Full wwPDB X-ray Structure Validation Report ⓘ

Nov 22, 2023 – 10:04 PM JST

PDB ID	:	7XI4
Title	:	Crystal Structure of the NPAS4-ARNT heterodimer in complex with DNA
Authors	:	Sun, X.N.; Jing, L.Q.; Li, F.W.; Wu, D.L.
Deposited on	:	2022-04-12
Resolution	:	4.71 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
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:

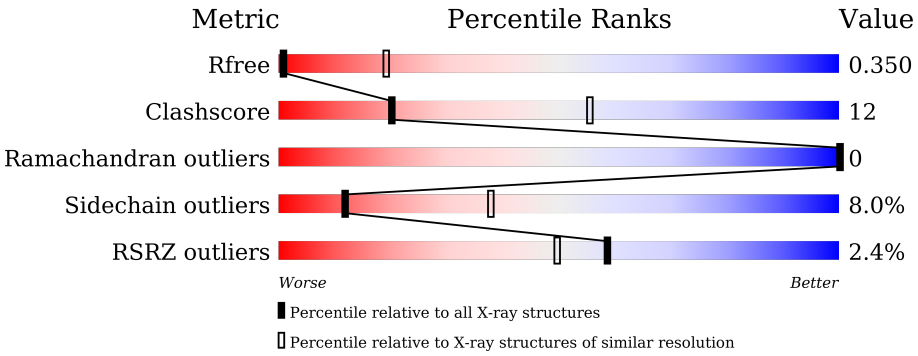
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 4.71 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}	130704	1085 (5.58-3.80)
Clashscore	141614	1159 (5.60-3.80)
Ramachandran outliers	138981	1094 (5.58-3.80)
Sidechain outliers	138945	1074 (5.58-3.80)
RSRZ outliers	127900	1118 (5.70-3.70)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=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	383	4%, 48%, 24%, ·, 26%
2	B	356	62%, 23%, ·, 14%
3	C	16	50%, 44%, 6%
4	D	16	62%, 38%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5300 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 Aryl hydrocarbon receptor nuclear translocator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	283	Total	C	N	O	S	0	0	0
			2280	1434	407	423	16			

- Molecule 2 is a protein called Neuronal PAS domain protein 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	306	Total	C	N	O	S	0	0	0
			2386	1519	411	445	11			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	349	LEU	-	expression tag	UNP A1L327
B	350	GLU	-	expression tag	UNP A1L327
B	351	HIS	-	expression tag	UNP A1L327
B	352	HIS	-	expression tag	UNP A1L327
B	353	HIS	-	expression tag	UNP A1L327
B	354	HIS	-	expression tag	UNP A1L327
B	355	HIS	-	expression tag	UNP A1L327
B	356	HIS	-	expression tag	UNP A1L327

- Molecule 3 is a DNA chain called DNA (5'-D(*GP*GP*AP*GP*GP*TP*CP*GP*TP*GP*AP*GP*TP*GP*AP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	15	Total	C	N	O	P	0	0	0
			316	149	61	91	15			

- Molecule 4 is a DNA chain called DNA (5'-D(P*CP*CP*AP*TP*CP*AP*CP*TP*CP*AP*CP*GP*AP*CP*CP*T)-3').

