



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:21 PM UTC

PDB ID : 3F5C / pdb_00003f5c
Title : Structure of Dax-1:LRH-1 complex
Authors : Fletterick, R.J.; Sablin, E.P.
Deposited on : 2008-11-03
Resolution : 3.00 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

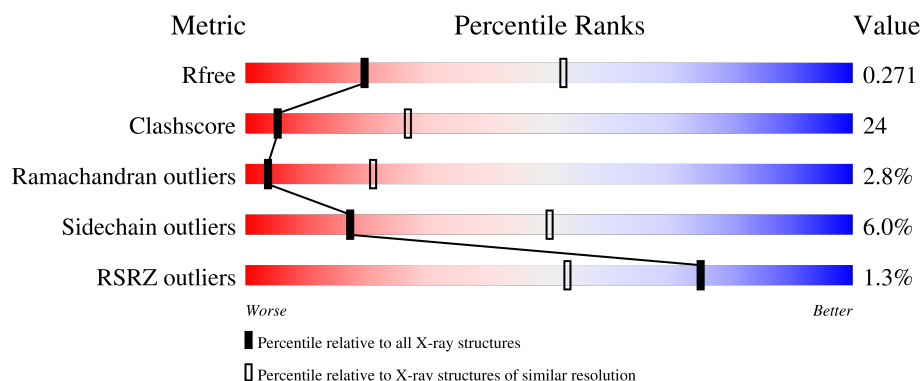
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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 $\leq 5\%$. 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	248	
2	B	268	
2	C	268	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4936 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 Nuclear receptor subfamily 5 group A member 2.

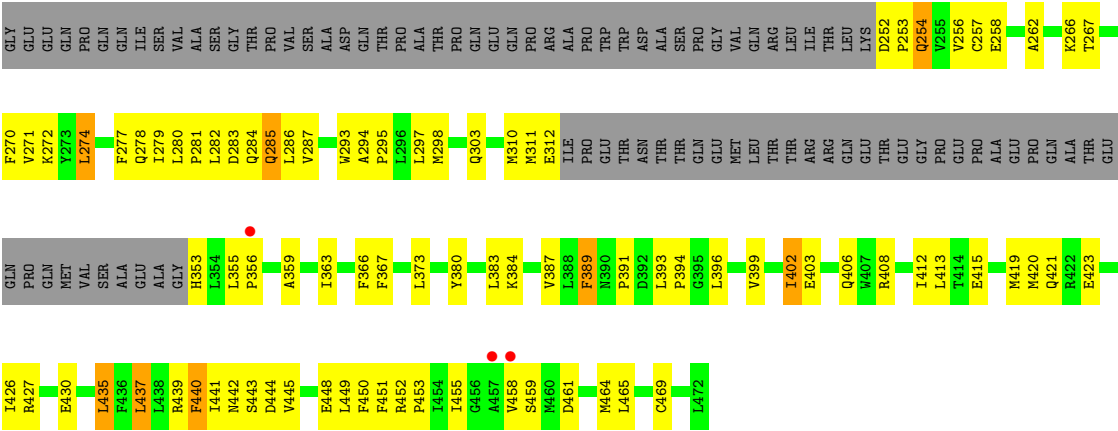
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	243	Total	C	N	O	S	0	0	0
			1983	1270	337	367	9			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	525	LEU	ILE	engineered mutation	UNP P45448

- Molecule 2 is a protein called Nuclear receptor subfamily 0 group B member 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	183	Total	C	N	O	S	0	0	0
			1485	970	243	257	15			
2	C	181	Total	C	N	O	S	0	0	0
			1468	958	240	255	15			



