



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 08:30 AM GMT

PDB ID : 4B7W
Title : Ligand binding domain human hepatocyte nuclear factor 4alpha: Apo form
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Deposited on : 2012-08-24
Resolution : 4.00 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

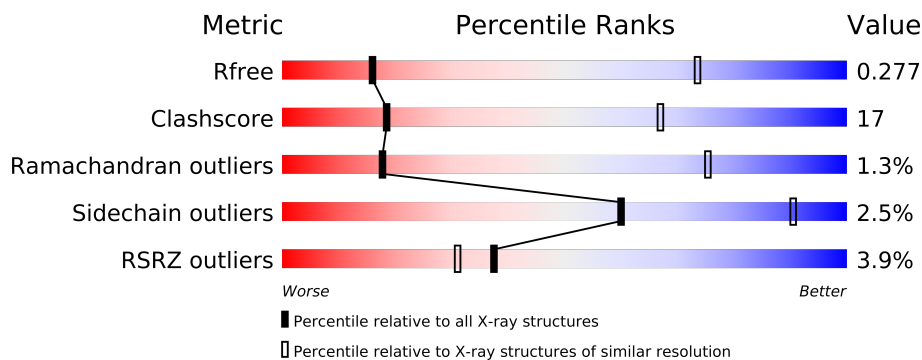
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 4.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1035 (4.52-3.46)
Clashscore	79885	1235 (4.50-3.50)
Ramachandran outliers	78287	1170 (4.50-3.50)
Sidechain outliers	78261	1156 (4.50-3.50)
RSRZ outliers	66119	1035 (4.52-3.46)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	239	
1	B	239	
1	C	239	
1	D	239	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6476 atoms, of which 0 are hydrogen and 0 are deuterium.

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 HEPATOCYTE NUCLEAR FACTOR 4-ALPHA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	202	Total	C	N	O	S	0	0	0
			1627	1050	271	297	9			
1	B	200	Total	C	N	O	S	0	0	0
			1611	1040	269	293	9			
1	C	202	Total	C	N	O	S	0	0	0
			1627	1050	271	297	9			
1	D	200	Total	C	N	O	S	0	0	0
			1611	1040	269	293	9			

There are 12 discrepancies between the modelled and reference sequences:

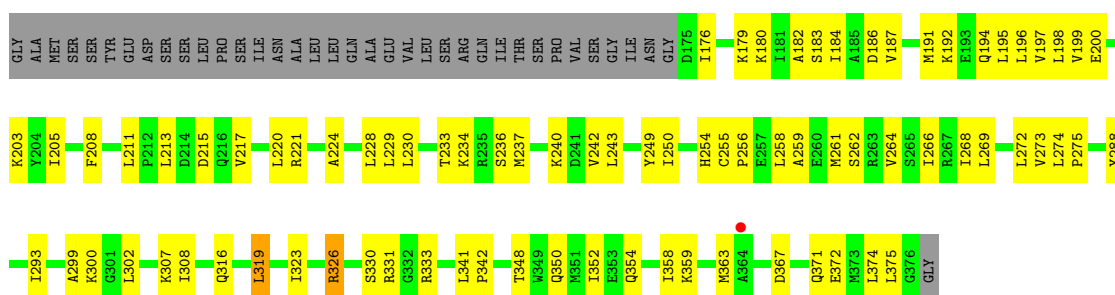
Chain	Residue	Modelled	Actual	Comment	Reference
A	139	GLY	-	EXPRESSION TAG	UNP P41235
A	140	ALA	-	EXPRESSION TAG	UNP P41235
A	141	MET	-	EXPRESSION TAG	UNP P41235
B	139	GLY	-	EXPRESSION TAG	UNP P41235
B	140	ALA	-	EXPRESSION TAG	UNP P41235
B	141	MET	-	EXPRESSION TAG	UNP P41235
C	139	GLY	-	EXPRESSION TAG	UNP P41235
C	140	ALA	-	EXPRESSION TAG	UNP P41235
C	141	MET	-	EXPRESSION TAG	UNP P41235
D	139	GLY	-	EXPRESSION TAG	UNP P41235
D	140	ALA	-	EXPRESSION TAG	UNP P41235
D	141	MET	-	EXPRESSION TAG	UNP P41235

3 Residue-property plots

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.

