



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:52 PM UTC

PDB ID : 1R0W / pdb_00001r0w
Title : Cystic fibrosis transmembrane conductance regulator (CFTR) nucleotide-binding domain one (NBD1) apo
Authors : Lewis, H.A.; Buchanan, S.G.; Burley, S.K.; Conners, K.; Dickey, M.; Dorwart, M.; Fowler, R.; Gao, X.; Guggino, W.B.; Hendrickson, W.A.
Deposited on : 2003-09-23
Resolution : 2.20 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
Mogul : 2022.3.0, CSD as543be (2022)
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

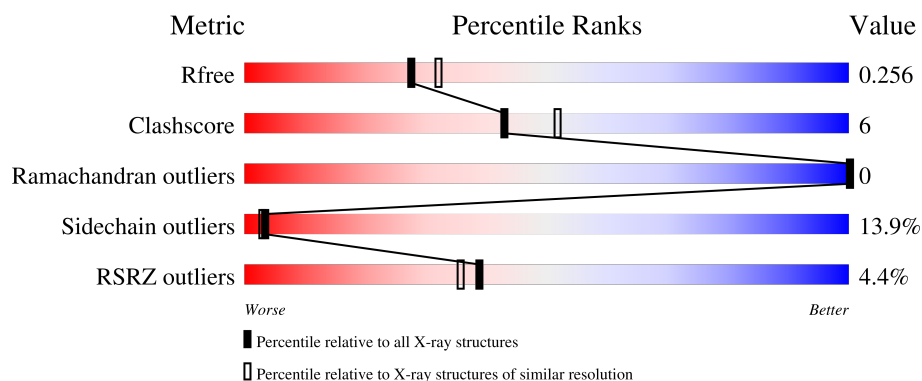
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (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 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	286	5% 74% 16% • 7%
1	B	286	5% 66% 21% 6% 7%
1	C	286	3% 77% 16% • 7%
1	D	286	5% 75% 14% • 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8723 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.

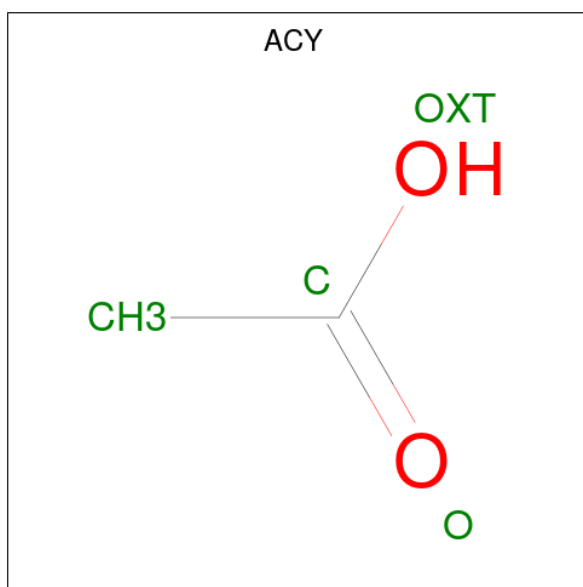
- Molecule 1 is a protein called Cystic fibrosis transmembrane conductance regulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	266	Total	C	N	O	S	0	0	0
			2098	1336	347	403	12			
1	B	267	Total	C	N	O	S	0	0	0
			2105	1340	348	405	12			
1	C	267	Total	C	N	O	S	0	0	0
			2105	1340	348	405	12			
1	D	264	Total	C	N	O	S	0	0	0
			2083	1328	344	399	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	388	SER	-	cloning artifact	UNP P26361
B	388	SER	-	cloning artifact	UNP P26361
C	388	SER	-	cloning artifact	UNP P26361
D	388	SER	-	cloning artifact	UNP P26361

