



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:46 AM GMT

PDB ID : 2BNX  
Title : CRYSTAL STRUCTURE OF THE DIMERIC REGULATORY DOMAIN OF  
MOUSE DIAPHANEOUS-RELATED FORMIN (DRF), MDIA1  
Authors : Otomo, T.; Otomo, C.; Tomchick, D.R.; Machius, M.; Rosen, M.K.  
Deposited on : 2005-04-05  
Resolution : 2.40 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  
<http://wwpdb.org/validation/2016/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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

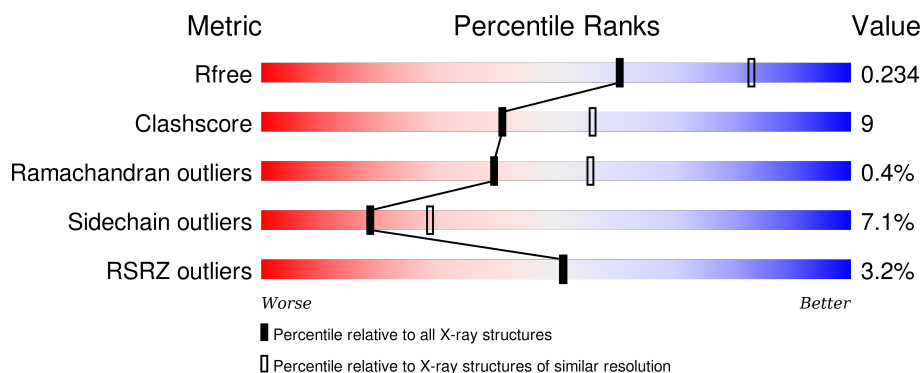
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*



The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	386	 4% 68% 16% • 12%
1	B	386	 2% 69% 16% • 12%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5687 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 DIAPHANOUS PROTEIN HOMOLOG 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	2	1
			2695	1689	467	517	22			
1	B	339	Total	C	N	O	S	0	2	0
			2742	1718	473	528	23			

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cl	0	0
			1	1		

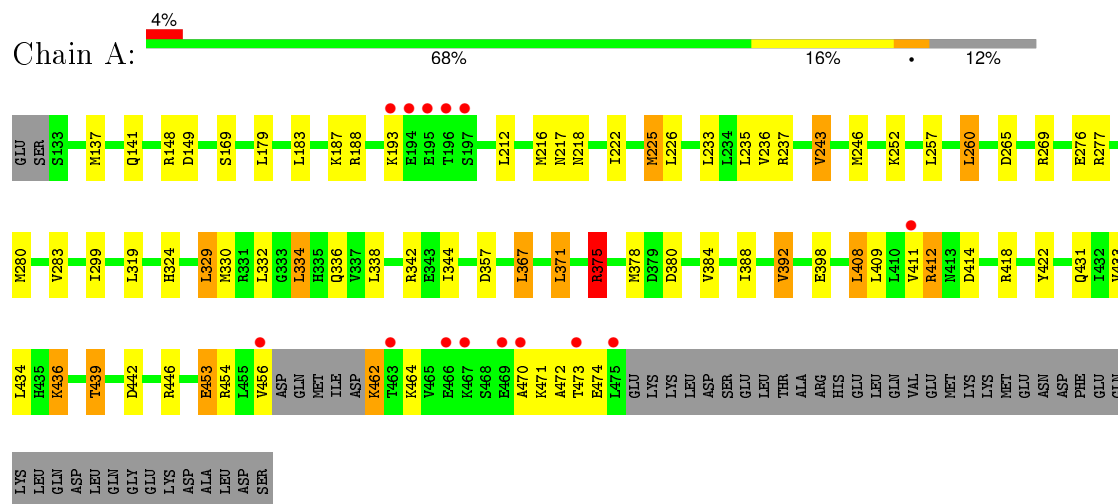
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	122	Total	O	0	2
			122	122		
3	B	127	Total	O	0	2
			127	127		