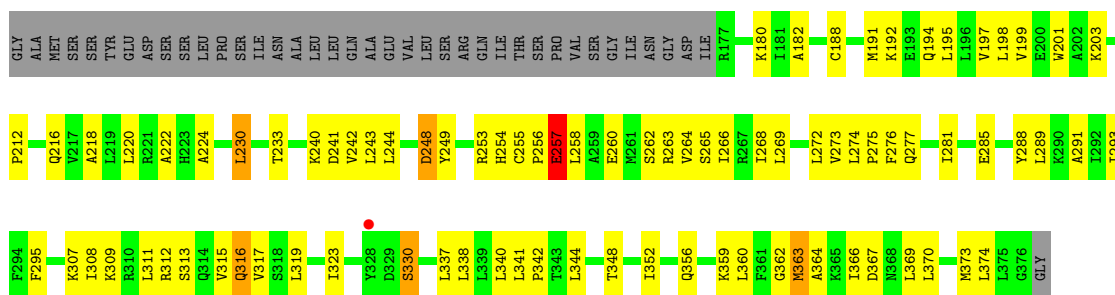
• Molecule 1: HEPATOCYTE NUCLEAR FACTOR 4-ALPHA

Chain A:



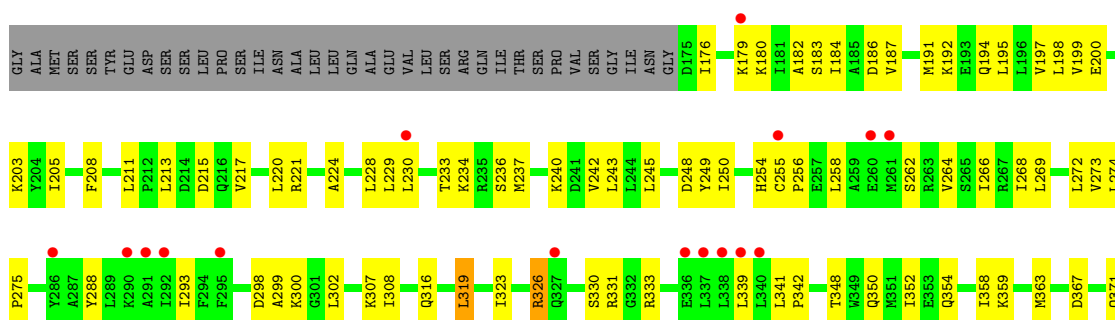
• Molecule 1: HEPATOCYTE NUCLEAR FACTOR 4-ALPHA

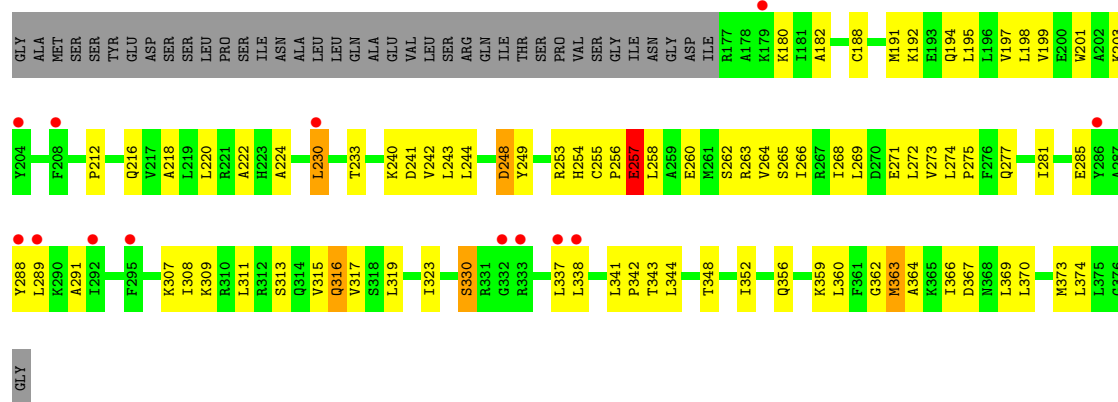
Chain B:



