Full wwPDB X-ray Structure Validation Report ⓘ

Feb 20, 2024 – 10:16 AM EST

PDB ID	:	4N1Y
Title	:	Crystal Structure of the Pacific Oyster Estrogen Receptor Ligand Binding Domain
Authors	:	Ortlund, E.O.
Deposited on	:	2013-10-04
Resolution	:	2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

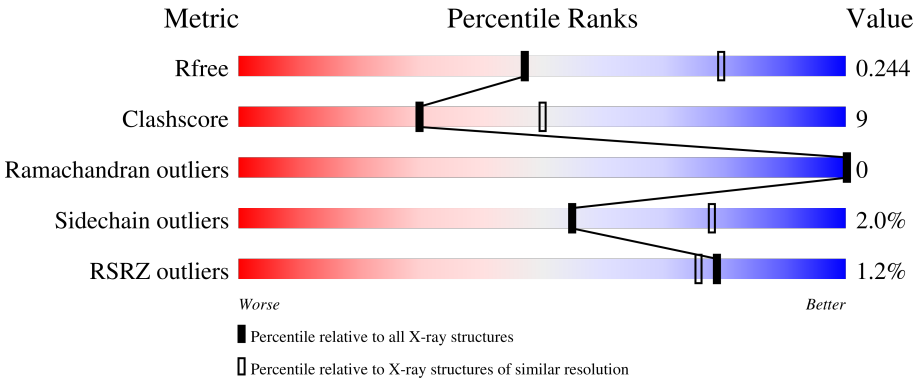
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.60 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	240	76% 18% 6%
1	B	240	% 72% 22% 5%
1	C	240	3% 72% 20% • 7%
1	D	240	77% 17% • 6%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7218 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 Estrogen receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	226	Total	C	N	O	S	0	0	0
			1794	1141	315	327	11			
1	B	227	Total	C	N	O	S	0	0	0
			1802	1145	316	330	11			
1	C	224	Total	C	N	O	S	0	0	0
			1776	1131	311	323	11			
1	D	226	Total	C	N	O	S	0	0	0
			1794	1141	315	327	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	243	SER	-	expression tag	UNP K1QUU5
A	244	ASN	-	expression tag	UNP K1QUU5
A	245	ALA	-	expression tag	UNP K1QUU5
B	243	SER	-	expression tag	UNP K1QUU5
B	244	ASN	-	expression tag	UNP K1QUU5
B	245	ALA	-	expression tag	UNP K1QUU5
C	243	SER	-	expression tag	UNP K1QUU5
C	244	ASN	-	expression tag	UNP K1QUU5
C	245	ALA	-	expression tag	UNP K1QUU5
D	243	SER	-	expression tag	UNP K1QUU5
D	244	ASN	-	expression tag	UNP K1QUU5
D	245	ALA	-	expression tag	UNP K1QUU5

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	20	Total	O	0	0
			20	20		
2	B	8	Total	O	0	0
			8	8		

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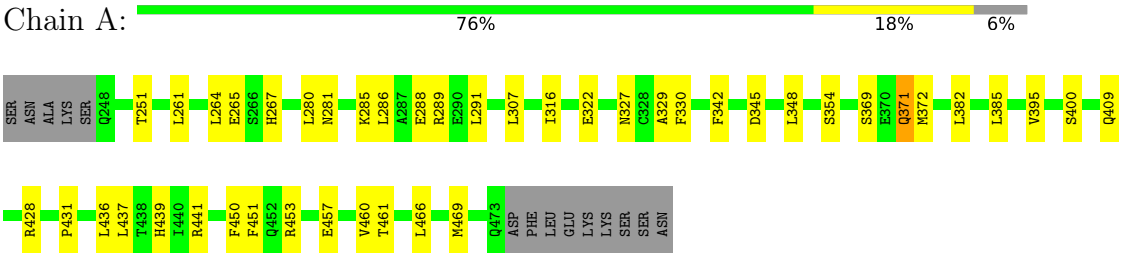
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	11	Total O 11 11	0	0
2	D	13	Total O 13 13	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