4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	103.36Å 103.36Å 117.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.79 – 3.00 24.79 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.4 (24.79-3.00) 98.2 (24.79-3.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 3.01Å)	Xtriage
Refinement program	PHENIX, CNS	Depositor
R, R_{free}	0.222 , 0.279 0.219 , 0.271	Depositor DCC
R_{free} test set	703 reflections (2.88%)	wwPDB-VP
Wilson B-factor (Å ²)	79.9	Xtriage
Anisotropy	0.004	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 58.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.053 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4936	wwPDB-VP
Average B, all atoms (Å ²)	117.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.17% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.66	0/2019	1.01	9/2731 (0.3%)
2	B	0.75	0/1517	1.03	6/2050 (0.3%)
2	C	0.67	0/1500	0.97	4/2028 (0.2%)
All	All	0.69	0/5036	1.01	19/6809 (0.3%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	444	ASP	N-CA-C	-11.37	99.94	114.04
1	A	508	TYR	CA-C-N	11.09	133.70	119.84
1	A	508	TYR	C-N-CA	11.09	133.70	119.84
1	A	356	GLU	N-CA-C	10.53	126.62	111.56
2	B	358	ALA	N-CA-C	-9.11	102.18	113.38
2	B	355	LEU	CA-C-N	7.95	129.78	119.84
2	B	355	LEU	C-N-CA	7.95	129.78	119.84
2	C	389	PHE	CB-CA-C	-7.50	99.15	111.68
2	C	274	LEU	CA-C-N	7.09	126.61	119.24
2	C	274	LEU	C-N-CA	7.09	126.61	119.24
1	A	357	LYS	N-CA-C	6.34	119.86	111.75
2	C	444	ASP	N-CA-C	-6.01	104.10	112.45
1	A	545	VAL	CA-C-N	5.63	126.87	119.84
1	A	545	VAL	C-N-CA	5.63	126.87	119.84
1	A	474	VAL	CB-CA-C	-5.40	104.94	112.02
2	B	441	ILE	N-CA-C	5.40	116.47	111.45
2	B	425	GLN	N-CA-C	-5.24	106.03	112.90
1	A	420	GLY	N-CA-C	-5.14	100.99	113.18
1	A	509	PRO	N-CA-C	5.11	122.99	112.47

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	1983	0	1997	105	0
2	B	1485	0	1523	71	0
2	C	1468	0	1499	70	0
All	All	4936	0	5019	242	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 24.

