



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 12:41 PM GMT

PDB ID : 3HM1
Title : Crystal structure of human Estrogen Receptor Alpha Ligand-Binding Domain in complex with a Glucocorticoid Receptor Interacting Protein 1 Nr Box II Peptide and estrone ((8R,9S,13S,14S)-3-hydroxy-13-methyl-7,8,9,11,12,14,15,16-octahydro-6H-cyclopenta[a]phenanthren-17-one)
Authors : Rajan, S.S.; Kim, Y.; Vanek, K.; Liwanag, M.; Joachimiak, A.; Greene, G.L.
Deposited on : 2009-05-28
Resolution : 2.33 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>

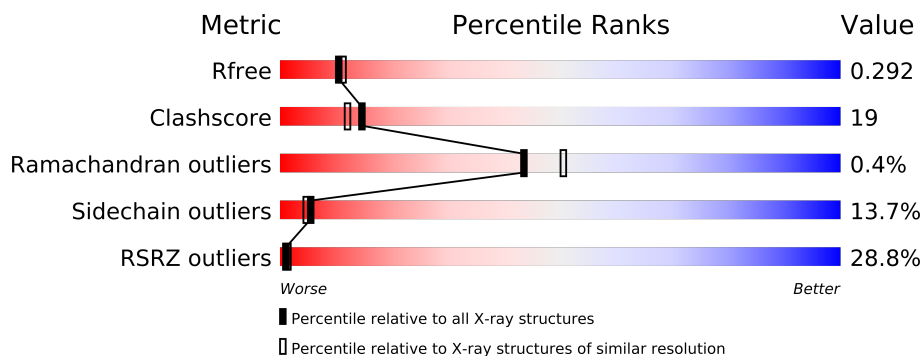
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.33 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	4049 (2.38-2.30)
Clashscore	79885	1094 (2.36-2.32)
Ramachandran outliers	78287	1080 (2.36-2.32)
Sidechain outliers	78261	1081 (2.36-2.32)
RSRZ outliers	66119	4050 (2.38-2.30)

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	253	
1	B	253	
2	C	13	
2	D	13	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4062 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 Estrogen receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	235	Total	C	N	O	S	0	3	0
			1911	1223	327	339	22			
1	B	239	Total	C	N	O	S	0	2	0
			1933	1237	334	340	22			

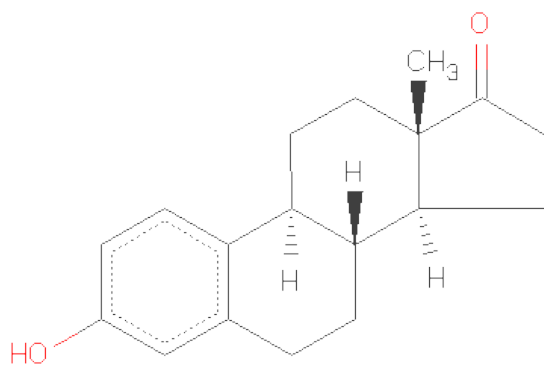
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	537	SER	TYR	ENGINEERED	UNP P03372
B	537	SER	TYR	ENGINEERED	UNP P03372

- Molecule 2 is a protein called Nuclear receptor coactivator 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	10	Total	C	N	O	0	0	0
			89	57	19	13			
2	D	9	Total	C	N	O	0	0	0
			79	51	16	12			

- Molecule 3 is (9BETA,13ALPHA)-3-HYDROXYESTRA-1,3,5(10)-TRIEN-17-ONE (three-letter code: J3Z) (formula: C₁₈H₂₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			20	18	2		
3	B	1	Total	C	O	0	0
			20	18	2		