• Molecule 1: HEPATOCYTE NUCLEAR FACTOR 4-ALPHA

Chain C:





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	101.05Å 105.28Å 98.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 4.00 46.69 – 4.02	Depositor EDS
% Data completeness (in resolution range)	85.9 (50.00-4.00) 87.4 (46.69-4.02)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 4.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.250 , 0.280 0.259 , 0.277	Depositor DCC
R_{free} test set	374 reflections (4.68%)	DCC
Wilson B-factor (Å ²)	129.2	Xtriage
Anisotropy	0.554	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 104.0	EDS
Estimated twinning fraction	0.079 for l,-k,h	Xtriage
L-test for twinning	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtriage
Outliers	0 of 8011 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6476	wwPDB-VP
Average B, all atoms (Å ²)	180.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.30% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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	0.24	0/1655	0.42	0/2235
1	B	0.24	0/1639	0.42	0/2213
1	C	0.24	0/1655	0.42	0/2235
1	D	0.24	0/1639	0.42	0/2213
All	All	0.24	0/6588	0.42	0/8896

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1627	0	1675	55	0
1	B	1611	0	1660	61	0
1	C	1627	0	1675	56	0
1	D	1611	0	1660	58	0
All	All	6476	0	6670	221	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 17.

All (221) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:358:ILE:HG23	1:A:363:MET:HB2	1.63	0.80
1:B:364:ALA:HA	1:B:367:ASP:HB3	1.62	0.80
1:D:364:ALA:HA	1:D:367:ASP:HB3	1.61	0.80
1:A:341:LEU:HB2	1:A:342:PRO:HD3	1.66	0.78
1:C:358:ILE:HG23	1:C:363:MET:HB2	1.64	0.78
1:C:341:LEU:HB2	1:C:342:PRO:HD3	1.66	0.76
1:B:260:GLU:HA	1:B:263:ARG:HH12	1.55	0.72
1:B:241:ASP:HB3	1:B:253:ARG:HB2	1.72	0.72
1:D:260:GLU:HA	1:D:263:ARG:HH12	1.55	0.71
1:D:241:ASP:HB3	1:D:253:ARG:HB2	1.73	0.70
1:D:274:LEU:HB3	1:D:275:PRO:HD3	1.73	0.70
1:B:274:LEU:HB3	1:B:275:PRO:HD3	1.73	0.69
1:A:184:ILE:HD12	1:A:184:ILE:H	1.57	0.69
1:C:184:ILE:HD12	1:C:184:ILE:H	1.59	0.68
1:B:230:LEU:HD23	1:B:344:LEU:HD22	1.75	0.67
1:C:182:ALA:HB2	1:C:249:TYR:HB3	1.75	0.67
1:A:182:ALA:HB2	1:A:249:TYR:HB3	1.77	0.67
1:D:230:LEU:HD23	1:D:344:LEU:HD22	1.75	0.66
1:D:341:LEU:HB2	1:D:342:PRO:HD3	1.78	0.66