All (242) 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:358:LEU:HB2	1:A:359:SER:HA	1.44	0.99
1:A:356:GLU:O	1:A:356:GLU:HG2	1.64	0.98
1:A:333:ASP:O	1:A:334:GLU:HB2	1.65	0.94
2:C:282:LEU:HA	2:C:285:GLN:HB3	1.52	0.91
1:A:358:LEU:CB	1:A:359:SER:HA	2.00	0.86
1:A:419:GLU:HG3	1:A:420:GLY:H	1.41	0.85
2:B:442:ASN:O	2:B:443:SER:HB2	1.74	0.85
2:B:411:GLN:HE21	2:B:411:GLN:HA	1.43	0.82
1:A:548:ASN:O	2:B:275:PRO:HG3	1.81	0.81
2:B:442:ASN:HB3	2:B:445:VAL:HG23	1.63	0.79
2:B:254:GLN:CD	2:B:254:GLN:H	1.90	0.77
1:A:444:ASN:C	1:A:446:LEU:H	1.93	0.75
2:C:294:ALA:HB3	2:C:295:PRO:HD3	1.68	0.75
1:A:442:ALA:HB2	2:C:281:PRO:HB3	1.70	0.73
1:A:511:GLN:HB3	1:A:514:LYS:HB2	1.68	0.73
2:B:294:ALA:HB3	2:B:295:PRO:HD3	1.70	0.73
1:A:324:ILE:HD12	1:A:324:ILE:H	1.54	0.72
2:C:310:MET:HE2	2:C:353:HIS:N	2.04	0.72
2:C:373:LEU:HD22	2:C:430:GLU:HG2	1.71	0.71
2:C:442:ASN:O	2:C:443:SER:HB3	1.90	0.70
1:A:356:GLU:O	1:A:356:GLU:CG	2.37	0.70
1:A:332:PRO:O	1:A:333:ASP:HB2	1.90	0.70
1:A:346:GLN:HA	1:A:349:GLN:HE21	1.55	0.70
2:B:378:LYS:HD3	2:B:416:HIS:CD2	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:424:TYR:CD2	2:B:424:TYR:O	2.45	0.69
2:B:252:ASP:O	2:B:256:VAL:HG22	1.93	0.69
2:C:461:ASP:O	2:C:465:LEU:HD13	1.93	0.69
1:A:333:ASP:O	1:A:334:GLU:CB	2.40	0.68
2:C:254:GLN:O	2:C:258:GLU:HB2	1.93	0.68
1:A:452:GLU:O	1:A:456:ARG:HB2	1.94	0.67
2:B:441:ILE:O	2:B:442:ASN:CB	2.44	0.65
1:A:332:PRO:O	1:A:333:ASP:CB	2.44	0.65
1:A:357:LYS:O	1:A:358:LEU:HB2	1.95	0.65
1:A:387:GLU:O	1:A:388:LEU:HB3	1.96	0.65
2:B:292:CYS:O	2:B:295:PRO:HD2	1.97	0.65
1:A:444:ASN:C	1:A:446:LEU:N	2.55	0.64
1:A:419:GLU:HG3	1:A:420:GLY:N	2.10	0.64
1:A:383:ILE:HA	1:A:386:ARG:HH21	1.63	0.63
1:A:486:LEU:O	1:A:490:GLU:HG2	1.99	0.63
2:C:281:PRO:O	2:C:282:LEU:HB3	1.98	0.63
2:B:455:ILE:HG12	2:B:458:VAL:HB	1.80	0.62
2:B:441:ILE:O	2:B:442:ASN:HB2	2.00	0.61
2:C:282:LEU:CA	2:C:285:GLN:HB3	2.28	0.61
2:B:460:MET:HE3	2:B:460:MET:HA	1.83	0.61
1:A:352:ARG:CG	1:A:352:ARG:O	2.48	0.60
1:A:444:ASN:O	1:A:446:LEU:N	2.34	0.60
2:B:424:TYR:O	2:B:424:TYR:CG	2.53	0.60
2:C:391:PRO:HB2	2:C:399:VAL:HG13	1.82	0.60
1:A:371:THR:O	1:A:375:ILE:HG13	2.01	0.60
1:A:394:MET:O	1:A:398:GLN:HG3	2.02	0.60
2:B:292:CYS:C	2:B:295:PRO:HD2	2.26	0.60
1:A:480:VAL:HG12	1:A:481:LYS:N	2.18	0.59
2:C:426:ILE:O	2:C:430:GLU:HB2	2.03	0.59
1:A:394:MET:HE1	2:B:279:ILE:HD13	1.84	0.59
1:A:372:LEU:O	1:A:376:VAL:HG23	2.03	0.59
1:A:409:HIS:HA	1:A:412:ARG:NH1	2.18	0.58
2:C:281:PRO:HB2	2:C:283:ASP:OD2	2.04	0.58
2:B:378:LYS:HD3	2:B:416:HIS:HD2	1.67	0.57
2:B:430:GLU:O	2:B:433:SER:HB3	2.05	0.57
2:B:300:GLU:OE2	2:B:384:LYS:HE2	2.05	0.57
2:B:459:SER:HB2	2:B:462:ASP:CG	2.29	0.57
2:C:420:MET:HG3	2:C:421:GLN:H	1.70	0.57