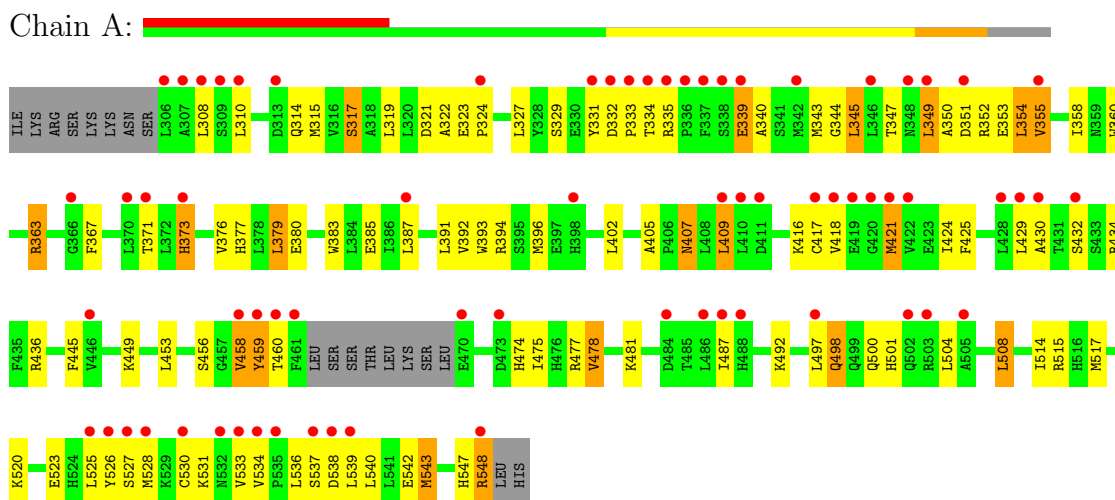
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	8	Total	O	0	0
			8	8		
4	B	2	Total	O	0	0
			2	2		

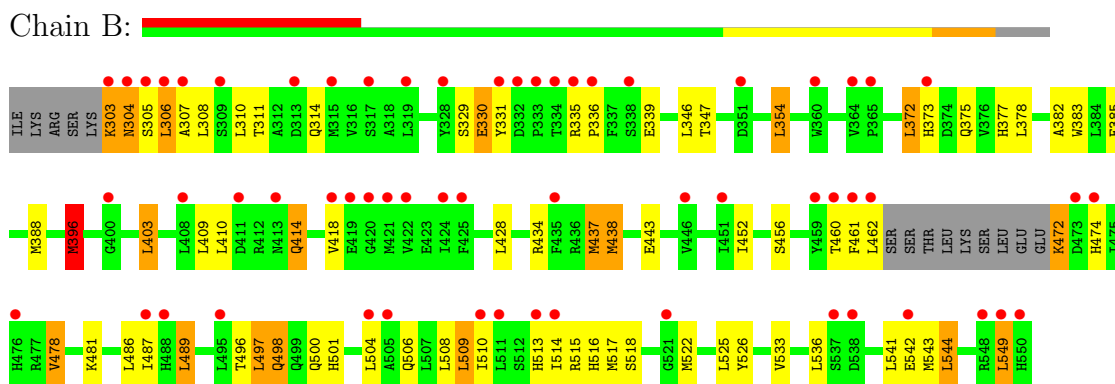
3 Residue-property plots

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: Estrogen receptor



• Molecule 1: Estrogen receptor

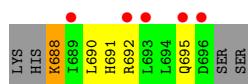


• Molecule 2: Nuclear receptor coactivator 2



• Molecule 2: Nuclear receptor coactivator 2





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.27Å 82.67Å 58.99Å 90.00° 109.18° 90.00°	Depositor
Resolution (Å)	33.37 – 2.33 33.37 – 2.33	Depositor EDS
% Data completeness (in resolution range)	86.0 (33.37-2.33) 75.0 (33.37-2.33)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.86 (at 2.34Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.231 , 0.289 0.240 , 0.292	Depositor DCC
R_{free} test set	965 reflections (5.12%)	DCC
Wilson B-factor (Å ²)	39.3	Xtriage
Anisotropy	0.919	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 47.0	EDS
Estimated twinning fraction	0.035 for l,-k,h	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 18885 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	4062	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% 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: CME, J3Z

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	0.30	0/1926	0.51	0/2595
1	B	0.31	0/1946	0.49	0/2624
2	C	0.21	0/90	0.35	0/119
2	D	0.24	0/79	0.39	0/104
All	All	0.30	0/4041	0.50	0/5442

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	1911	0	1951	95	0
1	B	1933	0	1981	66	0
2	C	89	0	95	4	0
2	D	79	0	88	6	0
3	A	20	0	22	1	0
3	B	20	0	22	2	0
4	A	8	0	0	1	0
4	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4062	0	4159	159	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 19.

