.45	2.26	9	1
1:C:216:SER:HB3	1:C:255:LEU:HD21	0.45	1.89	10	1
1:A:45:ASN:OD1	1:A:47:ARG:HD3	0.45	2.12	12	1
1:A:47:ARG:HE	1:A:49:VAL:HG12	0.45	1.72	6	1
1:A:10:PRO:HG3	1:A:29:LEU:HD11	0.45	1.87	5	1
1:A:29:LEU:HA	2:B:107:TYR:OH	0.45	2.12	6	1
1:C:254:LYS:HA	1:C:259:GLN:NE2	0.45	2.27	9	3
1:A:68:LYS:HG2	1:C:236:CYS:HB2	0.45	1.88	14	1
2:D:308:THR:HG23	2:D:311:ASN:HB3	0.45	1.88	14	1
1:A:51:ILE:CG2	1:A:55:LEU:HD12	0.45	2.41	19	2
1:C:209:CYS:SG	1:C:210:PRO:HD2	0.45	2.52	3	2
1:C:216:SER:OG	2:D:323:SER:HA	0.45	2.12	7	1
1:A:59:GLN:OE1	1:C:266:LEU:HB2	0.45	2.11	2	2
1:A:52:ASP:OD1	1:A:54:LYS:HB2	0.45	2.11	7	1
1:A:54:LYS:HE3	2:B:125:LYS:O	0.45	2.12	8	1
1:C:210:PRO:HD3	1:C:231:THR:OG1	0.45	2.12	9	1
1:A:15:GLU:HB2	2:B:121:TYR:HB3	0.45	1.88	14	1
1:A:27:LYS:HD2	1:C:225:HIS:CG	0.45	2.47	4	2
1:A:42:LEU:HB2	1:A:45:ASN:HB3	0.45	1.87	10	1
1:A:24:LYS:HA	2:D:309:SER:OG	0.45	2.12	18	1
1:A:24:LYS:HE2	1:A:42:LEU:O	0.44	2.12	5	1
2:B:107:TYR:CE1	1:C:225:HIS:HA	0.44	2.47	6	1
1:A:42:LEU:CB	1:A:45:ASN:HB3	0.44	2.42	10	1
2:D:306:ILE:HG22	2:D:307:TYR:N	0.44	2.28	3	1
1:A:54:LYS:HB3	2:B:127:PRO:HD3	0.44	1.88	9	1
1:A:54:LYS:HE2	2:B:126:GLU:H	0.44	1.71	18	1
1:C:266:LEU:HD12	1:C:267:ASN:N	0.44	2.28	2	1
1:A:24:LYS:CG	1:A:43:LYS:HA	0.44	2.42	7	2
1:A:20:ARG:NH1	1:A:57:TRP:HB2	0.44	2.28	8	1
1:C:258:ILE:O	1:C:262:LEU:HG	0.44	2.11	17	2
1:A:11:CYS:SG	1:A:39:VAL:HG22	0.44	2.53	15	1
1:C:252:ASP:HB2	1:C:255:LEU:HG	0.44	1.89	5	1
1:C:222:ASN:O	1:C:242:LEU:HA	0.44	2.12	8	3
1:A:17:HIS:HA	1:A:55:LEU:HD21	0.44	1.89	5	1
1:A:27:LYS:HA	1:C:226:LEU:O	0.43	2.13	10	1
1:A:20:ARG:NH1	2:D:307:TYR:HA	0.43	2.29	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:252:ASP:OD1	1:C:254:LYS:HB2	0.43	2.13	14	1
2:B:110:ASP:OD2	1:C:224:LYS:HB3	0.43	2.13	1	1
1:A:42:LEU:CD1	1:A:46:ASN:HB3	0.43	2.43	17	1
2:B:107:TYR:HA	1:C:220:ARG:O	0.43	2.12	18	1
1:A:15:GLU:HG2	1:A:49:VAL:HB	0.43	1.91	19	1
1:C:242:LEU:CD1	1:C:246:ASN:HB3	0.43	2.43	17	1
2:D:311:ASN:C	2:D:311:ASN:HD22	0.43	2.17	6	1
1:C:244:ASN:C	1:C:246:ASN:H	0.43	2.16	2	1
2:B:107:TYR:OH	1:C:226:LEU:HB2	0.43	2.13	5	1
1:A:22:ASN:ND2	1:A:42:LEU:HD22	0.43	2.29	11	1
1:A:20:ARG:HB2	2:D:307:TYR:CE1	0.43	2.49	12	1
1:C:215:GLU:CG	1:C:249:VAL:HB	0.43	2.43	13	1
1:C:215:GLU:OE2	2:D:321:TYR:HB2	0.43	2.14	15	2
1:A:26:LEU:HG	1:A:38:ILE:CG2	0.43	2.44	18	1
1:A:17:HIS:CE1	2:B:123:SER:HB3	0.43	2.49	4	1
1:A:63:GLU:HA	1:A:66:LEU:HD23	0.43	1.90	14	1
2:B:106:ILE:O	1:C:220:ARG:HD3	0.43	2.14	18	1
1:A:26:LEU:O	1:C:227:LYS:HA	0.43	2.14	18	1
1:A:61:TYR:O	1:A:65:CYS:HB2	0.43	2.14	9	1
1:A:26:LEU:HB2	2:D:307:TYR:OH	0.43	2.14	18	1
1:A:68:LYS:HD3	1:C:235:ALA:O	0.42	2.13	8	1
1:A:18:VAL:HG21	1:A:49:VAL:HG21	0.42	1.91	11	1
1:A:59:GLN:OE1	2:B:127:PRO:HB3	0.42	2.15	14	1
1:C:242:LEU:HD13	1:C:247:ARG:O	0.42	2.14	18	1