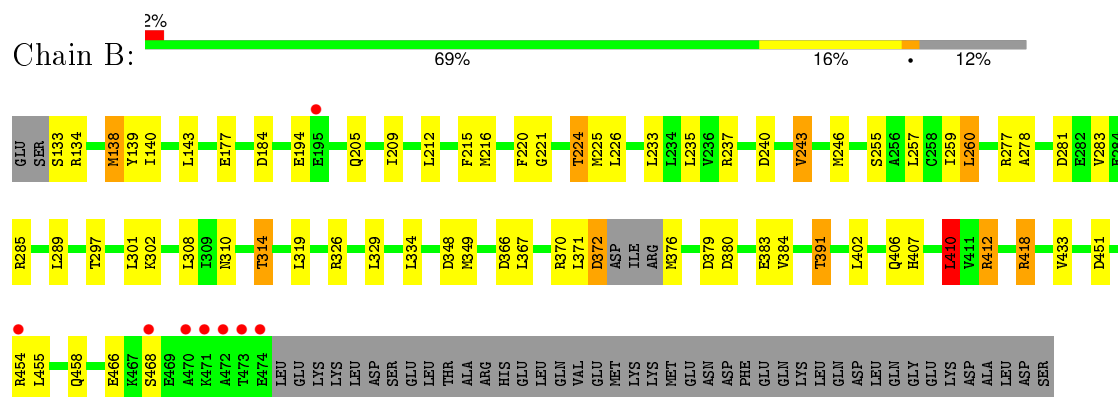
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: DIAPHANOUS PROTEIN HOMOLOG 1



#### • Molecule 1: DIAPHANOUS PROTEIN HOMOLOG 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	121.36 Å   121.36 Å   95.10 Å 90.00°   90.00°   120.00°	Depositor
Resolution (Å)	20.00 – 2.40 46.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (20.00-2.40) 99.8 (46.00-2.40)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.78 (at 2.39 Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, $R_{free}$	0.196 , 0.236 0.194 , 0.234	Depositor DCC
$R_{free}$ test set	1535 reflections (2.58%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.9	Xtriage
Anisotropy	0.595	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 49.9	EDS
Estimated twinning fraction	0.005 for -h,-k,l 0.024 for h,-h-k,-l 0.017 for -k,-h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 61285 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5687	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.39% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL

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	1.02	7/2731 (0.3%)	0.98	12/3680 (0.3%)
1	B	0.82	2/2778 (0.1%)	0.95	13/3736 (0.3%)
All	All	0.92	9/5509 (0.2%)	0.96	25/7416 (0.3%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	462	LYS	N-CA	19.66	1.85	1.46
1	A	453	GLU	CG-CD	19.20	1.80	1.51
1	A	453	GLU	CD-OE2	12.28	1.39	1.25
1	A	453	GLU	CD-OE1	10.37	1.37	1.25
1	B	466	GLU	CG-CD	7.77	1.63	1.51
1	A	462	LYS	CA-CB	7.62	1.70	1.53
1	A	473	THR	C-N	6.06	1.48	1.34
1	B	468	SER	CB-OG	5.83	1.49	1.42
1	A	453	GLU	CB-CG	5.37	1.62	1.52

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	375	ARG	NE-CZ-NH1	8.19	124.40	120.30
1	B	412	ARG	NE-CZ-NH2	-8.00	116.30	120.30
1	A	414	ASP	CB-CG-OD2	7.25	124.83	118.30
1	A	149	ASP	CB-CG-OD2	6.54	124.19	118.30
1	B	410	LEU	CA-CB-CG	6.34	129.88	115.30
1	B	326	ARG	NE-CZ-NH2	-6.31	117.14	120.30
1	B	418	ARG	NE-CZ-NH2	-6.15	117.23	120.30
1	A	371	LEU	CA-CB-CG	5.96	129.01	115.30
1	A	260	LEU	CA-CB-CG	5.84	128.74	115.30
1	B	412	ARG	CG-CD-NE	-5.83	99.56	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	366	ASP	CB-CG-OD2	5.81	123.53	118.30
1	B	281	ASP	CB-CG-OD1	5.76	123.48	118.30
1	B	260	LEU	CA-CB-CG	5.57	128.12	115.30
1	A	409	LEU	CA-CB-CG	5.55	128.07	115.30
1	B	348	ASP	CB-CG-OD1	5.53	123.28	118.30
1	B	379	ASP	CB-CG-OD2	5.51	123.26	118.30
1	A	265	ASP	CB-CG-OD2	5.46	123.21	118.30
1	A	453	GLU	CB-CG-CD	-5.43	99.53	114.20
1	B	240	ASP	CB-CG-OD2	5.41	123.17	118.30
1	A	371	LEU	CB-CG-CD2	5.35	120.09	111.00
1	A	380	ASP	CB-CG-OD2	5.18	122.96	118.30
1	A	375	ARG	CG-CD-NE	5.16	122.64	111.80
1	A	442	ASP	CB-CG-OD2	5.08	122.87	118.30
1	B	372	ASP	CB-CG-OD2	5.06	122.86	118.30
1	B	184	ASP	CB-CG-OD2	5.02	122.81	118.30