All (159) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:688:LYS:HG2	2:D:691:HIS:HB2	1.46	0.95
1:B:335:ARG:HG3	1:B:336:PRO:HD2	1.59	0.83
1:B:330:GLU:HG2	1:B:330:GLU:O	1.82	0.78
1:A:481:LYS:HZ2	1:A:481:LYS:HB3	1.48	0.78
1:A:393:TRP:O	1:A:396:MET:HB2	1.84	0.77
1:A:331:TYR:HB2	1:A:345:LEU:HD21	1.67	0.76
2:C:688:LYS:HG3	2:C:691:HIS:HB3	1.67	0.76
1:B:410:LEU:HD22	1:B:414:GLN:HG2	1.69	0.74
1:B:335:ARG:HG3	1:B:336:PRO:CD	2.17	0.74
2:D:688:LYS:HG3	2:D:691:HIS:H	1.54	0.73
1:A:526:TYR:CE2	1:A:530:CME:HE3	2.25	0.71
1:B:304:ASN:HD22	1:B:304:ASN:H	1.35	0.71
1:A:377:HIS:NE2	1:A:460:THR:HG23	2.06	0.71
1:A:498:GLN:HA	1:A:501[A]:HIS:NE2	2.07	0.70
1:B:525:LEU:HD11	1:B:536:LEU:HD11	1.72	0.70
1:A:391:LEU:HA	1:A:394:ARG:NH1	2.08	0.68
1:B:474:HIS:O	1:B:478:VAL:HG12	1.93	0.68
1:A:508:LEU:HG	1:B:509:LEU:CD1	2.24	0.67
1:A:526:TYR:HE2	1:A:530:CME:HE3	1.57	0.67
1:A:385:GLU:HG2	1:A:514:ILE:HG22	1.76	0.66
1:B:522:MET:HA	1:B:522:MET:CE	2.27	0.65
1:A:322:ALA:HA	1:A:363:ARG:NH2	2.12	0.64
1:A:481:LYS:NZ	1:A:481:LYS:HB3	2.13	0.64
1:A:354:LEU:O	1:A:358:ILE:HG12	1.97	0.64
1:B:383:TRP:NE1	1:B:543:MET:HB3	2.15	0.62
1:A:349:LEU:HD11	1:A:405:ALA:HB2	1.81	0.62
1:B:304:ASN:N	1:B:304:ASN:HD22	1.98	0.62
1:A:459[A]:TYR:CE2	1:B:513[A]:HIS:HB3	2.35	0.62
1:A:525:LEU:HD13	3:A:2:J3Z:H36	1.82	0.61
1:A:308:LEU:HD21	1:A:477:ARG:HB3	1.83	0.61
1:B:438:MET:O	1:B:438:MET:HG3	2.00	0.61
1:B:443:GLU:HB3	1:B:489:LEU:HD21	1.83	0.60
1:A:487:ILE:CD1	1:A:504:LEU:HD22	2.32	0.59
1:B:347:THR:HG21	1:B:536:LEU:HD21	1.85	0.59
1:A:429:LEU:HD12	1:A:430:ALA:N	2.17	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:688:LYS:CG	2:D:691:HIS:H	2.16	0.58
1:B:497:LEU:HD22	1:B:501[A]:HIS:HE2	1.68	0.57
1:B:496:THR:O	1:B:500:GLN:HG3	2.04	0.56
1:B:346:LEU:HB3	3:B:1:J3Z:H23	1.87	0.56
1:A:360:TRP:CZ2	1:A:449:LYS:HG2	2.40	0.56
1:A:371:THR:HG22	1:A:373:HIS:H	1.71	0.56
1:B:388:MET:HG2	1:B:428:LEU:HD21	1.87	0.56
1:A:391:LEU:HD11	1:A:402:LEU:HB3	1.88	0.56
1:B:437:MET:O	1:B:437:MET:HG2	2.06	0.55
1:B:549:LEU:HD22	1:B:549:LEU:N	2.22	0.55
1:A:329:SER:H	1:A:407:ASN:HD21	1.52	0.55
1:B:526:TYR:CD2	1:B:549:LEU:HD23	2.42	0.55
1:A:459[A]:TYR:CE1	1:B:513[A]:HIS:CD2	2.95	0.54
1:B:339:GLU:HA	1:B:418:VAL:HG22	1.90	0.53
1:B:311:THR:HG23	1:B:314:GLN:OE1	2.08	0.53
1:A:527:SER:O	1:A:531:LYS:HG2	2.08	0.53
1:B:377:HIS:CD2	1:B:461:PHE:CE2	2.97	0.53
1:B:497:LEU:HD22	1:B:501[A]:HIS:NE2	2.23	0.53
1:A:314:GLN:HA	1:A:317:SER:HB2	1.90	0.53