2:B:306:LEU:HD23	2:B:307:HIS:N	2.20	0.56
2:C:383:LEU:HD22	2:C:435:LEU:HD11	1.87	0.56
1:A:455:VAL:O	1:A:456:ARG:C	2.47	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:553:GLU:HG3	2:B:275:PRO:HB2	1.87	0.56
2:B:452:ARG:N	2:B:453:PRO:CD	2.69	0.56
2:C:423:GLU:HB3	2:C:426:ILE:HD12	1.88	0.56
1:A:388:LEU:HD13	1:A:485:ASN:HB3	1.89	0.55
1:A:516:GLY:O	1:A:520:LEU:HB2	2.05	0.55
2:C:295:PRO:HB2	2:C:387:VAL:HG11	1.88	0.55
1:A:451:GLN:O	1:A:452:GLU:C	2.48	0.55
2:C:274:LEU:O	2:C:277:PHE:HB3	2.07	0.55
1:A:403:GLU:HB3	1:A:525:LEU:HD21	1.88	0.54
2:B:379:GLU:CD	2:B:427:ARG:HH12	2.15	0.54
2:B:411:GLN:HA	2:B:411:GLN:NE2	2.20	0.54
1:A:522:LEU:HB2	1:A:523:PRO:HD3	1.89	0.54
1:A:333:ASP:OD1	1:A:335:PRO:HD2	2.08	0.54
2:C:391:PRO:HG3	2:C:403:GLU:HG2	1.89	0.54
1:A:324:ILE:O	1:A:328:LEU:HG	2.09	0.53
2:C:252:ASP:N	2:C:253:PRO:CD	2.71	0.53
2:C:452:ARG:HB2	2:C:453:PRO:HD3	1.90	0.53
1:A:436:ILE:HD13	1:A:436:ILE:O	2.09	0.53
1:A:467:PHE:CE2	1:A:471:LYS:HD2	2.44	0.53
1:A:513:GLU:O	1:A:517:GLN:HG2	2.08	0.53
1:A:403:GLU:OE1	1:A:526:ARG:HG2	2.09	0.53
1:A:462:PHE:HZ	1:A:467:PHE:HA	1.73	0.52
2:C:359:ALA:HB1	2:C:445:VAL:HG11	1.92	0.52
1:A:409:HIS:O	1:A:413:GLN:HG2	2.08	0.52
1:A:465:ARG:HD2	1:A:503:TYR:CE1	2.45	0.52
1:A:541:VAL:HG12	1:A:541:VAL:O	2.09	0.52
2:C:262:ALA:O	2:C:266:LYS:HB2	2.08	0.52
2:C:355:LEU:O	2:C:356:PRO:C	2.52	0.52
1:A:338:GLN:HG2	1:A:425:VAL:O	2.10	0.51
1:A:320:ILE:HG22	1:A:321:PRO:HD2	1.93	0.51
1:A:379:ALA:O	1:A:382:SER:HB3	2.11	0.51
2:B:268:LEU:O	2:B:272:LYS:HB2	2.10	0.50
2:C:303:GLN:HG3	2:C:380:TYR:CD2	2.46	0.50
1:A:352:ARG:O	1:A:352:ARG:HG2	2.10	0.50
2:C:448:GLU:HA	2:C:452:ARG:HG2	1.93	0.50
2:B:274:LEU:O	2:B:278:GLN:HG2	2.11	0.50
2:B:455:ILE:CG1	2:B:458:VAL:HB	2.40	0.50
2:B:306:LEU:HD23	2:B:306:LEU:C	2.37	0.50
1:A:524:GLU:O	1:A:528:ILE:HG13	2.12	0.50
1:A:321:PRO:O	1:A:325:LEU:HG	2.12	0.50
1:A:343:ALA:O	1:A:347:GLN:HB2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:391:ASP:O	1:A:395:LYS:HG3	2.12	0.50
1:A:467:PHE:CZ	1:A:471:LYS:HD2	2.46	0.50
2:B:293:TRP:CH2	2:B:447:THR:HG22	2.46	0.50
1:A:388:LEU:HD11	1:A:392:ASP:CB	2.42	0.49
1:A:455:VAL:HG22	1:A:458:ARG:HH12	1.77	0.49
2:B:361:GLN:HA	2:B:361:GLN:NE2	2.27	0.49
1:A:406:ILE:O	1:A:409:HIS:HB3	2.13	0.49
2:B:293:TRP:HH2	2:B:447:THR:HG22	1.78	0.49
2:C:458:VAL:O	2:C:459:SER:HB2	2.11	0.49
2:B:471:LYS:O	2:B:472:LEU:HG	2.12	0.49
2:C:298:MET:HA	2:C:298:MET:HE2	1.95	0.49
2:B:358:ALA:O	2:B:361:GLN:HB3	2.12	0.49
1:A:480:VAL:HG12	1:A:481:LYS:H	1.77	0.48
2:C:391:PRO:CB	2:C:399:VAL:HG13	2.43	0.48
1:A:511:GLN:CB	1:A:514:LYS:HB2	2.40	0.48
2:C:252:ASP:OD1	2:C:253:PRO:HD3	2.13	0.48
2:B:416:HIS:CE1	2:B:420:MET:HG3	2.49	0.48