1:A:274:LEU:HB3	1:A:275:PRO:HD3	1.78	0.66
1:B:341:LEU:HB2	1:B:342:PRO:HD3	1.77	0.65
1:D:269:LEU:HA	1:D:273:VAL:HB	1.79	0.65
1:C:274:LEU:HB3	1:C:275:PRO:HD3	1.78	0.65
1:B:182:ALA:HB2	1:B:249:TYR:HB3	1.78	0.64
1:D:263:ARG:HA	1:D:266:ILE:HD12	1.79	0.64
1:D:182:ALA:HB2	1:D:249:TYR:HB3	1.79	0.64
1:B:269:LEU:HA	1:B:273:VAL:HB	1.78	0.64
1:A:233:THR:HG21	1:A:272:LEU:HB3	1.79	0.63
1:C:233:THR:HG21	1:C:272:LEU:HB3	1.80	0.63
1:A:230:LEU:HD11	1:A:293:ILE:HD12	1.80	0.62
1:B:263:ARG:HA	1:B:266:ILE:HD12	1.82	0.62
1:B:269:LEU:HD23	1:B:273:VAL:HG21	1.81	0.62
1:D:269:LEU:HD23	1:D:273:VAL:HG21	1.81	0.61
1:D:313:SER:HA	1:D:316:GLN:HG2	1.83	0.61
1:C:230:LEU:HD11	1:C:293:ILE:HD12	1.81	0.60
1:B:244:LEU:HD11	1:B:248:ASP:HA	1.83	0.60
1:A:192:LYS:HE2	1:A:367:ASP:HB2	1.84	0.60
1:C:192:LYS:HE2	1:C:367:ASP:HB2	1.84	0.59
1:D:352:ILE:HG22	1:D:356:GLN:HE21	1.67	0.59
1:B:352:ILE:HG22	1:B:356:GLN:HE21	1.68	0.58
1:B:313:SER:HA	1:B:316:GLN:HG2	1.86	0.58
1:C:299:ALA:HB3	1:C:302:LEU:HG	1.87	0.56
1:A:299:ALA:HB3	1:A:302:LEU:HG	1.86	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:244:LEU:HD11	1:D:248:ASP:HA	1.86	0.56
1:C:323:ILE:HG21	1:C:333:ARG:HB3	1.88	0.55
1:A:323:ILE:HG21	1:A:333:ARG:HB3	1.89	0.55
1:A:220:LEU:O	1:A:224:ALA:HB2	2.07	0.54
1:A:217:VAL:HG12	1:A:221:ARG:HD3	1.90	0.54
1:B:289:LEU:HD11	1:B:337:LEU:HD22	1.89	0.54
1:D:289:LEU:HD11	1:D:337:LEU:HD22	1.89	0.54
1:C:220:LEU:O	1:C:224:ALA:HB2	2.07	0.53
1:B:220:LEU:O	1:B:224:ALA:HB2	2.08	0.53
1:D:220:LEU:O	1:D:224:ALA:HB2	2.08	0.53
1:B:360:LEU:O	1:D:360:LEU:HD13	2.08	0.53
1:D:233:THR:HG23	1:D:273:VAL:HA	1.91	0.53
1:B:233:THR:HG23	1:B:273:VAL:HA	1.91	0.53
1:C:268:ILE:HG22	1:C:273:VAL:HG23	1.90	0.53
1:A:194:GLN:HA	1:A:197:VAL:HG22	1.91	0.53
1:C:180:LYS:O	1:C:250:ILE:HG12	2.08	0.53
1:C:217:VAL:HG12	1:C:221:ARG:HD3	1.90	0.53
1:B:199:VAL:O	1:B:203:LYS:HG2	2.09	0.53
1:A:180:LYS:O	1:A:250:ILE:HG12	2.08	0.53
1:B:362:GLY:O	1:B:366:ILE:HG12	2.09	0.53
1:A:268:ILE:HG22	1:A:273:VAL:HG23	1.91	0.52
1:C:194:GLN:HA	1:C:197:VAL:HG22	1.91	0.52
1:B:323:ILE:HG22	1:B:330:SER:HB2	1.91	0.52
1:B:364:ALA:HB3	1:D:360:LEU:HD11	1.91	0.52
1:D:362:GLY:O	1:D:366:ILE:HG12	2.10	0.52
1:D:199:VAL:O	1:D:203:LYS:HG2	2.09	0.52
1:B:240:LYS:O	1:B:242:VAL:HG23	2.10	0.51
1:D:254:HIS:O	1:D:256:PRO:HD3	2.10	0.51
