



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 08:14 PM GMT

PDB ID : 3D5F
Title : Crystal Structure of PPAR-delta complex
Authors : Amano, Y.
Deposited on : 2008-05-16
Resolution : 2.20 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>

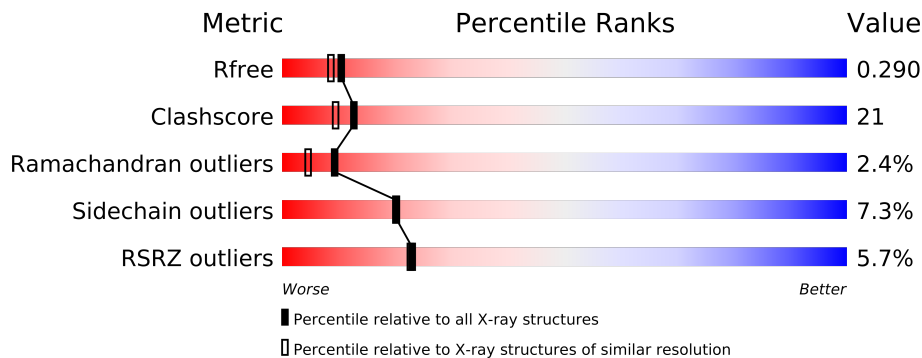
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.20 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	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

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	267	
1	B	267	

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			29	22	7		

- Molecule 3 is water.

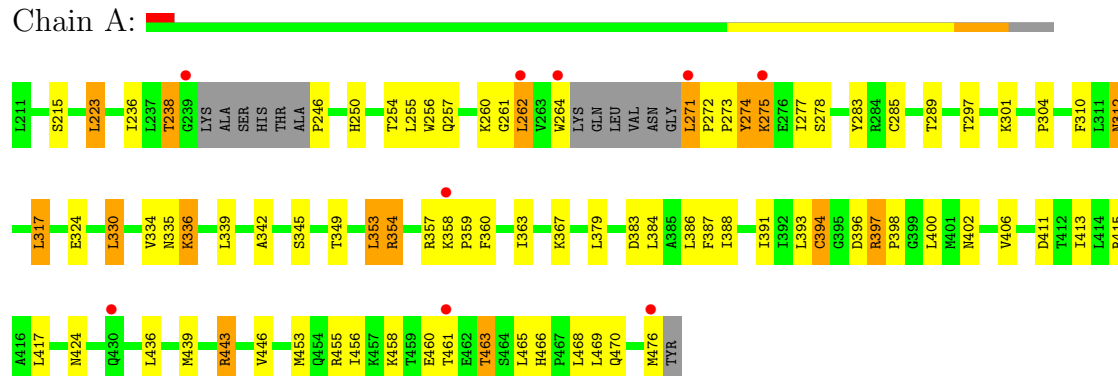
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	50	Total	O	0	0
			50	50		
3	B	37	Total	O	0	0
			37	37		

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.

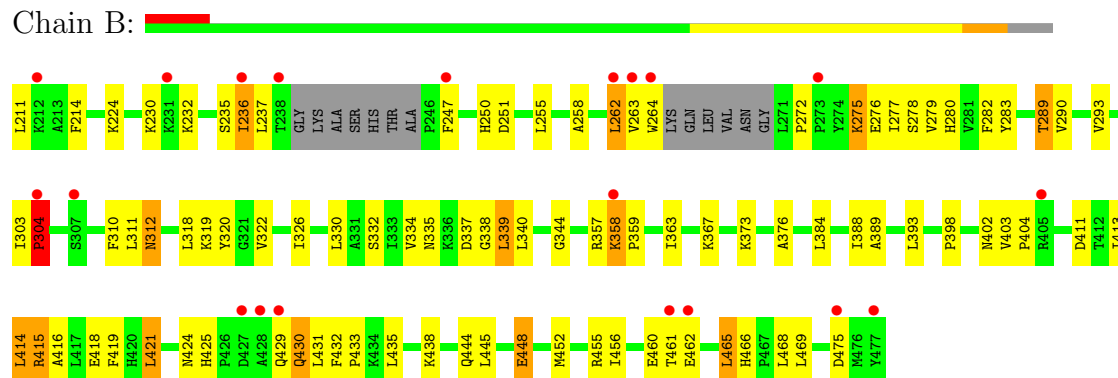
- Molecule 1: Peroxisome proliferator-activatedreceptor delta

Chain A:



- Molecule 1: Peroxisome proliferator-activatedreceptor delta

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	39.46Å 92.83Å 96.45Å 90.00° 98.02° 90.00°	Depositor
Resolution (Å)	42.47 – 2.20 42.47 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.9 (42.47-2.20) 97.0 (42.47-2.20)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.278 , 0.281 0.286 , 0.290	Depositor DCC
R_{free} test set	1698 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	32.4	Xtriage
Anisotropy	0.662	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 41.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Outliers	0 of 33944 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4245	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.64% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: L41

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	0.40	0/2091	0.65	0/2823
1	B	0.39	0/2096	0.63	0/2832
All	All	0.40	0/4187	0.64	0/5655

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	2048	0	2094	78	0
1	B	2052	0	2079	97	0
2	A	29	0	24	2	0
2	B	29	0	24	2	0
3	A	50	0	0	3	0
3	B	37	0	0	1	0
All	All	4245	0	4221	175	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 21.

All (175) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:293:VAL:HG22	1:B:322:VAL:HG11	1.23	1.13
1:B:247:PHE:HB3	1:B:262:LEU:HD11	1.48	0.95
1:B:275:LYS:HD3	1:B:275:LYS:H	1.32	0.93
1:B:275:LYS:HD3	1:B:275:LYS:N	1.84	0.92
1:A:465:LEU:HD23	1:A:470:GLN:HG2	1.53	0.90
1:A:312:ASN:H	1:A:312:ASN:HD22	1.18	0.90
1:B:275:LYS:H	1:B:275:LYS:CD	1.83	0.90
1:B:363:ILE:HG22	1:B:452:MET:SD	2.14	0.88
1:B:411:ASP:O	1:B:415:ARG:HG2	1.76	0.84
1:B:358:LYS:H	1:B:358:LYS:HE2	1.39	0.84
1:A:436:LEU:HA	1:A:439:MET:HE3	1.62	0.81
1:B:358:LYS:N	1:B:358:LYS:HE2	1.96	0.81
1:B:237:LEU:HD21	1:B:335:ASN:HD21	1.46	0.80
1:B:236:ILE:HD12	1:B:344:GLY:HA3	1.66	0.77
1:B:358:LYS:CE	1:B:358:LYS:H	1.98	0.76
1:A:312:ASN:N	1:A:312:ASN:HD22	1.85	0.75
1:A:285:CYS:O	1:A:289:THR:HG23	1.88	0.74
1:B:255:LEU:HD13	1:B:277:ILE:HD11	1.69	0.74
1:B:293:VAL:HG22	1:B:322:VAL:CG1	2.14	0.73
1:A:257:GLN:HG3	1:A:262:LEU:HD11	1.70	0.73
1:B:289:THR:HG21	2:B:501:L41:O28	1.88	0.72
1:B:456:ILE:O	1:B:460:GLU:HB2	1.90	0.71
1:B:335:ASN:HB3	1:B:337:ASP:H	1.55	0.71
1:A:460:GLU:HB3	1:A:463:THR:HG23	1.72	0.70
1:A:411:ASP:OD2	1:A:415:ARG:HD2	1.90	0.70
1:B:415:ARG:O	1:B:418:GLU:HB3	1.92	0.70
1:A:363:ILE:CD1	1:A:453:MET:HE2	2.23	0.69
1:B:237:LEU:HD23	1:B:237:LEU:O	1.93	0.69
1:A:466:HIS:CD2	1:A:468:LEU:H	2.11	0.69
1:B:461:THR:O	1:B:462:GLU:HB2	1.92	0.68
1:B:310:PHE:HB3	1:B:312:ASN:ND2	2.09	0.67
1:B:312:ASN:N	1:B:312:ASN:HD22	1.92	0.67
1:B:275:LYS:HG3	1:B:279:VAL:CG1	2.24	0.67
1:A:466:HIS:HD2	1:A:468:LEU:H	1.42	0.66
1:A:310:PHE:HB3	1:A:312:ASN:ND2	2.11	0.66
1:B:255:LEU:HD13	1:B:277:ILE:CD1	2.25	0.66
1:A:274:TYR:O	1:A:275:LYS:HG3	1.97	0.65
1:A:367:LYS:HD2	1:A:367:LYS:N	2.11	0.65
1:A:246:PRO:HA	1:A:345:SER:O	1.96	0.65
1:B:312:ASN:H	1:B:312:ASN:HD22	1.42	0.65
1:B:424:ASN:HD22	1:B:425:HIS:CE1	2.15	0.64