- Molecule 2 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		

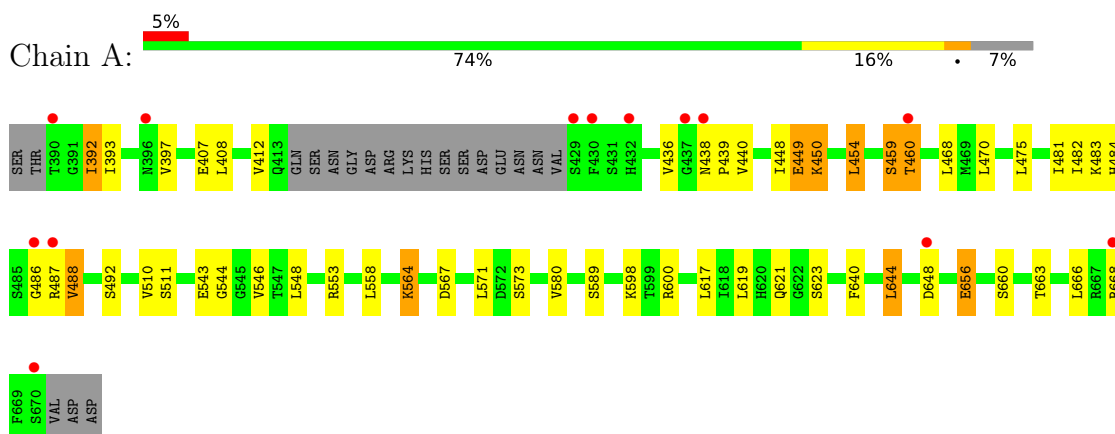
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	106	Total	O	0	0
			106	106		
3	B	92	Total	O	0	0
			92	92		
3	C	110	Total	O	0	0
			110	110		

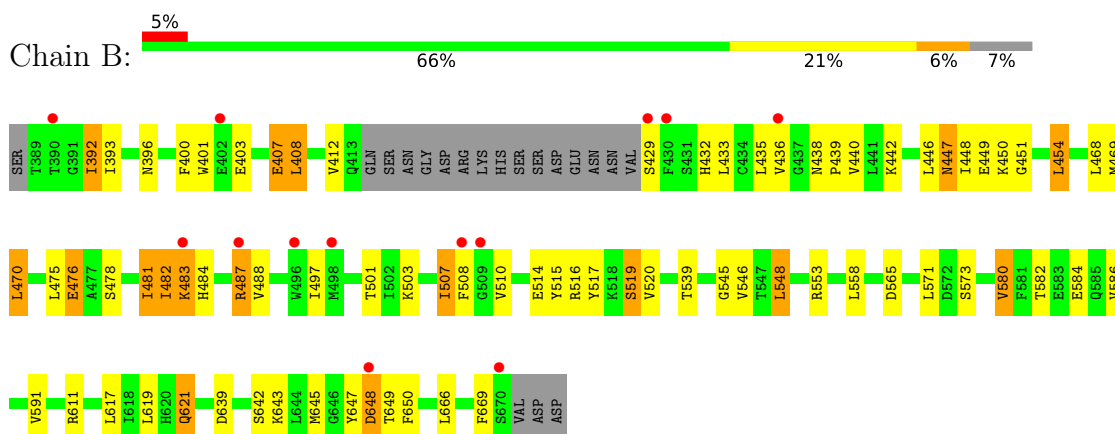
3 Residue-property plots [i](#)

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.

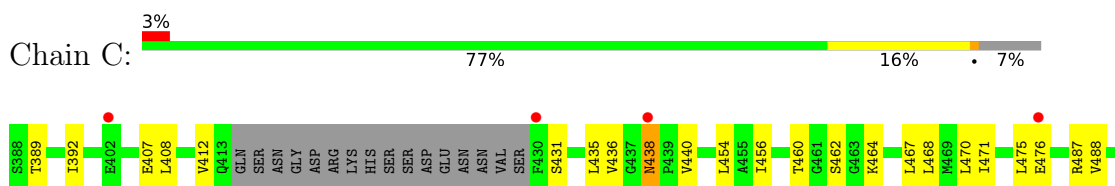
- Molecule 1: Cystic fibrosis transmembrane conductance regulator