1:A:456:SER:HA	1:A:515:ARG:NH2	2.25	0.52
1:A:344:GLY:HA2	1:A:534:VAL:HG21	1.90	0.52
1:A:351:ASP:OD2	1:A:540:LEU:HB2	2.09	0.52
1:A:498:GLN:HA	1:A:501[A]:HIS:CD2	2.45	0.52
1:A:329:SER:H	1:A:407:ASN:ND2	2.07	0.52
1:A:329:SER:HB3	1:A:407:ASN:HD21	1.75	0.52
1:B:522:MET:HA	1:B:522:MET:HE2	1.92	0.51
1:A:315:MET:HE3	1:A:481:LYS:NZ	2.26	0.51
1:A:514:ILE:HA	1:A:517:MET:HE2	1.93	0.50
1:A:344:GLY:CA	1:A:534:VAL:HG21	2.42	0.50
1:A:487:ILE:HD13	1:A:504:LEU:HD22	1.92	0.50
1:B:486:LEU:HD23	1:B:504:LEU:HD12	1.92	0.50
1:A:352:ARG:NH2	4:A:5:HOH:O	2.43	0.50
1:A:474:HIS:O	1:A:478:VAL:HG12	2.11	0.50
1:A:459[B]:TYR:HE2	1:B:434:ARG:HG2	1.76	0.49
1:A:498:GLN:HA	1:A:501[A]:HIS:CE1	2.48	0.49
1:B:382:ALA:HB2	1:B:456:SER:OG	2.12	0.49
1:B:506:GLN:O	1:B:510:ILE:HG13	2.13	0.48
1:A:497:LEU:O	1:A:500:GLN:HB2	2.14	0.48
1:A:416:LYS:O	1:A:417:CME:C	2.61	0.48
1:B:498:GLN:HA	1:B:501[B]:HIS:ND1	2.28	0.48
1:A:421:MET:HA	1:A:421:MET:CE	2.43	0.48
1:A:393:TRP:HB2	1:A:445:PHE:CE1	2.48	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:391:LEU:HA	1:A:394:ARG:HH12	1.77	0.48
1:A:376:VAL:O	1:A:380:GLU:HG3	2.14	0.48
1:B:525:LEU:HG	1:B:544:LEU:CD2	2.44	0.48
1:A:525:LEU:HD12	1:A:528:MET:CE	2.44	0.48
1:A:528:MET:HG3	1:A:533:VAL:HG23	1.95	0.48
1:B:487:ILE:HG23	1:B:500:GLN:NE2	2.29	0.47
1:A:331:TYR:CB	1:A:345:LEU:HD21	2.43	0.47
1:B:498:GLN:HA	1:B:501[B]:HIS:CE1	2.50	0.47
1:A:349:LEU:O	1:A:353:GLU:HG3	2.15	0.47
1:B:385:GLU:HG3	1:B:518:SER:HB2	1.98	0.46
1:A:343:MET:SD	1:A:418:VAL:HG21	2.55	0.46
1:B:410:LEU:HD23	1:B:414:GLN:HE21	1.80	0.46
1:B:329:SER:C	1:B:331:TYR:H	2.19	0.46
1:A:538:ASP:OD2	1:A:538:ASP:O	2.34	0.46
1:A:379:LEU:O	1:A:383:TRP:HB3	2.16	0.46
1:A:385:GLU:CG	1:A:514:ILE:HG22	2.44	0.45
1:A:352:ARG:O	1:A:355:VAL:HG13	2.16	0.45
1:A:367:PHE:CE1	1:A:453:LEU:HD11	2.51	0.45
1:A:523:GLU:CD	1:A:548[B]:ARG:HH12	2.20	0.45
1:B:514:ILE:HA	1:B:517:MET:HE2	1.99	0.45
1:A:343:MET:HE2	1:A:528:MET:SD	2.57	0.45
1:A:308:LEU:HD21	1:A:477:ARG:HE	1.82	0.45
1:A:351:ASP:OD1	1:A:537:SER:HB3	2.16	0.45
1:A:458:VAL:HG23	1:A:475:ILE:HD12	1.99	0.44
1:B:305:SER:C	1:B:307:ALA:H	2.20	0.44
2:D:688:LYS:HD2	2:D:690:LEU:HB3	2.00	0.44
1:B:307:ALA:HA	1:B:310:LEU:CD1	2.47	0.44
1:B:403:LEU:HD12	1:B:409:LEU:HD11	1.98	0.44
2:C:691:HIS:O	2:C:695:GLN:HG3	2.18	0.44
1:A:409:LEU:CD1	1:A:409:LEU:H	2.31	0.44
1:A:459[B]:TYR:CE2	1:B:434:ARG:HG2	2.51	0.44
1:A:396:MET:O	1:A:436:ARG:HD3	2.18	0.44