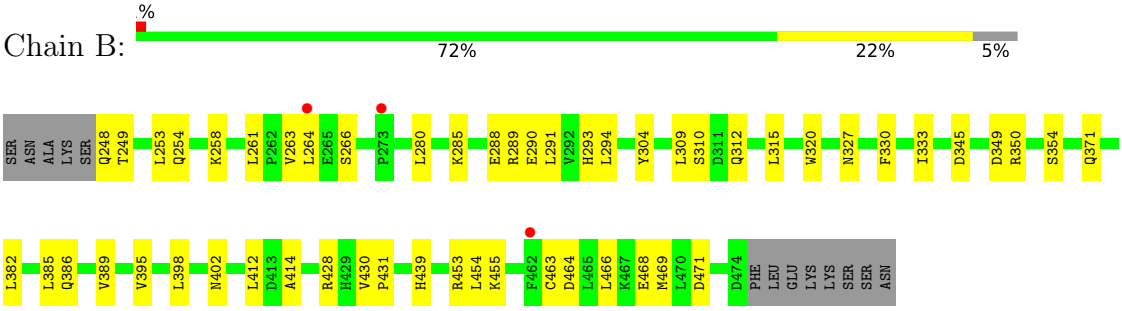
• Molecule 1: Estrogen receptor

Chain A:



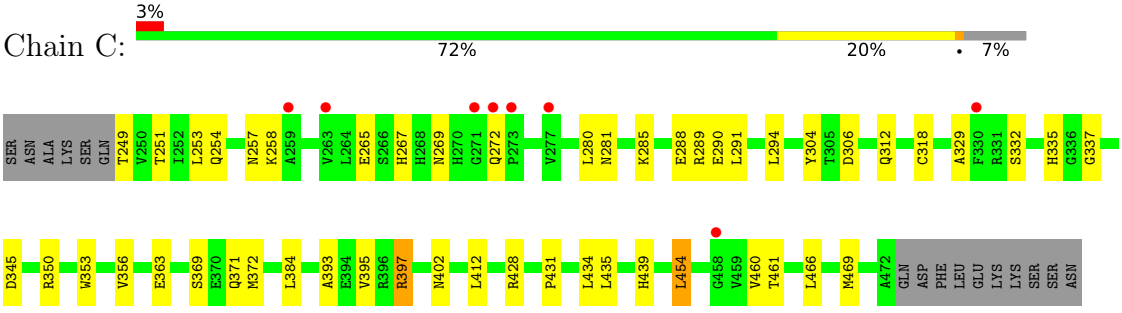
• Molecule 1: Estrogen receptor

Chain B:



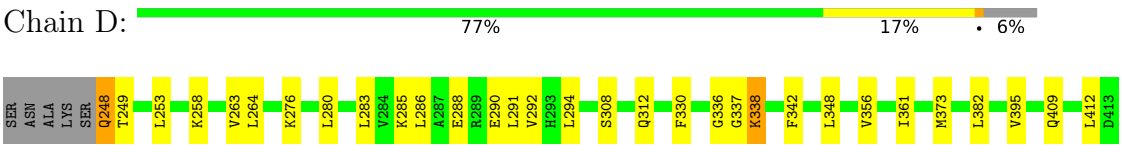
• Molecule 1: Estrogen receptor

Chain C:



• Molecule 1: Estrogen receptor

Chain D:




A414
P431
H439
G447
L454
C463
D464
L465
L466
K467
E468
M469
Q473
ASP
PHE
LEU
GLU
LYS
LYS
SER
SER
ASN

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	55.03Å 105.80Å 171.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.96 – 2.60 46.96 – 2.60	Depositor EDS
% Data completeness (in resolution range)	89.9 (46.96-2.60) 90.0 (46.96-2.60)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.20 (at 2.61Å)	Xtriage
Refinement program	PHENIX dev_1458	Depositor
R, R_{free}	0.170 , 0.243 0.174 , 0.244	Depositor DCC
R_{free} test set	1409 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	43.3	Xtriage
Anisotropy	0.671	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 53.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7218	wwPDB-VP
Average B, all atoms (Å^2)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.14% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.45	0/1828	0.62	0/2482
1	B	0.43	0/1836	0.65	0/2493
1	C	0.43	0/1810	0.62	1/2458 (0.0%)
1	D	0.44	0/1828	0.62	0/2482
All	All	0.44	0/7302	0.63	1/9915 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	397	ARG	NE-CZ-NH1	5.19	122.89	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1794	0	1815	34	0
1	B	1802	0	1819	47	0
1	C	1776	0	1799	35	0
1	D	1794	0	1815	30	0
2	A	20	0	0	2	0
2	B	8	0	0	3	0
2	C	11	0	0	2	0
2	D	13	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7218	0	7248	135	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 9.