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	2695	0	2673	58	0
1	B	2742	0	2754	44	0
2	A	1	0	0	0	0
3	A	122	0	0	5	0
3	B	127	0	0	5	0
All	All	5687	0	5427	93	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 9.

All (93) 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:453:GLU:CG	1:A:453:GLU:CD	1.80	1.48
1:A:462:LYS:CA	1:A:462:LYS:N	1.85	1.37
1:A:179:LEU:HD21	1:A:225:MET:HE3	1.51	0.90
1:A:217[B]:ASN:O	1:A:217[B]:ASN:OD1	2.02	0.77
1:A:319:LEU:HD21	1:A:367:LEU:HD22	1.67	0.77
1:A:436:LYS:H	1:A:436:LYS:HD2	1.49	0.76
1:A:411[A]:VAL:HG21	1:A:422:TYR:CE1	2.21	0.76
3:A:2096:HOH:O	1:B:418:ARG:HD2	1.86	0.74
1:A:137:MET:O	1:A:141:GLN:HG3	1.88	0.74
1:A:375:ARG:HG2	1:A:375:ARG:HH11	1.54	0.72
1:A:411[B]:VAL:HA	1:B:433:VAL:HG22	1.74	0.70
1:A:183:LEU:HD11	1:A:225:MET:HE1	1.75	0.69
1:A:212:LEU:HB3	1:A:216:MET:HE3	1.74	0.68
1:A:411[A]:VAL:HG21	1:A:422:TYR:HE1	1.56	0.68
1:B:205:GLN:HB3	1:B:246:MET:HE1	1.75	0.68
1:A:453:GLU:CD	1:A:453:GLU:CB	2.62	0.67
1:B:226:LEU:HD21	1:B:257:LEU:HD22	1.77	0.67
1:A:456:VAL:HG23	1:B:458:GLN:HB3	1.76	0.67
1:B:216:MET:HE1	1:B:225:MET:HG2	1.79	0.65
1:A:378:MET:HB3	1:A:384:VAL:HG22	1.82	0.62
1:A:408:LEU:O	1:A:411[A]:VAL:HG22	2.01	0.61
1:B:372:ASP:HA	3:B:2102:HOH:O	2.00	0.61
1:A:436:LYS:CD	1:A:436:LYS:H	2.13	0.61
1:A:334:LEU:HD22	1:A:338:LEU:HG	1.82	0.60
1:A:338:LEU:O	1:A:342:ARG:HG3	2.01	0.60
1:A:299:ILE:HD13	1:A:344:ILE:HG21	1.84	0.59
1:A:212:LEU:HB3	1:A:216:MET:CE	2.33	0.58
1:A:169:SER:HB2	3:A:2018:HOH:O	2.05	0.57
1:B:310:ASN:O	1:B:314:THR:HB	2.06	0.56
1:B:451:ASP:HB3	1:B:454:ARG:HB3	1.88	0.55
1:B:205:GLN:HB3	1:B:246:MET:CE	2.35	0.55
1:A:226:LEU:HD21	1:A:257:LEU:HD22	1.89	0.55
1:B:138:MET:HE1	3:B:2001[B]:HOH:O	2.07	0.54
1:A:436:LYS:N	1:A:436:LYS:HD2	2.21	0.54
1:A:225:MET:HE3	1:A:225:MET:HA	1.90	0.54
1:A:433:VAL:HG11	1:B:407:HIS:O	2.08	0.54
1:A:179:LEU:HD21	1:A:225:MET:CE	2.31	0.53
1:B:205:GLN:C	1:B:246:MET:HE3	2.28	0.53
1:B:302:LYS:HB3	1:B:349:MET:HE1	1.90	0.53
1:A:148:ARG:HG2	1:A:148:ARG:NH1	2.25	0.52
1:B:216:MET:CE	1:B:225:MET:HG2	2.38	0.52
1:A:243:VAL:HG22	1:A:246:MET:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:255:SER:O	1:B:259:ILE:HG12	2.09	0.51
1:A:470:ALA:C	1:A:472:ALA:H	2.14	0.51
1:B:194:GLU:HA	3:B:2017:HOH:O	2.12	0.50