1:A:528:MET:HE3	1:A:536:LEU:HD21	2.00	0.44
1:A:458:VAL:HG12	1:A:459[B]:TYR:CD1	2.53	0.44
1:A:347:THR:HG21	1:A:528:MET:HE1	1.99	0.43
1:B:385:GLU:HB3	1:B:452:ILE:HG21	2.00	0.43
1:A:339:GLU:HG3	1:A:340:ALA:N	2.34	0.43
2:C:691:HIS:CD2	2:C:692:ARG:HG3	2.54	0.43
1:A:525:LEU:HD12	1:A:528:MET:HE2	2.00	0.43
1:A:456:SER:HA	1:A:515:ARG:HH22	1.83	0.43
1:A:421:MET:CE	1:A:424:ILE:HD12	2.48	0.43
1:A:332:ASP:C	1:A:334:THR:H	2.21	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:343:MET:HG2	1:A:418:VAL:HG21	2.01	0.43
1:B:510:ILE:O	1:B:514:ILE:HG13	2.18	0.43
1:B:472:LYS:HE2	1:B:472:LYS:N	2.34	0.43
1:A:497:LEU:HD13	1:B:497:LEU:HD21	2.00	0.43
1:A:459[B]:TYR:HE2	1:B:434:ARG:CG	2.32	0.43
1:A:421:MET:HA	1:A:421:MET:HE2	2.00	0.43
1:A:387:LEU:HA	1:A:387:LEU:HD12	1.90	0.43
1:A:520:LYS:HD3	1:A:520:LYS:HA	1.83	0.42
2:D:688:LYS:CG	2:D:691:HIS:HB2	2.33	0.42
1:A:339:GLU:HG3	1:A:340:ALA:H	1.84	0.42
1:B:306:LEU:O	1:B:306:LEU:HG	2.19	0.42
1:B:541:LEU:HD12	1:B:541:LEU:HA	1.87	0.42
1:A:315:MET:O	1:A:319:LEU:HG	2.20	0.42
1:A:380:GLU:O	1:A:547:HIS:HE1	2.03	0.42
1:A:409:LEU:HD12	1:A:409:LEU:H	1.84	0.42
1:B:525:LEU:HD22	3:B:1:J3Z:H36	2.02	0.42
1:B:522:MET:HE1	1:B:525:LEU:HD23	2.01	0.42
1:B:544:LEU:HA	1:B:544:LEU:HD13	1.78	0.42
1:A:379:LEU:HD12	1:A:379:LEU:HA	1.82	0.42
1:B:354:LEU:HA	1:B:354:LEU:HD12	1.83	0.42
1:A:409:LEU:O	1:A:409:LEU:HD13	2.20	0.41
1:A:392:VAL:HG13	1:A:432:SER:HA	2.02	0.41
1:A:350:ALA:O	1:A:354:LEU:HB2	2.20	0.41
1:B:310:LEU:O	1:B:481:LYS:HE2	2.20	0.41
1:A:543:MET:CE	2:C:690:LEU:HD22	2.50	0.41
1:B:396:MET:HE3	1:B:396:MET:HB3	1.94	0.41
1:B:372:LEU:HD21	2:D:695:GLN:CD	2.40	0.41
1:A:508:LEU:HA	1:A:508:LEU:HD12	1.87	0.41
1:A:515:ARG:HD2	1:B:516:HIS:HB2	2.02	0.41
1:A:391:LEU:O	1:A:391:LEU:HD12	2.21	0.41
1:B:456:SER:HA	1:B:515:ARG:NH2	2.36	0.41
1:B:303:LYS:HE3	1:B:303:LYS:HB2	1.94	0.41
1:A:501[B]:HIS:CD2	1:B:501[B]:HIS:HB3	2.56	0.41
1:B:305:SER:C	1:B:307:ALA:N	2.74	0.41
1:A:407:ASN:H	1:A:407:ASN:HD22	1.69	0.41
1:B:403:LEU:CD1	1:B:409:LEU:HD11	2.51	0.40
1:A:459[A]:TYR:CE1	1:B:513[A]:HIS:HD2	2.39	0.40
1:B:372:LEU:HD22	1:B:375:GLN:NE2	2.37	0.40
1:A:323:GLU:HA	1:A:324:PRO:HD3	1.84	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	230/253 (91%)	224 (97%)	5 (2%)	1 (0%)	43	50
1	B	234/253 (92%)	225 (96%)	8 (3%)	1 (0%)	43	50
2	C	8/13 (62%)	8 (100%)	0	0	100	100
2	D	7/13 (54%)	7 (100%)	0	0	100	100
All	All	479/532 (90%)	464 (97%)	13 (3%)	2 (0%)	43	50