2:B:426:ILE:O	2:B:430:GLU:HG3	2.13	0.48
2:B:295:PRO:HB2	2:B:387:VAL:HG11	1.95	0.48
2:B:280:LEU:HD21	2:B:401:TYR:CE2	2.49	0.48
1:A:488:LEU:O	1:A:492:VAL:HG22	2.14	0.48
2:B:452:ARG:N	2:B:453:PRO:HD2	2.30	0.47
1:A:324:ILE:HD12	1:A:324:ILE:N	2.28	0.47
1:A:463:ASP:CG	1:A:464:GLN:H	2.22	0.47
1:A:464:GLN:O	1:A:464:GLN:HG2	2.15	0.47
2:C:380:TYR:O	2:C:384:LYS:HG3	2.15	0.47
1:A:323:LEU:O	1:A:327:LEU:HG	2.15	0.47
2:B:451:PHE:C	2:B:453:PRO:HD2	2.40	0.47
2:B:400:LYS:O	2:B:403:GLU:HB2	2.15	0.47
1:A:413:GLN:O	1:A:417:GLY:HA3	2.15	0.47
2:C:383:LEU:HD22	2:C:435:LEU:CD1	2.45	0.46
1:A:468:VAL:O	1:A:472:PHE:HD1	1.98	0.46
2:C:455:ILE:HD11	2:C:458:VAL:HB	1.97	0.46
2:B:268:LEU:HD12	2:B:467:MET:HB3	1.98	0.46
2:B:268:LEU:HD12	2:B:467:MET:HE2	1.97	0.46
2:C:280:LEU:C	2:C:282:LEU:H	2.22	0.46
2:C:280:LEU:HA	2:C:281:PRO:HD3	1.69	0.46
2:B:252:ASP:H	2:B:253:PRO:CD	2.29	0.46
2:B:272:LYS:HZ3	2:B:472:LEU:HB3	1.81	0.46
1:A:398:GLN:HA	1:A:554:MET:HE1	1.98	0.46
2:C:451:PHE:O	2:C:455:ILE:HG22	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:510:GLN:HE21	1:A:510:GLN:C	2.24	0.46
2:C:441:ILE:O	2:C:442:ASN:HB2	2.14	0.46
2:C:448:GLU:HA	2:C:452:ARG:CG	2.46	0.46
2:B:268:LEU:N	2:B:268:LEU:HD23	2.31	0.45
2:B:285:GLN:O	2:B:289:VAL:HG23	2.17	0.45
2:B:463:MET:HB2	2:B:463:MET:HE2	1.65	0.45
2:C:279:ILE:O	2:C:280:LEU:HG	2.16	0.45
1:A:451:GLN:C	1:A:453:LEU:N	2.70	0.45
1:A:456:ARG:O	1:A:459:SER:HB2	2.17	0.45
2:C:449:LEU:HB3	2:C:450:PHE:CD1	2.50	0.45
1:A:492:VAL:HA	1:A:495:GLN:HB3	1.98	0.45
1:A:492:VAL:O	1:A:496:VAL:HG23	2.16	0.45
1:A:451:GLN:O	1:A:453:LEU:N	2.50	0.45
2:C:373:LEU:CD2	2:C:430:GLU:HG2	2.43	0.45
2:C:312:GLU:CD	2:C:312:GLU:H	2.25	0.45
2:B:287:VAL:O	2:B:288:LEU:C	2.59	0.45
2:C:271:VAL:O	2:C:274:LEU:HB2	2.17	0.45
1:A:413:GLN:NE2	1:A:423:PHE:O	2.48	0.44
1:A:324:ILE:H	1:A:324:ILE:CD1	2.27	0.44
1:A:521:ARG:HD2	1:A:521:ARG:N	2.32	0.44
1:A:410:ILE:HG23	1:A:454:VAL:HG22	1.97	0.44
1:A:475:LEU:HD12	1:A:475:LEU:O	2.18	0.44
2:C:415:GLU:O	2:C:419:MET:HG2	2.17	0.44
2:B:451:PHE:O	2:B:455:ILE:HG22	2.17	0.44
2:B:293:TRP:CZ2	2:B:460:MET:HG2	2.52	0.44
2:B:306:LEU:CD2	2:B:308:PHE:HB3	2.48	0.44
2:C:389:PHE:O	2:C:406:GLN:NE2	2.51	0.44
1:A:345:LEU:O	1:A:349:GLN:HG2	2.18	0.44
1:A:455:VAL:C	1:A:457:LEU:N	2.71	0.44
1:A:508:TYR:HA	1:A:509:PRO:HD3	1.51	0.44
1:A:520:LEU:O	1:A:523:PRO:HD2	2.17	0.43
2:C:396:LEU:HD13	2:C:402:ILE:HD11	2.00	0.43
2:C:437:LEU:O	2:C:440:PHE:HD1	2.01	0.43
1:A:470:LEU:HD23	1:A:473:LEU:HD12	1.99	0.43
2:C:458:VAL:O	2:C:459:SER:CB	2.65	0.43
1:A:341:ILE:O	1:A:344:TYR:HB3	2.18	0.43
1:A:462:PHE:CZ	1:A:467:PHE:HA	2.53	0.43
2:B:436:PHE:O	2:B:439:ARG:HG3	2.18	0.43
2:C:256:VAL:HG23	2:C:257:CYS:N	2.33	0.43