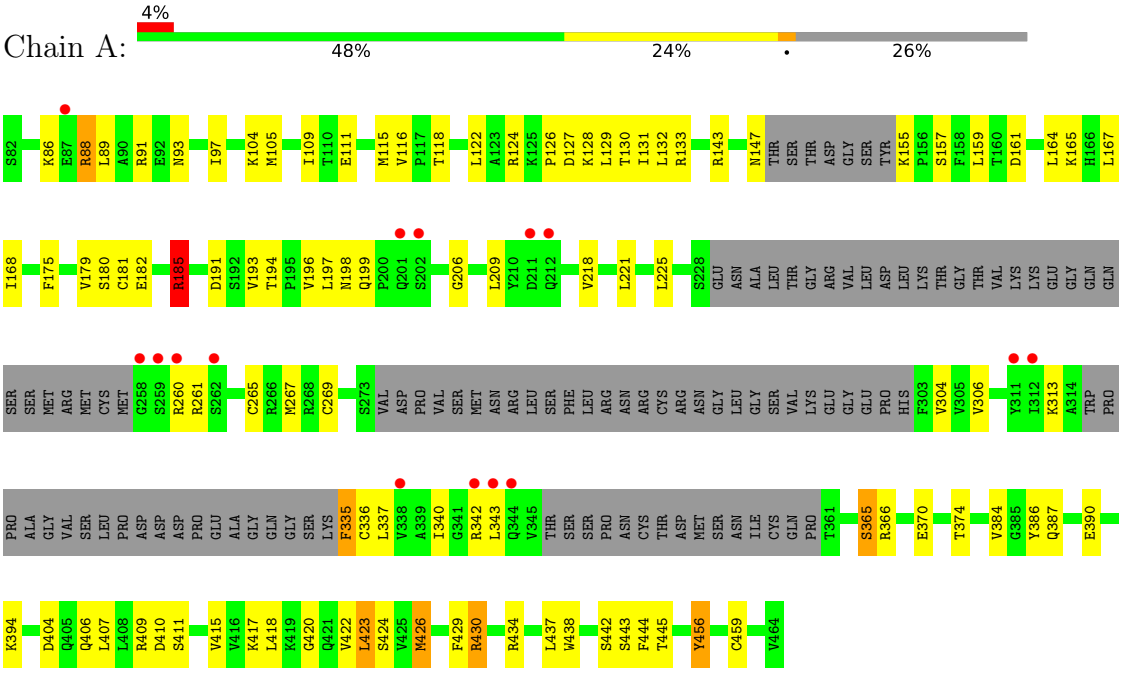
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	16	Total	C	N	O	P	0	0	0
			318	152	55	95	16			

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

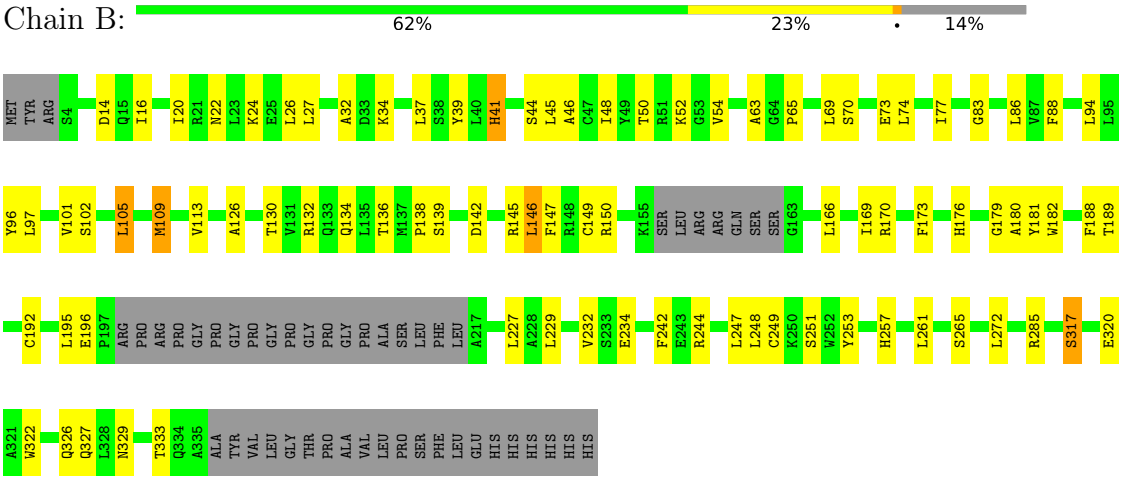
• Molecule 1: Aryl hydrocarbon receptor nuclear translocator

Chain A:



• Molecule 2: Neuronal PAS domain protein 4

Chain B:



• Molecule 3: DNA (5'-D(*GP*GP*AP*GP*GP*TP*CP*GP*TP*GP*AP*GP*TP*GP*AP*T)-3')

Chain C:

• Molecule 4: DNA (5'-D(P*CP*CP*AP*TP*CP*AP*CP*TP*CP*AP*CP*GP*AP*CP*CP*T)-3')

Chain D:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	105.24Å 105.24Å 215.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.63 – 4.71 29.63 – 4.71	Depositor EDS
% Data completeness (in resolution range)	84.6 (29.63-4.71) 84.7 (29.63-4.71)	Depositor EDS
R_{merge}	0.26	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.04 (at 4.61Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.314 , 0.351 0.314 , 0.350	Depositor DCC
R_{free} test set	299 reflections (5.26%)	wwPDB-VP
Wilson B-factor (Å^2)	56.9	Xtriage
Anisotropy	0.780	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.23 , 80.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.77	EDS
Total number of atoms	5300	wwPDB-VP
Average B, all atoms (Å^2)	109.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.27	0/2320	0.51	3/3124 (0.1%)
2	B	0.27	0/2440	0.48	1/3310 (0.0%)
3	C	0.59	0/355	0.92	0/548
4	D	0.57	0/354	0.88	0/541
All	All	0.32	0/5469	0.57	4/7523 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	185	ARG	NE-CZ-NH1	-6.86	116.87	120.30
1	A	423	LEU	CB-CG-CD1	-6.66	99.67	111.00
2	B	32	ALA	N-CA-C	5.39	125.56	111.00
1	A	122	LEU	CA-CB-CG	5.30	127.50	115.30

There are no chirality outliers.

There are no planarity outliers.

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	2280	0	2265	70	2
2	B	2386	0	2356	55	1
3	C	316	0	170	6	0
4	D	318	0	180	7	0
All	All	5300	0	4971	128	2

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 12.