All (135) 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:C:249:THR:N	2:C:508:HOH:O	1.92	1.03
1:D:288:GLU:HG3	1:D:466:LEU:HB2	1.51	0.92
1:C:265:GLU:O	1:C:289:ARG:NH2	2.04	0.90
1:D:249:THR:HG22	1:D:414:ALA:HA	1.58	0.84
1:A:322:GLU:OE2	2:A:513:HOH:O	1.94	0.83
1:A:261:LEU:HD22	1:A:327:ASN:HD22	1.44	0.82
1:B:288:GLU:HG3	1:B:466:LEU:HB2	1.63	0.81
1:D:291:LEU:HD21	1:D:469:MET:HG3	1.63	0.79
1:A:291:LEU:HD21	1:A:469:MET:HG3	1.66	0.76
1:C:288:GLU:HG2	1:C:466:LEU:HD22	1.66	0.76
1:B:285:LYS:HZ3	1:B:463:CYS:H	1.35	0.72
1:B:371:GLN:NE2	2:B:503:HOH:O	1.95	0.69
1:B:264:LEU:HD12	1:B:290:GLU:HG2	1.76	0.68
1:B:453:ARG:CZ	2:B:504:HOH:O	2.42	0.67
1:D:280:LEU:HD13	1:D:454:LEU:HD11	1.76	0.67
1:C:397:ARG:HG2	1:C:397:ARG:HH11	1.61	0.66
1:B:464:ASP:O	1:B:468:GLU:HG3	1.96	0.65
1:A:288:GLU:HG2	1:A:466:LEU:HD22	1.79	0.64
1:B:285:LYS:NZ	1:B:463:CYS:H	1.95	0.64
1:A:264:LEU:HB3	1:A:289:ARG:NH2	2.13	0.63
1:B:280:LEU:HD13	1:B:454:LEU:HD11	1.79	0.63
1:B:285:LYS:HZ3	1:B:463:CYS:N	1.96	0.63
1:A:354:SER:OG	1:D:338:LYS:HE3	1.99	0.63
1:C:397:ARG:HH11	1:C:397:ARG:CG	2.13	0.62
1:D:288:GLU:OE1	1:D:463:CYS:HB2	2.00	0.62
1:D:286:LEU:O	1:D:290:GLU:HG3	1.99	0.62
1:A:264:LEU:HB3	1:A:289:ARG:HH21	1.65	0.61
1:B:453:ARG:NH2	2:B:504:HOH:O	2.33	0.61
1:B:455:LYS:NZ	1:B:471:ASP:OD1	2.33	0.60
1:B:249:THR:HG22	1:B:414:ALA:HA	1.81	0.60
1:D:464:ASP:O	1:D:468:GLU:HG3	2.00	0.60
1:A:281:ASN:O	1:A:285:LYS:HG2	2.01	0.60
1:D:336:GLY:O	1:D:338:LYS:HD3	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:431:PRO:HB2	1:B:412:LEU:HD22	1.84	0.59
1:B:254:GLN:O	1:B:258:LYS:HG2	2.02	0.59
1:D:276:LYS:HG3	1:D:356:VAL:HA	1.83	0.59
1:B:264:LEU:HD11	1:B:293:HIS:CD2	2.37	0.58
1:C:353:TRP:HZ3	1:C:363:GLU:HG2	1.69	0.57
1:C:304:TYR:OH	1:C:312:GLN:O	2.23	0.56
1:B:349:ASP:OD1	1:B:350:ARG:N	2.35	0.56
1:B:248:GLN:HG2	1:B:249:THR:H	1.71	0.56
1:A:265:GLU:O	1:A:289:ARG:NH2	2.29	0.55
1:A:261:LEU:HD22	1:A:327:ASN:ND2	2.18	0.54
1:C:412:LEU:HD22	1:D:431:PRO:HB2	1.88	0.54
1:A:439:HIS:CE1	1:B:395:VAL:HB	2.43	0.53
1:A:267:HIS:N	1:A:345:ASP:OD2	2.42	0.53
1:D:249:THR:CG2	1:D:414:ALA:HA	2.34	0.53
1:C:291:LEU:HD21	1:C:469:MET:HG3	1.89	0.53
1:C:332:SER:HA	1:C:335:HIS:HD2	1.75	0.52
1:B:264:LEU:HB3	1:B:289:ARG:NH2	2.24	0.52
1:C:281:ASN:O	1:C:285:LYS:HG2	2.10	0.51
1:D:248:GLN:N	2:D:504:HOH:O	2.44	0.51
1:A:329:ALA:C	1:A:372:MET:HE1	2.31	0.51
1:C:353:TRP:CZ3	1:C:363:GLU:HG2	2.44	0.51
1:C:254:GLN:O	1:C:258:LYS:HG3	2.11	0.51
1:B:402:ASN:HD21	1:C:306:ASP:CG	2.14	0.51
1:C:329:ALA:C	1:C:372:MET:HE1	2.31	0.50
1:B:261:LEU:HD21	1:B:294:LEU:HD23	1.93	0.50
1:B:285:LYS:HE2	1:B:463:CYS:SG	2.51	0.50
1:B:291:LEU:HD21	1:B:469:MET:HG3	1.94	0.50
1:D:264:LEU:HD12	1:D:290:GLU:HG2	1.93	0.50
1:C:269:ASN:ND2	1:C:272:GLN:HG3	2.27	0.50
1:B:349:ASP:OD1	1:B:350:ARG:HG3	2.12	0.49
1:D:338:LYS:N	1:D:338:LYS:HD2	2.26	0.49
1:C:369:SER:HA	1:C:372:MET:HE2	1.94	0.48
1:C:439:HIS:CE1	1:D:395:VAL:HB	2.48	0.48
1:B:264:LEU:HD11	1:B:293:HIS:HD2	1.79	0.48
1:C:428:ARG:HD3	1:D:409:GLN:OE1	2.14	0.48
1:A:369:SER:HA	1:A:372:MET:HE2	1.96	0.48
1:C:253:LEU:O	1:C:257:ASN:HB2	2.13	0.48
1:A:371:GLN:HG2	1:A:436:LEU:HD21	1.96	0.47
1:D:464:ASP:HA	1:D:467:LYS:HB3	1.97	0.47
1:C:384:LEU:HA	1:C:384:LEU:HD23	1.74	0.46