1:A:212:LEU:O	1:A:216:MET:HG3	2.12	0.49
1:B:212:LEU:HB3	1:B:216:MET:HE3	1.95	0.48
1:A:392:VAL:HG13	1:A:398:GLU:HA	1.94	0.48
1:B:283:VAL:HG21	3:B:2035:HOH:O	2.14	0.48
3:A:2105:HOH:O	1:B:391:THR:HG21	2.14	0.47
1:B:371:LEU:O	1:B:372:ASP:HB2	2.15	0.46
1:A:367:LEU:HD12	1:B:410:LEU:CD2	2.46	0.46
1:A:148:ARG:HG2	1:A:148:ARG:HH11	1.81	0.46
1:A:324:HIS:ND1	1:B:412:ARG:NH2	2.63	0.46
1:B:209:ILE:HG13	1:B:246:MET:HE2	1.98	0.46
1:A:408:LEU:O	1:A:411[B]:VAL:HG13	2.16	0.45
1:A:375:ARG:HG2	1:B:406:GLN:OE1	2.17	0.45
1:A:233:LEU:O	1:A:237:ARG:HG3	2.16	0.45
1:B:140:ILE:HD13	1:B:177:GLU:HG2	1.97	0.45
1:B:243:VAL:HG22	1:B:246:MET:HB3	1.98	0.44
1:B:139:TYR:O	1:B:143:LEU:HG	2.17	0.44
1:B:319:LEU:HD23	1:B:370:ARG:NH2	2.33	0.44
1:A:217[B]:ASN:O	1:A:218:ASN:HB3	2.17	0.44
1:A:225:MET:HA	1:A:225:MET:CE	2.47	0.44
1:B:297:THR:HB	1:B:301:LEU:HD23	2.00	0.43
1:A:217[B]:ASN:O	1:A:217[B]:ASN:CG	2.57	0.43
1:A:433:VAL:HG12	1:B:410:LEU:HB3	2.01	0.43
1:B:209:ILE:CG1	1:B:246:MET:HE2	2.49	0.43
1:A:269:ARG:HD3	3:A:2053:HOH:O	2.18	0.43
1:B:380:ASP:O	1:B:384:VAL:HG23	2.18	0.43
1:A:388:ILE:O	1:A:392:VAL:HB	2.19	0.43
1:A:462:LYS:C	1:A:464:LYS:H	2.23	0.42
1:A:418:ARG:HD2	3:B:2103:HOH:O	2.19	0.42
1:A:342:ARG:NH1	3:A:2083:HOH:O	2.52	0.42
1:A:236:VAL:HG12	1:A:277:ARG:HD2	2.02	0.42
1:A:431:GLN:O	1:A:436:LYS:NZ	2.53	0.41
1:B:233:LEU:O	1:B:237:ARG:HG3	2.20	0.41
1:A:375:ARG:HG2	1:A:375:ARG:NH1	2.30	0.41
1:A:329:LEU:HB3	1:A:334:LEU:HD12	2.03	0.41
1:A:277:ARG:HA	1:A:280:MET:HG2	2.02	0.41
1:B:220:PHE:O	1:B:224:THR:HG23	2.20	0.41
1:B:278:ALA:HB2	1:B:285:ARG:HA	2.03	0.41
1:A:342:ARG:NH2	1:A:357:ASP:OD1	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:MET:HG3	1:A:439:THR:HG21	2.03	0.40
1:A:217[B]:ASN:C	1:A:217[B]:ASN:OD1	2.59	0.40
1:A:433:VAL:CG1	1:B:410:LEU:HB3	2.51	0.40
1:B:205:GLN:O	1:B:246:MET:HE3	2.21	0.40
1:B:220:PHE:O	1:B:224:THR:CG2	2.69	0.40
1:B:380:ASP:HB3	1:B:383:GLU:HB2	2.02	0.40
1:B:289:LEU:HD21	1:B:308:LEU:HD23	2.02	0.40
1:B:216:MET:HE1	1:B:225:MET:HE2	2.03	0.40
1:B:215:PHE:O	1:B:221:GLY:HA3	2.22	0.40
1:A:367:LEU:CD1	1:B:410:LEU:HD22	2.51	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	336/386 (87%)	326 (97%)	7 (2%)	3 (1%)	21	30
1	B	337/386 (87%)	328 (97%)	9 (3%)	0	100	100
All	All	673/772 (87%)	654 (97%)	16 (2%)	3 (0%)	39	56