All (128) 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)
2:B:86:LEU:HD13	2:B:97:LEU:HD21	1.45	0.95
1:A:415:VAL:HG12	1:A:423:LEU:HD23	1.49	0.93
2:B:86:LEU:HD13	2:B:97:LEU:CD2	2.01	0.90
1:A:404:ASP:HA	1:A:407:LEU:HD12	1.54	0.88
1:A:109:ILE:HG23	1:A:131:ILE:HD11	1.59	0.85
2:B:229:LEU:HD13	2:B:247:LEU:HB3	1.60	0.83
1:A:384:VAL:HG13	1:A:386:TYR:HB2	1.69	0.74
1:A:196:VAL:HG22	1:A:197:LEU:HD12	1.68	0.73
1:A:88:ARG:HA	1:A:91:ARG:HB2	1.69	0.72
1:A:175:PHE:HB2	1:A:193:VAL:HG22	1.73	0.71
1:A:127:ASP:OD1	1:A:130:THR:OG1	2.08	0.71
1:A:387:GLN:HG2	1:A:390:GLU:HG3	1.74	0.69
1:A:422:VAL:HA	1:A:444:PHE:HB3	1.75	0.69
2:B:48:ILE:HD11	2:B:94:LEU:HB3	1.75	0.69
1:A:180:SER:HA	1:A:336:CYS:HA	1.74	0.68
1:A:424:SER:HA	1:A:442:SER:HA	1.73	0.68
1:A:161:ASP:HA	2:B:74:LEU:HD22	1.76	0.66
2:B:317:SER:H	2:B:320:GLU:HB2	1.62	0.65
1:A:164:LEU:HB3	2:B:74:LEU:HD11	1.77	0.65
1:A:209:LEU:HD11	1:A:221:LEU:HD21	1.79	0.65
2:B:242:PHE:HB3	2:B:247:LEU:HD21	1.80	0.63
2:B:195:LEU:HD12	2:B:196:GLU:HG2	1.81	0.61
4:D:9:DC:H2"	4:D:10:DA:C8	2.37	0.60
2:B:257:HIS:HB2	2:B:285:ARG:HB2	1.83	0.60
2:B:146:LEU:HD12	2:B:170:ARG:HB3	1.84	0.59
1:A:181:CYS:HA	1:A:225:LEU:HD13	1.84	0.59
1:A:406:GLN:HG2	1:A:409:ARG:HH21	1.67	0.59
2:B:101:VAL:O	2:B:105:LEU:N	2.36	0.59
1:A:306:VAL:HG22	1:A:343:LEU:HD12	1.83	0.59
1:A:418:LEU:HD12	1:A:423:LEU:HD22	1.84	0.58
1:A:191:ASP:O	1:A:194:THR:HB	2.05	0.57
1:A:167:LEU:HD11	2:B:189:THR:HG21	1.85	0.57
2:B:39:TYR:HB2	4:D:9:DC:OP2	2.05	0.56
1:A:164:LEU:O	1:A:168:ILE:HG23	2.04	0.56
1:A:165:LYS:HD3	2:B:69:LEU:HD12	1.87	0.56
2:B:134:GLN:HG2	2:B:327:GLN:HE21	1.71	0.56
2:B:132:ARG:O	2:B:136:THR:N	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:11:DC:H2"	4:D:12:DG:C8	2.41	0.55
1:A:109:ILE:HG23	1:A:131:ILE:CD1	2.36	0.54
1:A:411:SER:O	1:A:415:VAL:HG13	2.07	0.53
2:B:329:ASN:O	2:B:333:THR:HG23	2.07	0.53
1:A:115:MET:HE2	2:B:181:TYR:CD2	2.44	0.53
3:C:15:DA:H61	4:D:3:DA:H61	1.57	0.53
2:B:244:ARG:HH11	2:B:248:LEU:HD11	1.73	0.52
1:A:175:PHE:CB	1:A:193:VAL:HG22	2.40	0.52
1:A:155:LYS:HG2	1:A:157:SER:O	2.10	0.52
2:B:130:THR:HG22	2:B:327:GLN:NE2	2.25	0.52
2:B:176:HIS:HB2	2:B:182:TRP:HB3	1.91	0.51
2:B:73:GLU:O	2:B:77:ILE:HG12	2.10	0.51
1:A:116:VAL:HG12	1:A:118:THR:HG22	1.92	0.51
2:B:50:THR:O	2:B:54:VAL:HG12	2.11	0.51
2:B:322:TRP:O	2:B:326:GLN:HG2	2.11	0.51
2:B:63:ALA:O	2:B:65:PRO:HD3	2.10	0.51
2:B:179:GLY:HA3	2:B:182:TRP:CE3	2.46	0.51
1:A:340:ILE:HD12	1:A:340:ILE:O	2.12	0.50
2:B:126:ALA:HB3	2:B:150:ARG:HH12	1.76	0.50
2:B:130:THR:HG22	2:B:327:GLN:CD	2.32	0.50
1:A:193:VAL:HG12	1:A:199:GLN:HB2	1.94	0.50
1:A:340:ILE:HD12	1:A:340:ILE:C	2.32	0.49
1:A:437:LEU:HD12	1:A:437:LEU:O	2.12	0.49
2:B:139:SER:O	2:B:145:ARG:NH2	2.45	0.49
2:B:45:LEU:O	2:B:48:ILE:HG22	2.13	0.48
2:B:37:LEU:HG	2:B:41:HIS:CD2	2.48	0.48