1:A:441:ARG:NH2	2:A:512:HOH:O	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:330:PHE:CD2	1:D:382:LEU:HD22	2.50	0.46
1:A:385:LEU:HD23	1:A:385:LEU:HA	1.75	0.46
1:A:330:PHE:HB2	1:A:382:LEU:HD13	1.98	0.45
1:D:412:LEU:HD23	1:D:412:LEU:HA	1.79	0.45
1:A:395:VAL:HB	1:B:439:HIS:CE1	2.51	0.45
1:A:437:LEU:HD23	1:A:437:LEU:HA	1.77	0.45
1:C:267:HIS:N	1:C:345:ASP:OD2	2.49	0.45
1:B:454:LEU:HD23	1:B:454:LEU:HA	1.83	0.45
1:B:266:SER:H	1:B:345:ASP:HB3	1.81	0.45
1:B:285:LYS:HZ2	1:B:285:LYS:HG3	1.59	0.45
1:B:248:GLN:HG2	1:B:249:THR:N	2.32	0.44
1:C:454:LEU:HD22	1:C:460:VAL:HB	1.99	0.44
1:A:307:LEU:HD22	1:A:400:SER:HB3	1.99	0.44
1:A:285:LYS:NZ	1:A:288:GLU:OE1	2.45	0.44
1:A:281:ASN:OD1	1:A:460:VAL:HG13	2.17	0.44
1:B:304:TYR:OH	1:B:312:GLN:O	2.36	0.44
1:B:288:GLU:CG	1:B:466:LEU:HB2	2.41	0.44
1:B:430:VAL:HB	1:B:431:PRO:HD3	1.99	0.44
1:D:285:LYS:HB3	1:D:285:LYS:HE3	1.56	0.43
1:B:320:TRP:CG	1:B:469:MET:HE3	2.53	0.43
1:D:288:GLU:O	1:D:292:VAL:HG23	2.19	0.43
1:C:395:VAL:HB	1:D:439:HIS:CE1	2.53	0.43
1:C:434:LEU:HD23	1:C:434:LEU:HA	1.81	0.43
1:B:327:ASN:OD1	1:B:386:GLN:NE2	2.52	0.43
1:B:466:LEU:HD12	1:B:466:LEU:HA	1.79	0.43
1:C:280:LEU:HD23	1:C:280:LEU:HA	1.88	0.42
1:A:329:ALA:O	1:A:372:MET:HE1	2.19	0.42
1:A:409:GLN:OE1	1:B:428:ARG:HD3	2.19	0.42
1:B:253:LEU:HD23	1:B:253:LEU:HA	1.84	0.42
1:B:385:LEU:O	1:B:389:VAL:HG23	2.19	0.42
1:A:453:ARG:O	1:A:457:GLU:HG3	2.19	0.42
1:C:318:CYS:HB2	1:C:393:ALA:HB1	2.02	0.42
1:A:280:LEU:HD23	1:A:280:LEU:HA	1.75	0.42
1:D:361:ILE:HD13	1:D:447:GLY:HA2	2.00	0.42
1:C:428:ARG:C	1:C:431:PRO:HD2	2.40	0.42
1:C:249:THR:N	2:C:503:HOH:O	2.53	0.41
1:D:342:PHE:HE2	1:D:348:LEU:HB2	1.86	0.41
1:B:264:LEU:HB3	1:B:289:ARG:HH21	1.84	0.41
1:B:315:LEU:HA	1:B:315:LEU:HD23	1.74	0.41
1:D:253:LEU:HA	1:D:253:LEU:HD23	1.79	0.41
1:C:280:LEU:HD21	1:C:356:VAL:HB	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:PHE:CE2	1:A:348:LEU:HD12	2.55	0.41
1:D:294:LEU:HA	1:D:294:LEU:HD23	1.81	0.41
1:B:330:PHE:HA	1:B:333:ILE:HG13	2.02	0.41
1:B:398:LEU:HA	1:C:402:ASN:HD22	1.85	0.41
1:C:337:GLY:O	1:C:350:ARG:NH1	2.52	0.41
1:C:290:GLU:O	1:C:294:LEU:HG	2.21	0.41
1:D:280:LEU:HD23	1:D:283:LEU:HD12	2.02	0.41
1:B:266:SER:H	1:B:345:ASP:CB	2.33	0.41
1:A:450:PHE:HD2	1:A:451:PHE:HD1	1.68	0.40
1:B:266:SER:OG	1:B:345:ASP:HB3	2.21	0.40
1:A:285:LYS:HA	1:A:288:GLU:HG3	2.03	0.40
1:A:286:LEU:HD12	1:A:286:LEU:HA	1.91	0.40
1:A:316:ILE:HG22	1:A:469:MET:HE2	2.03	0.40
1:B:330:PHE:HB2	1:B:382:LEU:HD13	2.04	0.40
1:A:428:ARG:C	1:A:431:PRO:HD2	2.41	0.40
1:C:372:MET:HE2	1:C:372:MET:HB2	1.65	0.40
1:D:308:SER:O	1:D:312:GLN:HG3	2.21	0.40
1:D:337:GLY:C	1:D:338:LYS:HD2	2.42	0.40
1:B:382:LEU:O	1:B:382:LEU:HG	2.18	0.40
1:C:435:LEU:HD23	1:C:435:LEU:HA	1.82	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	224/240 (93%)	222 (99%)	2 (1%)	0	100	100
1	B	225/240 (94%)	220 (98%)	5 (2%)	0	100	100
1	C	222/240 (92%)	219 (99%)	3 (1%)	0	100	100
1	D	224/240 (93%)	223 (100%)	1 (0%)	0	100	100
All	All	895/960 (93%)	884 (99%)	11 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	200/213 (94%)	197 (98%)	3 (2%)	65	83
1	B	201/213 (94%)	197 (98%)	4 (2%)	55	78
1	C	198/213 (93%)	194 (98%)	4 (2%)	55	78
1	D	200/213 (94%)	195 (98%)	5 (2%)	47	73
All	All	799/852 (94%)	783 (98%)	16 (2%)	55	78