2:C:393:LEU:HA	2:C:394:PRO:HD3	1.86	0.43
1:A:380:ARG:HA	1:A:385:PHE:CD2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:306:LEU:C	2:B:306:LEU:CD2	2.92	0.43
2:C:277:PHE:CZ	2:C:285:GLN:HG3	2.53	0.43
2:C:420:MET:HE2	2:C:420:MET:HB3	1.85	0.43
1:A:401:TRP:CG	1:A:554:MET:HE2	2.53	0.43
2:B:267:THR:O	2:B:270:PHE:HB3	2.19	0.43
2:C:427:ARG:O	2:C:427:ARG:HG3	2.15	0.43
2:C:452:ARG:N	2:C:453:PRO:CD	2.82	0.43
1:A:348:GLU:O	1:A:351:ASN:HB3	2.18	0.42
1:A:555:LEU:HD12	1:A:555:LEU:O	2.19	0.42
2:C:413:LEU:HD12	2:C:413:LEU:O	2.20	0.42
1:A:357:LYS:O	1:A:358:LEU:CB	2.65	0.42
1:A:388:LEU:HD11	1:A:392:ASP:HB2	2.00	0.42
1:A:422:ILE:HD11	1:A:451:GLN:HE21	1.83	0.42
2:B:313:ILE:HD12	2:B:313:ILE:C	2.45	0.42
2:C:298:MET:HB3	2:C:366:PHE:CE2	2.55	0.42
2:C:363:ILE:CG2	2:C:367:PHE:HE1	2.33	0.42
2:B:257:CYS:SG	2:B:453:PRO:HG2	2.60	0.42
2:C:408:ARG:O	2:C:412:ILE:HG22	2.20	0.42
1:A:481:LYS:HG3	1:A:482:ASN:ND2	2.34	0.41
2:C:284:GLN:C	2:C:286:LEU:N	2.77	0.41
2:C:458:VAL:O	2:C:458:VAL:HG12	2.19	0.41
2:B:436:PHE:O	2:B:439:ARG:CG	2.68	0.41
2:B:438:LEU:O	2:B:441:ILE:HG12	2.20	0.41
2:C:283:ASP:O	2:C:287:VAL:HG23	2.20	0.41
1:A:477:SER:O	1:A:480:VAL:HG23	2.20	0.41
1:A:440:GLU:OE2	1:A:539:LYS:HE2	2.20	0.41
2:B:272:LYS:NZ	2:B:472:LEU:HD23	2.36	0.41
2:C:293:TRP:CG	2:C:294:ALA:N	2.88	0.41
2:C:271:VAL:HG12	2:C:277:PHE:CE2	2.55	0.41
2:C:423:GLU:O	2:C:426:ILE:HB	2.20	0.41
1:A:432:TYR:CE2	1:A:451:GLN:HG3	2.55	0.41
2:C:311:MET:HE3	2:C:311:MET:HB2	1.92	0.41
1:A:462:PHE:CE1	1:A:466:GLU:HB2	2.56	0.41
2:B:366:PHE:CZ	2:B:438:LEU:HD13	2.56	0.41
1:A:390:VAL:O	1:A:391:ASP:C	2.64	0.41
2:B:401:TYR:CZ	2:B:405:LEU:HD11	2.56	0.41
2:B:452:ARG:HA	2:B:455:ILE:HG22	2.02	0.41
2:C:402:ILE:H	2:C:402:ILE:HG12	1.76	0.41
1:A:466:GLU:O	1:A:470:LEU:HG	2.21	0.41
1:A:488:LEU:O	1:A:488:LEU:HD12	2.21	0.41
2:B:393:LEU:HA	2:B:394:PRO:HD3	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:396:LEU:HD13	2:B:402:ILE:HD12	2.03	0.41
2:C:464:MET:O	2:C:465:LEU:C	2.64	0.41
1:A:490:GLU:OE2	1:A:490:GLU:HA	2.20	0.40
2:B:380:TYR:O	2:B:384:LYS:HG3	2.22	0.40
2:C:267:THR:O	2:C:270:PHE:HB3	2.20	0.40
1:A:545:VAL:HA	1:A:546:PRO:HD3	1.91	0.40
2:B:379:GLU:O	2:B:380:TYR:C	2.64	0.40
2:C:363:ILE:O	2:C:367:PHE:HD1	2.05	0.40
1:A:319:SER:C	1:A:320:ILE:HD13	2.46	0.40
2:B:373:LEU:O	2:B:427:ARG:NH2	2.55	0.40
2:C:437:LEU:HD13	2:C:437:LEU:HA	1.91	0.40
2:B:306:LEU:HB3	2:B:367:PHE:HE2	1.87	0.40
2:B:408:ARG:O	2:B:412:ILE:HG22	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	241/248 (97%)	205 (85%)	26 (11%)	10 (4%)	2	13
2	B	179/268 (67%)	154 (86%)	20 (11%)	5 (3%)	4	21
2	C	177/268 (66%)	144 (81%)	31 (18%)	2 (1%)	11	43
All	All	597/784 (76%)	503 (84%)	77 (13%)	17 (3%)	4	21