1:A:420:GLY:HA2	1:A:445:THR:H	1.78	0.48
2:B:179:GLY:HA3	2:B:182:TRP:HE3	1.78	0.48
3:C:10:DG:H2"	3:C:11:DA:C8	2.48	0.48
1:A:159:LEU:HD23	1:A:164:LEU:HB2	1.96	0.48
2:B:27:LEU:HD21	2:B:46:ALA:HA	1.95	0.48
1:A:197:LEU:HD21	1:A:304:VAL:HG11	1.95	0.48
1:A:365:SER:OG	1:A:366:ARG:N	2.46	0.48
4:D:10:DA:H2'	4:D:11:DC:C6	2.49	0.47
4:D:9:DC:H2"	4:D:10:DA:H8	1.78	0.47
3:C:9:DT:H2"	3:C:10:DG:C8	2.49	0.47
1:A:129:LEU:O	1:A:133:ARG:HG2	2.15	0.47
1:A:423:LEU:HD12	1:A:423:LEU:HA	1.51	0.47
1:A:267:MET:N	1:A:304:VAL:O	2.48	0.46
2:B:22:ASN:O	2:B:26:LEU:HB2	2.15	0.46
1:A:423:LEU:O	1:A:443:SER:N	2.39	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:ARG:HH12	1:A:89:LEU:HG	1.80	0.46
2:B:227:LEU:HD12	2:B:253:TYR:CZ	2.50	0.46
2:B:86:LEU:CD1	2:B:97:LEU:CD2	2.85	0.46
1:A:185:ARG:HH12	1:A:206:GLY:H	1.64	0.46
2:B:109:MET:O	2:B:113:VAL:HG23	2.16	0.46
2:B:136:THR:O	2:B:138:PRO:HD3	2.17	0.45
1:A:159:LEU:HD22	2:B:96:TYR:CZ	2.51	0.45
1:A:179:VAL:HG23	1:A:337:LEU:HB3	1.97	0.45
2:B:34:LYS:O	2:B:37:LEU:HB2	2.15	0.45
1:A:426:MET:N	1:A:426:MET:HE2	2.31	0.45
1:A:109:ILE:HG21	1:A:128:LYS:HG2	1.99	0.44
1:A:93:ASN:O	1:A:97:ILE:HG12	2.17	0.44
1:A:128:LYS:H	3:C:5:DG:P	2.40	0.44
1:A:194:THR:HA	1:A:199:GLN:O	2.16	0.44
2:B:70:SER:HB2	2:B:73:GLU:HG2	2.00	0.44
1:A:86:LYS:HA	1:A:86:LYS:HD2	1.90	0.43
1:A:197:LEU:CD2	1:A:304:VAL:HG21	2.48	0.43
1:A:418:LEU:HD23	1:A:418:LEU:HA	1.80	0.43
1:A:404:ASP:HA	1:A:407:LEU:CD1	2.38	0.43
1:A:126:PRO:HG2	1:A:131:ILE:HG22	2.00	0.43
1:A:109:ILE:HD13	1:A:128:LYS:HG2	2.01	0.43
4:D:3:DA:H2"	4:D:4:DT:C6	2.54	0.42
1:A:165:LYS:HE2	1:A:165:LYS:HB3	1.60	0.42
2:B:16:ILE:O	2:B:20:ILE:HG23	2.19	0.42
1:A:126:PRO:HB2	1:A:130:THR:HB	2.00	0.42
3:C:6:DT:H2"	3:C:7:DC:C6	2.54	0.42
2:B:83:GLY:HA3	2:B:192:CYS:O	2.19	0.42
1:A:340:ILE:C	1:A:340:ILE:CD1	2.88	0.42
2:B:97:LEU:HD23	2:B:97:LEU:HA	1.88	0.42
2:B:24:LYS:HE3	2:B:24:LYS:HB3	1.66	0.41
2:B:147:PHE:CZ	2:B:169:ILE:HD12	2.55	0.41
2:B:150:ARG:HG2	2:B:166:LEU:HD23	2.01	0.41
2:B:227:LEU:HD23	2:B:227:LEU:HA	1.74	0.41
2:B:229:LEU:HD21	2:B:232:VAL:HB	2.03	0.41
1:A:218:VAL:HA	1:A:221:LEU:HD23	2.03	0.41
1:A:430:ARG:HH11	1:A:434:ARG:HH11	1.67	0.41
2:B:173:PHE:CE1	2:B:188:PHE:HB2	2.55	0.41
3:C:10:DG:H2"	3:C:11:DA:H5'	2.02	0.41
1:A:181:CYS:HB2	1:A:335:PHE:HB2	2.01	0.41
1:A:131:ILE:HG21	1:A:131:ILE:HD13	1.84	0.41
1:A:197:LEU:HD22	1:A:304:VAL:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:374:THR:HG21	1:A:456:TYR:CE1	2.56	0.41
2:B:20:ILE:HD11	2:B:39:TYR:CE2	2.56	0.41
2:B:86:LEU:HG	2:B:88:PHE:HD1	1.86	0.41
1:A:366:ARG:HB3	1:A:374:THR:OG1	2.22	0.41
2:B:169:ILE:HG23	2:B:192:CYS:SG	2.61	0.40
1:A:128:LYS:O	1:A:131:ILE:HG12	2.21	0.40
1:A:132:LEU:HD21	2:B:16:ILE:HG23	2.02	0.40
1:A:111:GLU:O	1:A:115:MET:HG3	2.22	0.40
1:A:194:THR:O	1:A:198:ASN:HA	2.21	0.40