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	396	MET
1	A	333	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	211/226 (93%)	181 (86%)	30 (14%)	5	4
1	B	214/226 (95%)	187 (87%)	27 (13%)	7	6
2	C	10/13 (77%)	7 (70%)	3 (30%)	0	0
2	D	9/13 (69%)	7 (78%)	2 (22%)	1	1
All	All	444/478 (93%)	382 (86%)	62 (14%)	5	4

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	310	LEU

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Mol	Chain	Res	Type
1	A	317	SER
1	A	321	ASP
1	A	327	LEU
1	A	335	ARG
1	A	339	GLU
1	A	345	LEU
1	A	349	LEU
1	A	354	LEU
1	A	355	VAL
1	A	363	ARG
1	A	373	HIS
1	A	379	LEU
1	A	407	ASN
1	A	409	LEU
1	A	421	MET
1	A	425	PHE
1	A	434	ARG
1	A	458	VAL
1	A	459[A]	TYR
1	A	459[B]	TYR
1	A	478	VAL
1	A	492	LYS
1	A	498	GLN
1	A	508	LEU
1	A	539	LEU
1	A	542	GLU
1	A	543	MET
1	A	548[A]	ARG
1	A	548[B]	ARG
1	B	303	LYS
1	B	304	ASN
1	B	306	LEU
1	B	308	LEU
1	B	330	GLU
1	B	354	LEU
1	B	372	LEU
1	B	373	HIS
1	B	378	LEU
1	B	396	MET
1	B	403	LEU
1	B	414	GLN
1	B	437	MET

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Mol	Chain	Res	Type
1	B	438	MET
1	B	460	THR
1	B	462	LEU
1	B	472	LYS
1	B	478	VAL
1	B	489	LEU
1	B	497	LEU
1	B	498	GLN
1	B	508	LEU
1	B	509	LEU
1	B	533	VAL
1	B	542	GLU
1	B	544	LEU
1	B	549	LEU
2	C	688	LYS
2	C	689	ILE
2	C	691	HIS
2	D	688	LYS
2	D	692	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	375	GLN
1	A	407	ASN
1	A	474	HIS
1	A	499	GLN
1	A	502	GLN
1	A	519	ASN
1	A	547	HIS
1	B	304	ASN
1	B	375	GLN
1	B	377	HIS
1	B	414	GLN
1	B	476	HIS
1	B	500	GLN
1	B	502	GLN
1	B	506	GLN
1	B	519	ASN
1	B	532	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

6 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CME	A	381	1	9,9,10	6.06	2 (22%)	7,9,11	0.92	0
1	CME	A	417	1	9,9,10	5.93	2 (22%)	7,9,11	4.03	3 (42%)
1	CME	A	530	1	9,9,10	6.05	2 (22%)	7,9,11	1.48	1 (14%)
1	CME	B	381	1	9,9,10	5.80	2 (22%)	7,9,11	2.43	1 (14%)
1	CME	B	417	1	9,9,10	5.46	1 (11%)	7,9,11	2.02	2 (28%)
1	CME	B	530	1	9,9,10	5.67	2 (22%)	7,9,11	1.05	1 (14%)

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
1	CME	A	381	1	-	0/6/8/10	0/0/0/0
1	CME	A	417	1	-	0/6/8/10	0/0/0/0
1	CME	A	530	1	-	0/6/8/10	0/0/0/0
1	CME	B	381	1	-	0/6/8/10	0/0/0/0
1	CME	B	417	1	-	0/6/8/10	0/0/0/0
1	CME	B	530	1	-	0/6/8/10	0/0/0/0