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	412	ARG
1	A	474	GLU
1	A	471	LYS

### 5.3.2 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 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	298/351 (85%)	272 (91%)	26 (9%)	13	19
1	B	309/351 (88%)	292 (94%)	17 (6%)	27	42
All	All	607/702 (86%)	564 (93%)	43 (7%)	18	28

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	187	LYS
1	A	188	ARG
1	A	193	LYS
1	A	222	ILE
1	A	225	MET
1	A	235	LEU
1	A	243	VAL
1	A	252	LYS
1	A	260	LEU
1	A	276	GLU
1	A	283	VAL
1	A	329	LEU
1	A	332	LEU
1	A	334	LEU
1	A	336	GLN
1	A	367	LEU
1	A	371	LEU
1	A	375	ARG
1	A	392	VAL
1	A	408	LEU
1	A	412	ARG
1	A	434	LEU
1	A	436	LYS
1	A	439	THR
1	A	446	ARG
1	A	454	ARG
1	B	133	SER

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Mol	Chain	Res	Type
1	B	134	ARG
1	B	138	MET
1	B	224	THR
1	B	235	LEU
1	B	243	VAL
1	B	260	LEU
1	B	277	ARG
1	B	314	THR
1	B	329	LEU
1	B	334	LEU
1	B	367	LEU
1	B	376	MET
1	B	391	THR
1	B	402	LEU
1	B	410	LEU
1	B	455	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	262	GLN
1	A	336	GLN
1	B	339	GLN
1	B	437	ASN

### 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

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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	338/386 (87%)	0.07	14 (4%)	41 42	42, 52, 75, 86	0
1	B	339/386 (87%)	0.08	8 (2%)	62 61	41, 54, 71, 91	0
All	All	677/772 (87%)	0.07	22 (3%)	51 51	41, 53, 73, 91	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	470	ALA	5.1
1	A	195	GLU	5.0
1	A	194	GLU	4.9
1	B	472	ALA	4.2
1	A	193	LYS	3.7
1	B	470	ALA	3.7
1	A	196	THR	3.4
1	A	467	LYS	3.1
1	B	473	THR	3.0
1	A	466	GLU	2.8
1	B	468	SER	2.7
1	A	475	LEU	2.7
1	B	471	LYS	2.6
1	A	473	THR	2.6
1	B	195	GLU	2.6
1	B	454	ARG	2.4
1	A	463	THR	2.3
1	A	411[A]	VAL	2.3
1	A	469	GLU	2.1
1	B	474	GLU	2.1
1	A	197	SER	2.0
1	A	456	VAL	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	CL	A	1500	1/1	0.88	0.10	-	80,80,80,80	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.