1:C:224:LYS:HG3	1:C:243:LYS:HA	0.42	1.90	3	1
1:C:213:PHE:O	1:C:250:CYS:HB3	0.42	2.13	18	1
1:C:220:ARG:HE	1:C:220:ARG:C	0.42	2.17	15	1
1:A:15:GLU:CG	1:A:49:VAL:HB	0.42	2.43	4	1
1:C:217:HIS:CD2	2:D:324:MET:HB2	0.42	2.49	7	1
1:C:224:LYS:HG2	1:C:243:LYS:HG2	0.42	1.91	4	1
1:A:25:HIS:CD2	1:C:227:LYS:HD2	0.42	2.49	4	2
2:B:107:TYR:O	2:B:108:THR:HG23	0.42	2.14	5	1
1:C:254:LYS:O	2:D:327:PRO:HD3	0.42	2.15	8	1
2:B:108:THR:OG1	1:C:224:LYS:HA	0.42	2.15	10	1
2:D:307:TYR:N	2:D:307:TYR:CD1	0.42	2.88	10	2
1:C:251:ILE:CG2	1:C:255:LEU:HD12	0.42	2.45	18	2
1:C:218:VAL:HG23	2:D:321:TYR:CE1	0.42	2.50	3	1
1:A:54:LYS:O	2:B:127:PRO:HA	0.42	2.14	18	1
1:C:210:PRO:HG3	1:C:229:LEU:HD11	0.42	1.91	20	1
1:A:57:TRP:HE3	2:D:307:TYR:HH	0.42	1.55	14	1
1:C:216:SER:HA	1:C:252:ASP:OD1	0.41	2.14	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:107:TYR:CD1	1:C:223:VAL:HG13	0.41	2.50	7	1
1:A:24:LYS:HG3	1:A:43:LYS:HA	0.41	1.91	8	1
1:C:215:GLU:HB2	2:D:321:TYR:CD2	0.41	2.50	12	1
1:A:47:ARG:NH1	1:A:49:VAL:HA	0.41	2.29	18	1
1:C:220:ARG:O	1:C:223:VAL:HG12	0.41	2.15	1	1
2:B:107:TYR:CD2	1:C:223:VAL:HG13	0.41	2.50	10	1
1:A:20:ARG:O	1:A:23:VAL:HG12	0.41	2.16	10	1
1:A:15:GLU:O	1:A:51:ILE:HA	0.41	2.15	9	1
1:A:55:LEU:HD13	1:A:57:TRP:NE1	0.41	2.30	15	1
1:A:68:LYS:HZ2	1:A:68:LYS:HB3	0.41	1.76	20	1
1:A:10:PRO:HG2	1:A:37:GLN:OE1	0.41	2.15	1	1
1:A:10:PRO:HG3	1:A:37:GLN:CG	0.41	2.45	7	1
1:A:10:PRO:HG3	1:A:37:GLN:HG2	0.41	1.91	7	1
1:A:15:GLU:HB2	2:B:121:TYR:CG	0.41	2.51	12	1
1:A:29:LEU:CD1	1:A:31:THR:HG23	0.41	2.45	19	1
1:C:214:PHE:CE1	2:D:324:MET:HB3	0.41	2.51	19	1
1:C:210:PRO:HD3	1:C:231:THR:HG21	0.41	1.93	5	1
1:C:254:LYS:HZ2	1:C:254:LYS:HB2	0.41	1.76	15	1
1:A:65:CYS:O	1:A:68:LYS:HE3	0.41	2.16	2	1
1:C:237:GLN:HG3	1:C:250:CYS:SG	0.41	2.56	19	1
1:A:9:CYS:HB3	1:A:10:PRO:HD2	0.41	1.93	19	1
1:C:224:LYS:CG	1:C:243:LYS:HA	0.41	2.46	7	1
1:C:215:GLU:HG3	2:D:322:ASP:HB3	0.40	1.94	8	1
1:C:217:HIS:HB3	2:D:322:ASP:HB3	0.40	1.92	16	1
1:C:246:ASN:OD1	1:C:247:ARG:HD2	0.40	2.16	17	1
1:C:215:GLU:HG2	1:C:217:HIS:H	0.40	1.76	8	1
1:A:64:LYS:HD2	1:A:65:CYS:N	0.40	2.31	6	1
1:C:211:CYS:SG	1:C:239:VAL:HG22	0.40	2.57	15	1
1:C:217:HIS:H	1:C:255:LEU:HD21	0.40	1.77	1	1
1:C:223:VAL:CG2	1:C:240:ALA:HB1	0.40	2.47	3	1
1:A:65:CYS:HA	1:A:68:LYS:HB3	0.40	1.93	7	1
2:B:107:TYR:CD1	2:B:107:TYR:N	0.40	2.90	10	1
1:C:215:GLU:HB2	2:D:321:TYR:HB3	0.40	1.92	14	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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	59/70 (84%)	52±2 (89±3%)	5±1 (8±2%)	2±2 (3±3%)	8	41
1	C	59/70 (84%)	52±2 (88±4%)	5±2 (9±4%)	2±2 (3±3%)	9	42
2	B	13/40 (32%)	8±2 (63±13%)	4±1 (28±10%)	1±1 (9±7%)	2	12
2	D	13/40 (32%)	8±2 (61±13%)	3±1 (25±11%)	2±1 (14±11%)	1	5
All	All	2880/4400 (65%)	2408 (84%)	341 (12%)	131 (5%)	5	29