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	381	CME	O-C	17.95	1.23	1.11
1	A	530	CME	O-C	17.87	1.23	1.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	417	CME	O-C	17.46	1.23	1.11
1	B	381	CME	O-C	16.91	1.23	1.11
1	B	530	CME	O-C	16.79	1.22	1.11
1	B	417	CME	O-C	16.21	1.22	1.11
1	B	381	CME	CA-C	3.83	1.55	1.48
1	A	417	CME	CA-C	3.14	1.54	1.48
1	A	530	CME	CA-C	2.87	1.53	1.48
1	A	381	CME	CA-C	2.65	1.53	1.48
1	B	530	CME	CA-C	2.58	1.53	1.48

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	417	CME	C-CA-N	-8.48	105.36	113.83
1	B	381	CME	CB-SG-SD	-6.22	91.46	103.87
1	A	417	CME	CB-SG-SD	4.38	112.61	103.87
1	A	417	CME	CB-CA-N	-4.31	102.95	110.27
1	B	417	CME	C-CA-N	-4.18	109.65	113.83
1	A	530	CME	C-CA-N	-3.37	110.47	113.83
1	B	417	CME	CB-CA-N	2.60	114.68	110.27
1	B	530	CME	C-CA-N	-2.14	111.69	113.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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
3	J3Z	A	2	-	23,23,23	0.84	0	36,36,36	1.51	7 (19%)
3	J3Z	B	1	-	23,23,23	0.86	0	36,36,36	1.49	8 (22%)

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
3	J3Z	A	2	-	-	0/0/40/40	0/0/4/4
3	J3Z	B	1	-	-	0/0/40/40	0/0/4/4

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	2	J3Z	C8-C7-C5	3.62	112.24	108.60
3	B	1	J3Z	C2-C12-C10	-3.49	103.44	108.91
3	A	2	J3Z	C9-C10-C5	3.27	106.89	104.06
3	A	2	J3Z	C2-C12-C10	-3.10	104.03	108.91
3	B	1	J3Z	C15-C14-C12	2.98	115.11	110.68
3	B	1	J3Z	C5-C10-C12	-2.93	110.04	113.13
3	B	1	J3Z	C8-C7-C5	2.76	111.38	108.60
3	B	1	J3Z	C9-C8-C7	-2.57	103.01	105.67
3	A	2	J3Z	C5-C10-C12	-2.54	110.44	113.13
3	B	1	J3Z	C6-C5-C7	2.38	110.01	105.21
3	A	2	J3Z	C14-C12-C2	2.38	111.76	109.28
3	A	2	J3Z	C15-C14-C12	2.27	114.05	110.68
3	B	1	J3Z	C9-C10-C5	2.14	105.92	104.06
3	A	2	J3Z	C9-C8-C7	-2.12	103.47	105.67
3	B	1	J3Z	C14-C12-C2	2.01	111.38	109.28

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	235/253 (92%)	1.80	69 (29%) 1 1	40, 65, 115, 139	3 (1%)
1	B	239/253 (94%)	1.66	60 (25%) 1 2	40, 64, 103, 137	2 (0%)
2	C	10/13 (76%)	4.21	8 (80%) 0 0	92, 112, 126, 128	0
2	D	9/13 (69%)	2.36	5 (55%) 0 0	77, 94, 106, 108	0
All	All	493/532 (92%)	1.79	142 (28%) 1 1	40, 65, 112, 139	5 (1%)

All (142) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	336	PRO	16.7
1	B	460	THR	10.6
1	B	548	ARG	9.5
1	B	304	ASN	9.3
1	B	462	LEU	9.2
1	B	550	HIS	9.0
2	C	696	ASP	8.6
1	A	533	VAL	8.4
1	A	309	SER	7.7
1	A	535	PRO	7.2
1	B	334	THR	7.2
2	C	692	ARG	7.2
2	C	689	ILE	7.2
1	A	459[A]	TYR	7.1
1	A	473	ASP	6.9
1	A	418	VAL	6.0
1	A	306	LEU	5.9
1	A	351	ASP	5.9
1	A	525	LEU	5.9
1	B	332	ASP	5.8
1	A	428	LEU	5.8