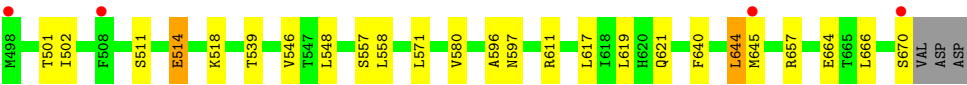


- Molecule 1: Cystic fibrosis transmembrane conductance regulator

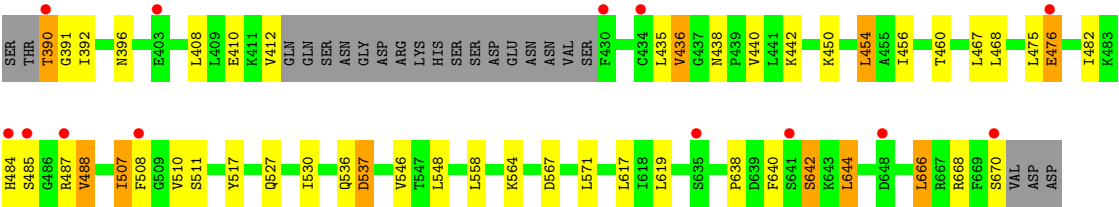
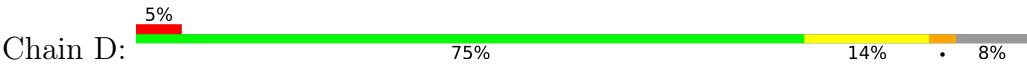


- Molecule 1: Cystic fibrosis transmembrane conductance regulator





● Molecule 1: Cystic fibrosis transmembrane conductance regulator



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α , β , γ	172.25Å 172.25Å 110.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.90 – 2.20 38.90 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (38.90-2.20) 93.2 (38.90-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.95 (at 2.20Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.212 , 0.262 0.210 , 0.256	Depositor DCC
R_{free} test set	4212 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	31.2	Xtriage
Anisotropy	0.092	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 31.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8723	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% 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

5.1 Standard geometry

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

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	0.98	0/2133	1.08	2/2868 (0.1%)
1	B	0.99	1/2140 (0.0%)	1.11	4/2878 (0.1%)
1	C	0.97	0/2140	1.07	2/2878 (0.1%)
1	D	0.97	0/2118	1.08	2/2848 (0.1%)
All	All	0.98	1/8531 (0.0%)	1.08	10/11472 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	591	VAL	CA-CB	5.15	1.60	1.54

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	481	ILE	N-CA-C	8.32	120.76	108.45
1	C	502	ILE	N-CA-C	-7.50	103.15	110.72
1	D	536	GLN	CA-C-N	6.77	130.02	120.28
1	D	536	GLN	C-N-CA	6.77	130.02	120.28
1	B	508	PHE	N-CA-C	6.66	120.03	110.24
1	A	589	SER	N-CA-C	6.47	118.41	111.36
1	B	580	VAL	N-CA-CB	-5.24	101.29	110.77
1	C	462	SER	N-CA-C	5.18	119.22	113.01
1	A	656	GLU	N-CA-C	-5.17	105.55	111.14
1	B	470	LEU	N-CA-C	-5.16	105.55	111.07

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	2098	0	2096	21	0
1	B	2105	0	2103	45	0
1	C	2105	0	2103	16	0
1	D	2083	0	2083	22	0
2	A	8	0	6	0	0
2	B	4	0	3	0	0
2	C	4	0	3	0	0
2	D	8	0	6	0	0
3	A	106	0	0	5	0
3	B	92	0	0	3	0
3	C	110	0	0	3	0
All	All	8723	0	8403	104	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 6.