1:A:310:PHE:CB	1:A:312:ASN:HD21	2.11	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:256:TRP:CZ2	1:A:260:LYS:HD2	2.33	0.63
1:A:272:PRO:HG2	1:A:283:TYR:CE2	2.34	0.62
1:A:310:PHE:HB3	1:A:312:ASN:HD21	1.65	0.61
1:B:358:LYS:HB2	1:B:359:PRO:HD3	1.82	0.61
1:B:373:LYS:HB2	3:B:66:HOH:O	2.00	0.61
1:B:310:PHE:HB3	1:B:312:ASN:HD21	1.65	0.60
1:A:470:GLN:HG3	3:A:42:HOH:O	2.02	0.60
1:B:275:LYS:HG2	1:B:276:GLU:H	1.67	0.60
1:A:386:LEU:HD13	1:A:417:LEU:HA	1.84	0.60
1:A:402:ASN:O	1:A:406:VAL:HG23	2.02	0.59
1:A:236:ILE:C	1:A:238:THR:H	2.05	0.59
1:B:264:TRP:H	1:B:264:TRP:HD1	1.49	0.59
1:B:432:PHE:HB3	1:B:433:PRO:HD3	1.85	0.58
1:A:363:ILE:HD13	1:A:453:MET:CE	2.34	0.58
1:B:214:PHE:CE2	1:B:304:PRO:HG2	2.39	0.57
1:A:215:SER:OG	1:A:386:LEU:HD11	2.04	0.56
1:A:363:ILE:CD1	1:A:453:MET:CE	2.84	0.55
1:B:275:LYS:HD2	1:B:283:TYR:HE2	1.70	0.55
1:A:336:LYS:HE3	3:A:29:HOH:O	2.06	0.55
1:B:255:LEU:HD23	1:B:255:LEU:C	2.28	0.54
1:B:430:GLN:O	1:B:433:PRO:HD2	2.08	0.54
1:A:393:LEU:HD13	1:A:413:ILE:HD11	1.90	0.53
1:B:465:LEU:CD1	1:B:469:LEU:HB2	2.39	0.53
1:B:236:ILE:CD1	1:B:344:GLY:HA3	2.37	0.53
1:B:275:LYS:HE3	1:B:280:HIS:HA	1.90	0.53
1:A:317:LEU:HD13	1:A:400:LEU:HD21	1.91	0.53
1:B:389:ALA:O	1:B:393:LEU:HD23	2.09	0.52
1:A:250:HIS:CD2	1:A:254:THR:HG21	2.44	0.52
1:A:357:ARG:HB3	1:A:359:PRO:HD2	1.91	0.52
1:A:310:PHE:CB	1:A:312:ASN:ND2	2.72	0.52
1:B:358:LYS:HB2	1:B:359:PRO:CD	2.40	0.52
1:B:340:LEU:HB3	1:B:344:GLY:HA2	1.91	0.52
1:A:465:LEU:HD23	1:A:470:GLN:HE21	1.75	0.52
1:A:312:ASN:ND2	1:A:312:ASN:N	2.56	0.52
1:B:237:LEU:HD21	1:B:335:ASN:ND2	2.18	0.52
1:A:324:GLU:HG3	1:A:446:VAL:HG21	1.92	0.51
1:A:411:ASP:O	1:A:415:ARG:HG3	2.10	0.51
1:A:277:ILE:HG23	1:A:278:SER:N	2.25	0.51
1:B:318:LEU:O	1:B:322:VAL:HG23	2.11	0.50
1:B:258:ALA:HB1	1:B:262:LEU:HD12	1.93	0.50
1:B:384:LEU:O	1:B:388:ILE:HG12	2.12	0.50
1:A:289:THR:HG22	2:A:501:L41:H13	1.93	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:340:LEU:HD22	1:B:344:GLY:HA2	1.94	0.50
1:B:319:LYS:NZ	1:B:475:ASP:HB2	2.28	0.49
1:B:211:LEU:HD23	1:B:419:PHE:CD2	2.48	0.49
1:A:394:CYS:SG	1:A:396:ASP:HB2	2.52	0.49
1:B:262:LEU:O	1:B:264:TRP:N	2.46	0.49
1:B:393:LEU:N	1:B:393:LEU:HD22	2.27	0.49
1:B:444:GLN:NE2	1:B:448:GLU:OE2	2.45	0.49
1:A:255:LEU:HD23	1:A:255:LEU:C	2.33	0.49
1:B:465:LEU:HD12	1:B:469:LEU:HB2	1.94	0.49
1:A:379:LEU:HB3	1:A:383:ASP:HB2	1.95	0.49
1:B:403:VAL:HB	1:B:404:PRO:HD3	1.95	0.48
1:B:320:TYR:CZ	1:B:398:PRO:HG2	2.48	0.48
1:B:264:TRP:N	1:B:264:TRP:CD1	2.78	0.48
1:B:275:LYS:HE3	1:B:283:TYR:HD2	1.79	0.48
1:A:310:PHE:HB2	1:A:312:ASN:HD21	1.79	0.48
1:B:461:THR:O	1:B:462:GLU:CB	2.60	0.48
1:A:312:ASN:ND2	1:A:312:ASN:H	1.97	0.47
1:B:339:LEU:HD12	1:B:340:LEU:O	2.13	0.47
1:A:255:LEU:HD13	1:A:277:ILE:HD11	1.96	0.47
1:A:465:LEU:HD23	1:A:470:GLN:CG	2.36	0.47
1:B:230:LYS:HA	1:B:332:SER:HB3	1.97	0.47
1:A:367:LYS:HG2	2:A:501:L41:H17	1.96	0.47
1:B:312:ASN:ND2	1:B:312:ASN:N	2.62	0.47
1:A:334:VAL:CG1	1:A:335:ASN:N	2.77	0.47
1:B:335:ASN:HB2	1:B:338:GLY:O	2.15	0.46
1:A:384:LEU:O	1:A:388:ILE:HG12	2.15	0.46