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Mol	Chain	Res	Type	RSRZ
1	A	421	MET	5.8
1	A	371	THR	5.7
1	A	337	PHE	5.7
1	A	534	VAL	5.5
1	A	310	LEU	5.2
1	A	537	SER	5.1
1	A	505	ALA	5.1
1	A	333	PRO	5.0
1	B	338	SER	4.9
1	B	365	PRO	4.9
1	B	510	ILE	4.7
2	C	690	LEU	4.7
1	B	336	PRO	4.7
1	B	537	SER	4.5
1	A	334	THR	4.5
2	D	689	ILE	4.5
1	A	548[A]	ARG	4.4
1	B	307	ALA	4.3
1	B	459	TYR	4.2
1	A	458	VAL	4.2
1	B	487	ILE	4.2
1	B	317	SER	4.2
1	B	400	GLY	4.0
1	A	398	HIS	3.9
1	A	461	PHE	3.8
1	A	539	LEU	3.7
1	A	417	CME	3.6
1	B	549	LEU	3.6
2	D	692	ARG	3.6
1	B	319	LEU	3.6
1	A	307	ALA	3.4
1	A	470	GLU	3.4
1	B	315	MET	3.4
2	C	691	HIS	3.4
1	A	348	ASN	3.3
2	D	696	ASP	3.3
1	A	497	LEU	3.2
2	C	687	HIS	3.2
1	A	349	LEU	3.2
1	A	422	VAL	3.2
1	B	351	ASP	3.2
1	B	305	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	513[A]	HIS	3.1
1	B	422	VAL	3.1
1	B	542	GLU	3.0
1	B	306	LEU	3.0
1	B	309	SER	3.0
1	B	421	MET	3.0
1	A	527	SER	2.9
1	A	339	GLU	2.9
1	B	461	PHE	2.9
1	B	303	LYS	2.9
1	B	328	TYR	2.9
1	B	521	GLY	2.9
1	A	429	LEU	2.8
1	B	408	LEU	2.8
1	A	324	PRO	2.8
1	A	488	HIS	2.7
1	A	355	VAL	2.7
1	A	486	LEU	2.7
1	B	331	TYR	2.7
1	B	476	HIS	2.7
1	A	332	ASP	2.7
1	B	335	ARG	2.7
2	D	695	GLN	2.6
1	A	526	TYR	2.6
1	B	418	VAL	2.6
1	A	532	ASN	2.6
1	A	420	GLY	2.6
1	B	514	ILE	2.6
1	A	411	ASP	2.6
1	A	430	ALA	2.5
1	A	331	TYR	2.5
1	A	313	ASP	2.5
1	B	473	ASP	2.5
1	A	366	GLY	2.5
1	B	451	ILE	2.5
1	A	460	THR	2.5
1	A	419	GLU	2.5
1	B	413	ASN	2.5
1	A	373	HIS	2.5
1	A	308	LEU	2.5
1	B	488	HIS	2.5
1	B	420	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	333	PRO	2.4
1	A	338	SER	2.4
2	D	693	LEU	2.4
1	A	484	ASP	2.4
2	C	694	LEU	2.4
1	A	346	LEU	2.4
1	B	446	VAL	2.4
2	C	693	LEU	2.3
1	A	409	LEU	2.3
1	B	373	HIS	2.3
1	A	530	CME	2.3
1	B	505	ALA	2.3
1	A	487	ILE	2.2
1	A	410	LEU	2.2
1	A	528	MET	2.2
1	B	411	ASP	2.2
1	B	474	HIS	2.2
1	A	370	LEU	2.2
1	A	538	ASP	2.2
1	B	313	ASP	2.2
1	B	424	ILE	2.2
1	B	538	ASP	2.2
1	A	432	SER	2.2
1	A	335	ARG	2.1
1	A	502	GLN	2.1
1	A	446	VAL	2.1
1	B	364	VAL	2.1
1	B	419	GLU	2.1
1	B	435	PHE	2.1
1	B	511	LEU	2.1
1	B	425	PHE	2.1
1	A	342	MET	2.1
1	B	495	LEU	2.1
1	A	387	LEU	2.1
1	B	504	LEU	2.1
1	B	360	TRP	2.1
1	A	503	ARG	2.0

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

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
1	CME	A	417	10/11	0.36	0.63	87,115,118,119	4
1	CME	B	530	10/11	0.21	0.11	61,67,109,109	0
1	CME	B	381	10/11	0.24	-0.03	42,75,107,192	3
1	CME	A	530	10/11	0.28	-0.44	88,90,126,196	3
1	CME	A	381	10/11	0.16	-0.68	42,53,77,129	4
1	CME	B	417	10/11	0.16	-1.39	69,78,132,155	4

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
3	J3Z	B	1	20/20	0.25	1.07	41,51,61,63	0
3	J3Z	A	2	20/20	0.18	-0.82	38,51,64,65	0

6.5 Other polymers ⓘ

There are no such residues in this entry.