1:B:212:PRO:O	1:B:216:GLN:HG3	2.10	0.51
1:B:360:LEU:HD13	1:D:360:LEU:O	2.11	0.51
1:D:212:PRO:O	1:D:216:GLN:HG3	2.11	0.51
1:D:323:ILE:HG22	1:D:330:SER:HB2	1.92	0.51
1:D:240:LYS:O	1:D:242:VAL:HG23	2.11	0.51
1:A:234:LYS:O	1:A:237:MET:HG2	2.12	0.50
1:D:264:VAL:O	1:D:268:ILE:HG13	2.12	0.50
1:D:243:LEU:HG	1:D:269:LEU:HD21	1.93	0.50
1:B:254:HIS:O	1:B:256:PRO:HD3	2.11	0.50
1:B:272:LEU:C	1:B:275:PRO:HD2	2.32	0.50
1:D:359:LYS:O	1:D:363:MET:HG2	2.12	0.50
1:A:211:LEU:HD23	1:A:307:LYS:HE3	1.94	0.50
1:A:269:LEU:HA	1:A:273:VAL:HB	1.94	0.49
1:C:200:GLU:OE1	1:C:203:LYS:HD2	2.11	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:240:LYS:O	1:A:242:VAL:HG23	2.13	0.49
1:A:183:SER:H	1:A:186:ASP:HB2	1.77	0.49
1:A:350:GLN:O	1:A:354:GLN:HG2	2.13	0.49
1:B:367:ASP:HA	1:B:370:LEU:HD12	1.95	0.49
1:C:350:GLN:O	1:C:354:GLN:HG2	2.12	0.49
1:B:264:VAL:O	1:B:268:ILE:HG13	2.12	0.49
1:C:269:LEU:HA	1:C:273:VAL:HB	1.95	0.49
1:B:288:TYR:CD2	1:B:319:LEU:HD23	2.48	0.49
1:B:359:LYS:O	1:B:363:MET:HG2	2.13	0.49
1:A:200:GLU:OE1	1:A:203:LYS:HD2	2.12	0.49
1:C:359:LYS:NZ	1:C:375:LEU:HD13	2.27	0.49
1:D:367:ASP:HA	1:D:370:LEU:HD12	1.95	0.48
1:D:272:LEU:C	1:D:275:PRO:HD2	2.33	0.48
1:C:272:LEU:C	1:C:275:PRO:HD2	2.34	0.48
1:B:265:SER:HA	1:B:268:ILE:HD12	1.95	0.48
1:C:183:SER:H	1:C:186:ASP:HB2	1.78	0.48
1:C:211:LEU:HD23	1:C:307:LYS:HE3	1.94	0.48
1:C:234:LYS:O	1:C:237:MET:HG2	2.13	0.48
1:D:308:ILE:HA	1:D:311:LEU:HD12	1.94	0.48
1:C:240:LYS:O	1:C:242:VAL:HG23	2.13	0.48
1:B:243:LEU:HG	1:B:269:LEU:HD21	1.93	0.48
1:A:272:LEU:C	1:A:275:PRO:HD2	2.34	0.48
1:D:288:TYR:CD2	1:D:319:LEU:HD23	2.48	0.48
1:B:308:ILE:HA	1:B:311:LEU:HD12	1.95	0.48
1:D:366:ILE:O	1:D:370:LEU:HG	2.14	0.48
1:D:319:LEU:O	1:D:323:ILE:HG12	2.13	0.48
1:D:262:SER:O	1:D:266:ILE:HG13	2.14	0.47
1:A:359:LYS:NZ	1:A:375:LEU:HD13	2.29	0.47
1:B:268:ILE:HG22	1:B:273:VAL:HG23	1.95	0.47
1:B:366:ILE:O	1:B:370:LEU:HG	2.14	0.47
1:D:268:ILE:HG22	1:D:273:VAL:HG23	1.95	0.47
1:C:323:ILE:HG22	1:C:330:SER:HB2	1.96	0.47
1:A:323:ILE:HG22	1:A:330:SER:HB2	1.97	0.47
1:B:262:SER:O	1:B:266:ILE:HG13	2.14	0.47
1:A:236:SER:OG	1:A:243:LEU:HA	2.15	0.47
1:D:291:ALA:HB3	1:D:315:VAL:HG11	1.97	0.47
1:D:265:SER:HA	1:D:268:ILE:HD12	1.97	0.47
1:B:194:GLN:HA	1:B:197:VAL:HG22	1.96	0.47
1:A:187:VAL:O	1:A:191:MET:HG3	2.15	0.47
1:C:187:VAL:O	1:C:191:MET:HG3	2.15	0.47