All 42 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	D	308	THR	9
1	A	35	ALA	7
1	C	235	ALA	7
2	D	326	GLU	6
2	B	126	GLU	6
2	D	322	ASP	5
1	A	10	PRO	5
2	D	306	ILE	5
1	C	245	ASN	5
1	A	32	PRO	4
2	B	122	ASP	4
2	B	106	ILE	4
2	D	323	SER	4
1	C	246	ASN	4
2	D	311	ASN	3
1	C	210	PRO	3
1	A	46	ASN	3
1	A	17	HIS	3
1	A	18	VAL	3
1	A	45	ASN	3
2	D	324	MET	3
1	A	43	LYS	3
1	C	243	LYS	3
1	C	218	VAL	3
2	B	123	SER	2
1	C	217	HIS	2
2	B	124	MET	2
2	B	111	ASN	2
1	C	244	ASN	2
1	A	55	LEU	2

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Mol	Chain	Res	Type	Models (Total)
2	B	121	TYR	2
1	C	232	PRO	2
1	A	44	ASN	1
2	B	108	THR	1
1	C	216	SER	1
1	C	233	ASN	1
1	A	36	CYS	1
2	D	321	TYR	1
1	C	256	LYS	1
1	C	255	LEU	1
2	D	309	SER	1
1	A	16	SER	1

6.3.2 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 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	56/65 (86%)	52±1 (92±3%)	4±1 (8±3%)	20	66
1	C	56/65 (86%)	52±1 (92±3%)	4±1 (8±3%)	19	65
2	B	13/34 (38%)	13±1 (97±5%)	0±1 (3±5%)	45	87
2	D	13/34 (38%)	12±1 (93±7%)	1±1 (7±7%)	24	71
All	All	2760/3960 (70%)	2563 (93%)	197 (7%)	22	68

All 53 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	25	HIS	20
1	C	225	HIS	19
1	A	47	ARG	9
1	A	20	ARG	8
1	C	247	ARG	8
1	C	227	LYS	7
1	C	220	ARG	7
1	A	48	GLN	6
2	D	321	TYR	6

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Mol	Chain	Res	Type	Models (Total)
1	A	68	LYS	5
1	C	230	ASN	5
1	C	229	LEU	5
1	C	215	GLU	4
1	A	12	ARG	4
2	D	311	ASN	4
1	C	248	GLN	4
1	C	268	LYS	4
1	A	15	GLU	4
1	A	29	LEU	4
1	A	67	ASN	4
1	C	237	GLN	4
1	C	217	HIS	3
1	A	37	GLN	3
2	B	111	ASN	3
2	D	307	TYR	3
1	A	33	ASN	3
2	B	121	TYR	3
1	A	27	LYS	2
1	A	46	ASN	2
1	A	17	HIS	2
1	A	23	VAL	2
2	D	326	GLU	2
1	C	256	LYS	2
1	C	255	LEU	2
2	B	126	GLU	2
1	A	55	LEU	2
1	A	64	LYS	2
1	C	266	LEU	2
1	C	244	ASN	2
2	D	324	MET	1
1	A	44	ASN	1
1	C	212	ARG	1
1	A	66	LEU	1
2	B	124	MET	1
1	C	264	LYS	1
1	C	267	ASN	1
1	C	233	ASN	1
2	D	327	PRO	1
1	C	243	LYS	1
1	C	218	VAL	1
1	C	241	ARG	1

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Mol	Chain	Res	Type	Models (Total)
1	C	223	VAL	1
1	A	56	LYS	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 carbohydrates 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