All (104) 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:580:VAL:CG2	3:C:217:HOH:O	2.15	0.95
1:C:456:ILE:HD13	1:C:467:LEU:HD23	1.55	0.89
1:B:429:SER:HB3	1:B:432:HIS:HB2	1.58	0.84
1:C:436:VAL:HB	1:C:438:ASN:HD21	1.51	0.74
1:B:584:GLU:OE1	3:B:173:HOH:O	2.06	0.74
1:B:481:ILE:HG23	1:B:483:LYS:NZ	2.06	0.70
1:B:481:ILE:HD12	1:B:482:ILE:H	1.56	0.70
1:D:390:THR:HG23	1:D:450:LYS:HB2	1.74	0.69
1:D:436:VAL:HG12	1:D:438:ASN:HD21	1.57	0.68
1:A:440:VAL:HG11	1:A:475:LEU:HD21	1.74	0.68
1:C:596:ALA:O	3:C:297:HOH:O	2.12	0.67
1:B:487:ARG:HH11	1:B:565:ASP:CG	2.04	0.66
1:B:487:ARG:HG3	1:B:487:ARG:HH21	1.61	0.65
1:B:393:ILE:HB	1:B:483:LYS:HG3	1.80	0.64
1:D:436:VAL:HG12	1:D:438:ASN:ND2	2.14	0.63
1:D:488:VAL:O	1:D:564:LYS:NZ	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:460:THR:CG2	3:A:165:HOH:O	2.48	0.62
1:B:487:ARG:HG3	1:B:487:ARG:NH2	2.15	0.62
1:D:517:TYR:HH	1:D:537:ASP:CG	2.09	0.61
1:C:389:THR:HG21	1:C:597:ASN:O	2.00	0.61
1:D:487:ARG:HH21	1:D:487:ARG:HG3	1.65	0.61
1:B:481:ILE:HG23	1:B:483:LYS:HZ1	1.63	0.60
1:A:486:GLY:HA3	1:A:567:ASP:OD2	2.03	0.59
1:B:515:TYR:O	1:B:519:SER:HB3	2.03	0.58
1:C:580:VAL:HG23	3:C:217:HOH:O	1.93	0.58
1:D:476:GLU:H	1:D:476:GLU:CD	2.10	0.58
1:D:527:GLN:OE1	1:D:530:ILE:HD11	2.03	0.58
1:C:611:ARG:HH22	1:C:645:MET:HE2	1.69	0.57
1:B:436:VAL:HB	1:B:438:ASN:HD21	1.68	0.57
1:B:481:ILE:CG2	1:B:483:LYS:HZ1	2.18	0.56
1:B:408:LEU:HD11	1:B:469:MET:SD	2.46	0.56
1:B:440:VAL:HG11	1:B:475:LEU:HD21	1.88	0.56
1:D:436:VAL:CG1	1:D:438:ASN:HD21	2.19	0.55
1:B:407:GLU:H	1:B:407:GLU:CD	2.14	0.55
1:D:638:PRO:O	1:D:642:SER:HB3	2.06	0.55
1:C:440:VAL:HG11	1:C:475:LEU:HD21	1.89	0.55
1:C:456:ILE:CD1	1:C:467:LEU:HD23	2.32	0.54
1:B:448:ILE:HD11	1:B:454:LEU:HG	1.90	0.54
1:A:397:VAL:HG11	1:A:470:LEU:HD21	1.91	0.52
1:A:460:THR:HG21	3:A:165:HOH:O	2.07	0.52
1:D:390:THR:HG22	1:D:391:GLY:N	2.26	0.51
1:C:392:ILE:CD1	1:C:471:ILE:HG12	2.41	0.51
1:C:514:GLU:HG3	1:C:518:LYS:HD2	1.93	0.51
1:B:481:ILE:HG13	1:B:483:LYS:HZ2	1.75	0.51
1:A:448:ILE:HD11	1:A:454:LEU:HG	1.92	0.50
1:A:449:GLU:CD	3:A:182:HOH:O	2.54	0.50
1:B:476:GLU:H	1:B:476:GLU:CD	2.19	0.50
1:B:447:ASN:HD22	1:B:447:ASN:C	2.20	0.50
1:A:448:ILE:CD1	1:A:454:LEU:HG	2.43	0.49
1:D:487:ARG:NH2	1:D:567:ASP:OD2	2.45	0.49
1:A:436:VAL:HB	1:A:438:ASN:HD21	1.76	0.49
1:A:450:LYS:NZ	3:A:154:HOH:O	2.45	0.49
1:B:487:ARG:NH1	1:B:565:ASP:OD1	2.45	0.48
1:C:392:ILE:HD11	1:C:471:ILE:HG12	1.94	0.48
1:B:436:VAL:HB	1:B:438:ASN:ND2	2.29	0.48