1:A:360:PHE:O	1:A:363:ILE:HG22	2.15	0.46
1:A:466:HIS:CD2	1:A:468:LEU:HB3	2.51	0.46
1:A:317:LEU:HD12	1:A:397:ARG:HG3	1.98	0.46
1:B:367:LYS:HD2	1:B:367:LYS:N	2.29	0.46
1:A:396:ASP:CB	1:A:443:ARG:HH22	2.28	0.46
1:A:264:TRP:CE2	1:A:342:ALA:HB2	2.50	0.46
1:B:235:SER:C	1:B:237:LEU:H	2.18	0.46
1:A:466:HIS:HD2	1:A:468:LEU:N	2.10	0.46
1:B:330:LEU:HD21	2:B:501:L41:H14A	1.97	0.46
1:B:279:VAL:HG12	1:B:283:TYR:CE2	2.50	0.46
1:A:297:THR:HG22	1:A:301:LYS:HD3	1.98	0.46
1:B:358:LYS:CA	1:B:358:LYS:HE2	2.46	0.46
1:A:330:LEU:HD21	1:A:339:LEU:HD12	1.98	0.46
1:B:414:LEU:O	1:B:418:GLU:N	2.41	0.45
1:A:397:ARG:H	1:A:397:ARG:HG2	1.38	0.45
1:A:354:ARG:HD2	3:A:59:HOH:O	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:430:GLN:C	1:B:433:PRO:HD2	2.38	0.45
1:B:303:ILE:HG23	1:B:304:PRO:HD2	1.99	0.45
1:A:393:LEU:CD1	1:A:413:ILE:HD11	2.47	0.44
1:A:317:LEU:CD1	1:A:400:LEU:HD21	2.46	0.44
1:B:322:VAL:HG12	1:B:326:ILE:CD1	2.48	0.44
1:A:274:TYR:CG	1:A:275:LYS:N	2.84	0.44
1:A:367:LYS:N	1:A:367:LYS:CD	2.80	0.44
1:B:320:TYR:CE2	1:B:398:PRO:HG2	2.52	0.44
1:B:310:PHE:CB	1:B:312:ASN:HD21	2.30	0.44
1:B:415:ARG:H	1:B:415:ARG:HG2	1.62	0.43
1:B:224:LYS:HE2	1:B:224:LYS:HB3	1.83	0.43
1:A:272:PRO:HG2	1:A:283:TYR:CD2	2.54	0.43
1:B:373:LYS:O	1:B:376:ALA:HB3	2.18	0.43
1:B:275:LYS:HG3	1:B:279:VAL:HG12	1.98	0.43
1:B:393:LEU:N	1:B:393:LEU:CD2	2.81	0.43
1:A:236:ILE:C	1:A:238:THR:N	2.71	0.43
1:B:334:VAL:CG1	1:B:335:ASN:N	2.82	0.43
1:A:387:PHE:CE2	1:A:391:ILE:HD11	2.52	0.43
1:B:430:GLN:HB3	1:B:430:GLN:HE21	1.63	0.43
1:B:277:ILE:HG23	1:B:278:SER:N	2.34	0.43
1:B:466:HIS:HB3	1:B:469:LEU:HG	2.01	0.43
1:B:444:GLN:HE21	1:B:448:GLU:CD	2.22	0.43
1:B:272:PRO:O	1:B:275:LYS:NZ	2.49	0.42
1:A:397:ARG:HA	1:A:398:PRO:HD3	1.81	0.42
1:B:421:LEU:HD21	1:B:435:LEU:HD12	2.01	0.42
1:B:272:PRO:HG2	1:B:283:TYR:CE2	2.53	0.42
1:A:396:ASP:CG	1:A:443:ARG:HH12	2.23	0.42
1:A:357:ARG:C	1:A:359:PRO:HD2	2.40	0.42
1:A:273:PRO:O	1:A:274:TYR:O	2.38	0.42
1:B:438:LYS:HA	1:B:438:LYS:HD3	1.84	0.42
1:A:349:THR:O	1:A:353:LEU:HD22	2.20	0.42
1:B:322:VAL:HG12	1:B:326:ILE:HD12	2.00	0.42
1:B:290:VAL:HG21	1:B:466:HIS:CD2	2.55	0.42
1:B:413:ILE:O	1:B:416:ALA:HB3	2.20	0.41
1:B:275:LYS:HG3	1:B:279:VAL:HG11	1.99	0.41
1:A:223:LEU:HD12	1:A:223:LEU:HA	1.87	0.41
1:A:460:GLU:HB3	1:A:463:THR:CG2	2.47	0.41
1:A:363:ILE:HD13	1:A:453:MET:HE3	2.03	0.41
1:B:250:HIS:CE1	1:B:251:ASP:OD2	2.74	0.41
1:A:257:GLN:CG	1:A:262:LEU:HD11	2.46	0.41
1:A:271:LEU:N	1:A:272:PRO:HD2	2.36	0.41
1:B:429:GLN:O	1:B:430:GLN:HB2	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:455:ARG:NH1	1:A:458:LYS:HG2	2.36	0.41
1:B:311:LEU:HD12	1:B:311:LEU:HA	1.84	0.41
1:B:357:ARG:HG2	1:B:359:PRO:HD2	2.03	0.40
1:B:275:LYS:HE3	1:B:283:TYR:CD2	2.56	0.40
1:B:279:VAL:O	1:B:282:PHE:HB3	2.22	0.40
1:A:367:LYS:HD2	1:A:367:LYS:H	1.85	0.40
1:A:456:ILE:O	1:A:460:GLU:HB2	2.22	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	248/267 (93%)	228 (92%)	14 (6%)	6 (2%)	9	4
1	B	248/267 (93%)	226 (91%)	16 (6%)	6 (2%)	9	4
All	All	496/534 (93%)	454 (92%)	30 (6%)	12 (2%)	9	4