1:C:236:SER:OG	1:C:243:LEU:HA	2.15	0.47
1:C:255:CYS:SG	1:C:258:LEU:HD12	2.55	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:348:THR:O	1:A:352:ILE:HG13	2.16	0.46
1:B:255:CYS:SG	1:B:257:GLU:HG2	2.56	0.46
1:B:256:PRO:C	1:B:258:LEU:H	2.19	0.46
1:B:291:ALA:HB3	1:B:315:VAL:HG11	1.96	0.46
1:B:319:LEU:O	1:B:323:ILE:HG12	2.15	0.46
1:D:255:CYS:SG	1:D:257:GLU:HG2	2.56	0.46
1:A:308:ILE:H	1:A:308:ILE:HD12	1.79	0.46
1:D:194:GLN:HA	1:D:197:VAL:HG22	1.98	0.46
1:B:268:ILE:O	1:B:273:VAL:HG23	2.16	0.46
1:D:256:PRO:C	1:D:258:LEU:H	2.19	0.46
1:C:195:LEU:HD21	1:C:374:LEU:HD11	1.98	0.46
1:C:331:ARG:NH1	1:D:317:VAL:HG11	2.30	0.45
1:C:348:THR:O	1:C:352:ILE:HG13	2.16	0.45
1:A:221:ARG:HG2	1:A:372:GLU:O	2.16	0.45
1:A:255:CYS:SG	1:A:258:LEU:HD12	2.56	0.45
1:C:213:LEU:O	1:C:217:VAL:HG23	2.17	0.45
1:A:299:ALA:HB3	1:A:302:LEU:CG	2.47	0.45
1:A:359:LYS:NZ	1:A:371:GLN:HE22	2.15	0.45
1:C:221:ARG:HG2	1:C:372:GLU:O	2.17	0.45
1:C:359:LYS:NZ	1:C:371:GLN:HE22	2.15	0.45
1:C:308:ILE:H	1:C:308:ILE:HD12	1.81	0.44
1:A:195:LEU:HD21	1:A:374:LEU:HD11	1.98	0.44
1:C:354:GLN:O	1:C:358:ILE:HG13	2.17	0.44
1:C:300:LYS:NZ	1:C:300:LYS:HB2	2.32	0.44
1:C:229:LEU:O	1:C:233:THR:HG23	2.17	0.44
1:A:213:LEU:O	1:A:217:VAL:HG23	2.17	0.44
1:C:195:LEU:HD21	1:C:228:LEU:HD11	1.98	0.44
1:A:354:GLN:O	1:A:358:ILE:HG13	2.17	0.44
1:B:348:THR:O	1:B:352:ILE:HG13	2.17	0.44
1:D:188:CYS:O	1:D:192:LYS:HG3	2.17	0.44
1:D:370:LEU:O	1:D:374:LEU:HB2	2.18	0.44
1:D:268:ILE:O	1:D:273:VAL:HG23	2.17	0.44
1:B:191:MET:O	1:B:195:LEU:HB2	2.17	0.44
1:C:299:ALA:HB3	1:C:302:LEU:CG	2.47	0.44
1:C:319:LEU:HD22	1:C:323:ILE:HD11	2.00	0.44
1:D:198:LEU:O	1:D:201:TRP:HB3	2.18	0.44
1:C:176:ILE:HA	1:C:179:LYS:HD2	2.00	0.44
1:D:307:LYS:O	1:D:311:LEU:HG	2.18	0.44
1:A:195:LEU:HD21	1:A:228:LEU:HD11	1.99	0.44
1:A:300:LYS:NZ	1:A:300:LYS:HB2	2.33	0.44
1:A:176:ILE:HA	1:A:179:LYS:HD2	2.00	0.43
1:B:370:LEU:O	1:B:374:LEU:HB2	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:264:VAL:O	1:A:268:ILE:HG13	2.19	0.43
1:A:268:ILE:O	1:A:273:VAL:HG23	2.18	0.43
1:A:262:SER:O	1:A:266:ILE:HG13	2.18	0.43
1:A:199:VAL:O	1:A:203:LYS:HG3	2.18	0.43
1:B:188:CYS:O	1:B:192:LYS:HG3	2.19	0.43
1:C:319:LEU:O	1:C:323:ILE:HG13	2.19	0.43
1:B:307:LYS:O	1:B:311:LEU:HG	2.19	0.43
1:B:198:LEU:O	1:B:201:TRP:HB3	2.19	0.43