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	251	THR
1	A	371	GLN
1	A	461	THR
1	B	263	VAL
1	B	309	LEU
1	B	310	SER
1	B	354	SER
1	C	251	THR
1	C	371	GLN
1	C	454	LEU
1	C	461	THR
1	D	248	GLN
1	D	258	LYS
1	D	263	VAL
1	D	338	LYS
1	D	373	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	420	GLN

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Mol	Chain	Res	Type
1	B	293	HIS
1	B	327	ASN
1	B	374	GLN
1	B	386	GLN
1	C	335	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	226/240 (94%)	-0.30	0 100 100	31, 45, 68, 88	0
1	B	227/240 (94%)	-0.08	3 (1%) 77 73	32, 57, 87, 115	0
1	C	224/240 (93%)	-0.02	8 (3%) 42 35	36, 59, 90, 117	0
1	D	226/240 (94%)	-0.27	0 100 100	33, 47, 72, 88	0
All	All	903/960 (94%)	-0.17	11 (1%) 79 76	31, 51, 84, 117	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	462	PHE	3.7
1	B	264	LEU	3.1
1	B	273	PRO	3.0
1	C	277	VAL	2.6
1	C	271	GLY	2.6
1	C	272	GLN	2.5
1	C	263	VAL	2.5
1	C	259	ALA	2.3
1	C	273	PRO	2.3
1	C	458	GLY	2.2
1	C	330	PHE	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 monosaccharides 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.