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	274	TYR
1	B	263	VAL
1	B	304	PRO
1	B	358	LYS
1	A	275	LYS
1	B	232	LYS
1	A	238	THR
1	A	261	GLY
1	B	236	ILE
1	B	262	LEU
1	A	262	LEU
1	A	358	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	225/236 (95%)	208 (92%)	17 (8%)	19	18
1	B	224/236 (95%)	208 (93%)	16 (7%)	21	21
All	All	449/472 (95%)	416 (93%)	33 (7%)	20	20

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

Mol	Chain	Res	Type
1	A	223	LEU
1	A	271	LEU
1	A	304	PRO
1	A	312	ASN
1	A	317	LEU
1	A	330	LEU
1	A	336	LYS
1	A	353	LEU
1	A	354	ARG
1	A	394	CYS
1	A	397	ARG
1	A	424	ASN
1	A	443	ARG
1	A	461	THR
1	A	463	THR
1	A	469	LEU
1	A	476	MET
1	B	275	LYS
1	B	289	THR
1	B	304	PRO
1	B	312	ASN
1	B	339	LEU
1	B	402	ASN
1	B	414	LEU
1	B	415	ARG
1	B	421	LEU
1	B	430	GLN
1	B	431	LEU
1	B	445	LEU

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Mol	Chain	Res	Type
1	B	448	GLU
1	B	455	ARG
1	B	465	LEU
1	B	468	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	220	ASN
1	A	227	ASN
1	A	250	HIS
1	A	312	ASN
1	A	314	GLN
1	A	402	ASN
1	A	420	HIS
1	A	422	GLN
1	A	424	ASN
1	A	437	GLN
1	A	466	HIS
1	A	470	GLN
1	B	225	ASN
1	B	250	HIS
1	B	257	GLN
1	B	312	ASN
1	B	335	ASN
1	B	402	ASN
1	B	425	HIS
1	B	430	GLN
1	B	444	GLN
1	B	470	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 ⓘ