1:A:229:LEU:O	1:A:233:THR:HG23	2.19	0.43
1:C:199:VAL:O	1:C:203:LYS:HG3	2.18	0.43
1:D:191:MET:O	1:D:195:LEU:HB2	2.19	0.43
1:D:348:THR:O	1:D:352:ILE:HG13	2.19	0.43
1:A:319:LEU:O	1:A:323:ILE:HG13	2.19	0.43
1:A:255:CYS:SG	1:A:258:LEU:HB2	2.59	0.42
1:D:281:ILE:HG23	1:D:285:GLU:HB2	2.01	0.42
1:B:364:ALA:HB2	1:D:360:LEU:HD21	2.01	0.42
1:A:288:TYR:CD2	1:A:319:LEU:HG	2.54	0.42
1:C:262:SER:O	1:C:266:ILE:HG13	2.19	0.42
1:A:342:PRO:HG3	1:B:342:PRO:HG3	2.00	0.42
1:C:198:LEU:HD13	1:C:198:LEU:O	2.19	0.42
1:B:289:LEU:O	1:B:293:ILE:HG13	2.19	0.42
1:D:273:VAL:O	1:D:277:GLN:HG3	2.20	0.42
1:A:319:LEU:HD22	1:A:323:ILE:HD11	2.00	0.42
1:C:268:ILE:O	1:C:273:VAL:HG23	2.19	0.42
1:D:218:ALA:O	1:D:222:ALA:HB2	2.20	0.42
1:A:254:HIS:O	1:A:256:PRO:HD3	2.20	0.41
1:B:218:ALA:O	1:B:222:ALA:HB2	2.20	0.41
1:C:254:HIS:O	1:C:256:PRO:HD3	2.21	0.41
1:B:369:LEU:O	1:B:373:MET:HG2	2.20	0.41
1:A:198:LEU:O	1:A:198:LEU:HD13	2.19	0.41
1:D:369:LEU:O	1:D:373:MET:HG2	2.20	0.41
1:C:205:ILE:HG22	1:C:208:PHE:H	1.84	0.41
1:B:276:PHE:CD2	1:B:281:ILE:HD12	2.55	0.41
1:B:281:ILE:HG23	1:B:285:GLU:HB2	2.03	0.41
1:A:205:ILE:HG22	1:A:208:PHE:H	1.84	0.41
1:C:288:TYR:CD2	1:C:319:LEU:HG	2.55	0.41
1:C:264:VAL:O	1:C:268:ILE:HG13	2.21	0.41
1:B:244:LEU:CD1	1:B:248:ASP:HA	2.51	0.41
1:A:192:LYS:O	1:A:196:LEU:HG	2.20	0.41
1:C:255:CYS:SG	1:C:258:LEU:HB2	2.61	0.41
1:B:338:LEU:C	1:B:340:LEU:H	2.24	0.41
1:C:323:ILE:CG2	1:C:330:SER:HB2	2.51	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:352:ILE:HG22	1:D:356:GLN:NE2	2.35	0.40
1:A:331:ARG:NH1	1:B:317:VAL:HG11	2.35	0.40
1:C:339:LEU:HD21	1:D:338:LEU:HD22	2.02	0.40
1:B:198:LEU:O	1:B:198:LEU:HD23	2.21	0.40
1:C:298:ASP:OD1	1:D:271:GLU:HG2	2.21	0.40
1:B:273:VAL:O	1:B:277:GLN:HG3	2.21	0.40
1:A:259:ALA:C	1:A:261:MET:H	2.25	0.40
1:D:271:GLU:HB3	1:D:343:THR:HG21	2.04	0.40
1:C:245:LEU:HB2	1:C:248:ASP:O	2.22	0.40
1:B:295:PHE:O	1:B:312:ARG:HB2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 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 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	200/239 (84%)	176 (88%)	23 (12%)	1 (0%)	38	88
1	B	198/239 (83%)	176 (89%)	18 (9%)	4 (2%)	11	68
1	C	200/239 (84%)	175 (88%)	24 (12%)	1 (0%)	38	88
1	D	198/239 (83%)	177 (89%)	17 (9%)	4 (2%)	11	68
All	All	796/956 (83%)	704 (88%)	82 (10%)	10 (1%)	18	75