All (2) 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:370:GLU:OE2	2:B:180:ALA:N[5_545]	2.15	0.05
1:A:406:GLN:NE2	1:A:410:ASP:OD2[8_555]	2.18	0.02

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	271/383 (71%)	254 (94%)	17 (6%)	0	100	100
2	B	300/356 (84%)	282 (94%)	18 (6%)	0	100	100
All	All	571/739 (77%)	536 (94%)	35 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	259/346 (75%)	235 (91%)	24 (9%)	9 30
2	B	253/294 (86%)	236 (93%)	17 (7%)	16 43
All	All	512/640 (80%)	471 (92%)	41 (8%)	12 38

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88	ARG
1	A	104	LYS
1	A	105	MET
1	A	124	ARG
1	A	143	ARG
1	A	147	ASN
1	A	182	GLU
1	A	185	ARG
1	A	260	ARG
1	A	261	ARG
1	A	265	CYS
1	A	269	CYS
1	A	313	LYS
1	A	335	PHE
1	A	342	ARG
1	A	365	SER
1	A	394	LYS
1	A	417	LYS
1	A	426	MET
1	A	429	PHE
1	A	430	ARG
1	A	438	TRP
1	A	456	TYR
1	A	459	CYS
2	B	14	ASP
2	B	41	HIS
2	B	44	SER
2	B	52	LYS
2	B	102	SER
2	B	105	LEU
2	B	109	MET

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Mol	Chain	Res	Type
2	B	142	ASP
2	B	146	LEU
2	B	149	CYS
2	B	234	GLU
2	B	249	CYS
2	B	251	SER
2	B	261	LEU
2	B	265	SER
2	B	272	LEU
2	B	317	SER

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

Mol	Chain	Res	Type
2	B	128	HIS
2	B	327	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

There are no monosaccharides 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)

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^{th} 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	283/383 (73%)	0.13	15 (5%) 26 24	56, 98, 219, 235	0
2	B	306/356 (85%)	-0.29	0 100 100	50, 88, 158, 180	0
3	C	15/16 (93%)	0.07	0 100 100	85, 103, 124, 145	0
4	D	16/16 (100%)	0.22	0 100 100	88, 110, 141, 142	0
All	All	620/771 (80%)	-0.08	15 (2%) 59 50	50, 94, 216, 235	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	311	TYR	4.0
1	A	259	SER	3.4
1	A	262	SER	3.2
1	A	342	ARG	3.0
1	A	312	ILE	2.8
1	A	202	SER	2.8
1	A	344	GLN	2.7
1	A	212	GLN	2.7
1	A	338	VAL	2.4
1	A	258	GLY	2.4
1	A	260	ARG	2.4
1	A	201	GLN	2.2
1	A	343	LEU	2.2
1	A	87	GLU	2.1
1	A	211	ASP	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates (i)

There are no monosaccharides 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.