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	L41	A	501	-	30,30,30	2.24	11 (36%)	39,39,39	1.58	6 (15%)
2	L41	B	501	-	30,30,30	2.13	10 (33%)	39,39,39	1.33	6 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	L41	A	501	-	-	0/20/20/20	0/2/2/2
2	L41	B	501	-	-	0/20/20/20	0/2/2/2

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	L41	O8-C3	-5.65	1.23	1.37
2	B	501	L41	O8-C3	-5.03	1.24	1.37
2	A	501	L41	C20-C19	4.28	1.47	1.38
2	B	501	L41	C20-C19	4.19	1.47	1.38
2	B	501	L41	C21-C19	3.86	1.46	1.38
2	B	501	L41	C20-C22	3.72	1.45	1.38
2	A	501	L41	O18-C19	3.58	1.46	1.37
2	A	501	L41	C20-C22	3.39	1.45	1.38
2	B	501	L41	C23-C24	3.32	1.45	1.38
2	A	501	L41	C22-C24	3.22	1.45	1.38
2	A	501	L41	C10-C7	3.19	1.45	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	L41	C3-C1	3.04	1.45	1.40
2	A	501	L41	C21-C19	2.99	1.44	1.38
2	B	501	L41	C22-C24	2.77	1.44	1.38
2	B	501	L41	C21-C23	2.70	1.43	1.38
2	A	501	L41	C4-C1	2.61	1.56	1.52
2	A	501	L41	C23-C24	2.55	1.44	1.38
2	B	501	L41	O18-C19	2.54	1.43	1.37
2	A	501	L41	C2-C1	2.44	1.43	1.40
2	B	501	L41	O25-C26	2.31	1.48	1.42
2	B	501	L41	C15-C12	2.17	1.56	1.49

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	L41	C7-C3-C1	-4.17	118.18	121.64
2	A	501	L41	C26-O25-C24	4.06	125.41	117.73
2	A	501	L41	O16-C12-C7	3.57	125.34	120.54
2	A	501	L41	C7-C3-C1	-3.28	118.91	121.64
2	B	501	L41	C2-C1-C3	2.36	120.58	117.27
2	B	501	L41	C11-O6-C2	2.33	123.36	117.65
2	B	501	L41	C4-C1-C2	-2.29	118.11	121.50
2	B	501	L41	O16-C12-C7	2.29	123.62	120.54
2	A	501	L41	C23-C24-C22	2.28	124.12	120.21
2	A	501	L41	C21-C19-C20	2.14	123.89	120.21
2	B	501	L41	C23-C24-C22	2.05	123.73	120.21
2	A	501	L41	C10-C7-C3	2.05	120.92	118.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	254/267 (95%)	0.40	9 (3%) 42 42	20, 34, 54, 72	0
1	B	254/267 (95%)	0.61	20 (7%) 13 12	23, 38, 64, 78	0
All	All	508/534 (95%)	0.51	29 (5%) 23 23	20, 36, 62, 78	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	263	VAL	7.5
1	A	262	LEU	5.3
1	A	239	GLY	4.7
1	B	262	LEU	4.6
1	B	264	TRP	4.1
1	B	477	TYR	4.1
1	B	428	ALA	3.9
1	B	461	THR	3.7
1	B	475	ASP	3.6
1	B	236	ILE	3.4
1	A	271	LEU	3.2
1	B	238	THR	3.2
1	B	304	PRO	3.1
1	B	429	GLN	2.9
1	A	476	MET	2.9
1	B	231	LYS	2.9
1	A	461	THR	2.8
1	B	427	ASP	2.8
1	A	358	LYS	2.8
1	A	264	TRP	2.6
1	A	430	GLN	2.5
1	B	462	GLU	2.4
1	B	273	PRO	2.2
1	B	358	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	275	LYS	2.1
1	B	247	PHE	2.1
1	B	212	LYS	2.0
1	B	307	SER	2.0
1	B	405	ARG	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

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, 95th 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	L41	B	501	29/29	0.14	-0.20	23,29,34,40	0
2	L41	A	501	29/29	0.13	-0.72	16,25,31,32	0

6.5 Other polymers

There are no such residues in this entry.