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	330	SER
1	D	330	SER
1	B	363	MET
1	D	363	MET
1	B	180	LYS
1	D	180	LYS
1	A	326	ARG
1	B	257	GLU

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Mol	Chain	Res	Type
1	C	326	ARG
1	D	257	GLU

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	179/209 (86%)	175 (98%)	4 (2%)	64	91
1	B	177/209 (85%)	172 (97%)	5 (3%)	56	89
1	C	179/209 (86%)	175 (98%)	4 (2%)	64	91
1	D	177/209 (85%)	172 (97%)	5 (3%)	56	89
All	All	712/836 (85%)	694 (98%)	18 (2%)	60	90

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	215	ASP
1	A	316	GLN
1	A	319	LEU
1	A	326	ARG
1	B	230	LEU
1	B	248	ASP
1	B	257	GLU
1	B	309	LYS
1	B	316	GLN
1	C	215	ASP
1	C	316	GLN
1	C	319	LEU
1	C	326	ARG
1	D	230	LEU
1	D	248	ASP
1	D	257	GLU
1	D	309	LYS
1	D	316	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	277	GLN
1	A	284	ASN
1	A	324	ASN
1	A	350	GLN
1	A	356	GLN
1	B	227	HIS
1	B	277	GLN
1	B	354	GLN
1	B	356	GLN
1	C	277	GLN
1	C	284	ASN
1	C	324	ASN
1	C	350	GLN
1	C	356	GLN
1	C	371	GLN
1	D	227	HIS
1	D	277	GLN
1	D	345	GLN
1	D	354	GLN
1	D	356	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no ligands in this entry.

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	202/239 (84%)	0.18	1 (0%) 88 78	81, 158, 228, 285	0
1	B	200/239 (83%)	0.04	1 (0%) 88 78	53, 134, 205, 267	0
1	C	202/239 (84%)	0.60	16 (7%) 13 14	135, 204, 262, 306	0
1	D	200/239 (83%)	0.43	13 (6%) 18 19	134, 210, 254, 286	0
All	All	804/956 (84%)	0.31	31 (3%) 37 31	53, 184, 252, 306	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	179	LYS	4.1
1	C	286	TYR	3.7
1	C	338	LEU	3.7
1	D	289	LEU	3.6
1	D	338	LEU	3.6
1	C	290	LYS	3.6
1	C	337	LEU	3.2
1	C	339	LEU	3.2
1	C	327	GLN	3.1
1	C	291	ALA	3.0
1	D	230	LEU	3.0
1	C	260	GLU	2.8
1	C	255	CYS	2.7
1	C	340	LEU	2.7
1	D	286	TYR	2.7
1	D	204	TYR	2.6
1	D	337	LEU	2.6
1	D	288	TYR	2.6
1	D	333	ARG	2.5
1	C	292	ILE	2.4
1	B	328	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	332	GLY	2.3
1	D	295	PHE	2.2
1	C	336	GLU	2.2
1	C	261	MET	2.2
1	C	230	LEU	2.1
1	D	208	PHE	2.1
1	C	295	PHE	2.0
1	A	364	ALA	2.0
1	D	292	ILE	2.0
1	D	179	LYS	2.0

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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.