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	333	ASP
1	A	334	GLU
1	A	358	LEU
2	B	423	GLU

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Mol	Chain	Res	Type
1	A	480	VAL
1	A	481	LYS
2	B	442	ASN
1	A	445	ASN
1	A	464	GLN
2	B	356	PRO
2	C	439	ARG
1	A	452	GLU
1	A	509	PRO
2	B	252	ASP
2	C	285	GLN
2	B	253	PRO
1	A	335	PRO

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	221/226 (98%)	208 (94%)	13 (6%)	18	50
2	B	164/235 (70%)	153 (93%)	11 (7%)	15	46
2	C	162/235 (69%)	153 (94%)	9 (6%)	19	52
All	All	547/696 (79%)	514 (94%)	33 (6%)	17	50

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	320	ILE
1	A	334	GLU
1	A	352	ARG
1	A	355	GLN
1	A	372	LEU
1	A	391	ASP
1	A	436	ILE
1	A	483	LEU
1	A	487	GLN

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Mol	Chain	Res	Type
1	A	510	GLN
1	A	521	ARG
1	A	525	LEU
1	A	553	GLU
2	B	252	ASP
2	B	254	GLN
2	B	264	LEU
2	B	268	LEU
2	B	297	LEU
2	B	299	LEU
2	B	310	MET
2	B	311	MET
2	B	411	GLN
2	B	427	ARG
2	B	442	ASN
2	C	254	GLN
2	C	272	LYS
2	C	278	GLN
2	C	297	LEU
2	C	402	ILE
2	C	435	LEU
2	C	437	LEU
2	C	440	PHE
2	C	469	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	336	GLN
1	A	349	GLN
1	A	370	GLN
1	A	398	GLN
1	A	399	ASN
1	A	482	ASN
1	A	497	ASN
1	A	510	GLN
2	B	278	GLN
2	B	361	GLN
2	B	416	HIS
2	B	425	GLN
2	B	442	ASN
2	C	254	GLN

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Mol	Chain	Res	Type
2	C	278	GLN
2	C	285	GLN
2	C	397	GLN
2	C	406	GLN
2	C	410	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 oligosaccharides 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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	243/248 (97%)	-0.43	1 (0%) 88 76	68, 121, 197, 256	0
2	B	183/268 (68%)	-0.48	4 (2%) 62 39	64, 97, 156, 190	0
2	C	181/268 (67%)	-0.45	3 (1%) 69 45	75, 105, 180, 207	0
All	All	607/784 (77%)	-0.45	8 (1%) 75 53	64, 108, 182, 256	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	356	PRO	3.0
2	C	457	ALA	2.6
2	B	356	PRO	2.5
2	B	354	LEU	2.4
2	B	472	LEU	2.3
2	B	310	MET	2.2
2	C	458	VAL	2.2
1	A	445	ASN	2.2

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 oligosaccharides 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.