1:B:448:ILE:CD1	1:B:454:LEU:HG	2.45	0.47
1:B:582:THR:O	1:B:586:VAL:HG23	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:544:GLY:O	1:A:553:ARG:HD3	2.15	0.46
1:B:400:PHE:HA	1:B:439:PRO:HA	1.98	0.46
1:B:436:VAL:CG1	1:B:438:ASN:HD21	2.29	0.46
1:A:510:VAL:HG12	1:A:511:SER:N	2.31	0.46
3:A:104:HOH:O	1:B:621:GLN:HG2	2.16	0.46
1:D:476:GLU:CD	1:D:476:GLU:N	2.73	0.45
1:D:440:VAL:HG11	1:D:475:LEU:HD21	1.98	0.45
1:A:392:ILE:HD12	1:A:484:HIS:CD2	2.52	0.45
1:A:459:SER:HB3	1:A:663:THR:HA	1.98	0.45
1:B:647:TYR:HB2	1:B:650:PHE:HB2	1.98	0.45
1:D:640:PHE:CZ	1:D:644:LEU:HD13	2.52	0.45
1:A:488:VAL:O	1:A:564:LYS:NZ	2.43	0.45
1:D:510:VAL:HG12	1:D:511:SER:N	2.32	0.45
1:B:545:GLY:O	1:B:548:LEU:HB2	2.16	0.45
1:B:481:ILE:CG2	1:B:483:LYS:NZ	2.75	0.45
1:B:451:GLY:O	3:B:122:HOH:O	2.21	0.44
1:B:507:ILE:CD1	1:B:517:TYR:CD1	3.01	0.44
1:B:487:ARG:HH21	1:B:487:ARG:CG	2.29	0.44
1:D:640:PHE:CE2	1:D:666:LEU:HD13	2.52	0.44
1:B:392:ILE:HD12	1:B:484:HIS:CD2	2.53	0.43
1:B:507:ILE:O	1:B:507:ILE:HG23	2.18	0.43
1:B:446:LEU:C	1:B:446:LEU:HD12	2.43	0.43
1:A:510:VAL:CG1	1:A:511:SER:N	2.81	0.43
1:B:497:ILE:HG13	1:B:553:ARG:HG2	2.01	0.43
1:A:392:ILE:HG13	1:A:393:ILE:N	2.33	0.43
1:D:507:ILE:HG23	1:D:507:ILE:O	2.18	0.42
1:B:503:LYS:HG3	1:B:517:TYR:CZ	2.54	0.42
1:C:501:THR:HA	1:C:539:THR:O	2.19	0.42
1:C:611:ARG:NH2	1:C:645:MET:HE2	2.34	0.42
1:B:639:ASP:HB3	1:B:669:PHE:CE1	2.54	0.42
1:B:648:ASP:HB3	1:B:649:THR:HG23	2.02	0.42
1:D:467:LEU:HA	1:D:467:LEU:HD12	1.62	0.42
1:B:481:ILE:HD12	1:B:482:ILE:N	2.30	0.41
1:B:446:LEU:HD12	1:B:446:LEU:O	2.21	0.41
1:D:454:LEU:HD13	1:D:456:ILE:HG13	2.02	0.41
1:D:508:PHE:CD1	1:D:508:PHE:C	2.97	0.41
1:B:401:TRP:CE2	1:B:433:LEU:HD13	2.56	0.41
1:B:501:THR:HA	1:B:539:THR:O	2.21	0.41
1:B:516:ARG:O	1:B:520:VAL:HG23	2.20	0.41
1:C:436:VAL:CB	1:C:438:ASN:HD21	2.28	0.41
1:A:481:ILE:HG21	1:A:483:LYS:HE2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:640:PHE:CZ	1:C:644:LEU:HD13	2.56	0.40
1:D:640:PHE:HE2	1:D:666:LEU:HD13	1.86	0.40
1:A:640:PHE:CZ	1:A:644:LEU:HD13	2.57	0.40
1:B:639:ASP:HB2	3:B:96:HOH:O	2.21	0.40
1:A:438:ASN:HA	1:A:439:PRO:HD3	1.93	0.40
1:A:598:LYS:O	1:A:600:ARG:HD3	2.21	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	262/286 (92%)	255 (97%)	7 (3%)	0	100	100
1	B	263/286 (92%)	261 (99%)	2 (1%)	0	100	100
1	C	263/286 (92%)	257 (98%)	6 (2%)	0	100	100
1	D	260/286 (91%)	250 (96%)	10 (4%)	0	100	100
All	All	1048/1144 (92%)	1023 (98%)	25 (2%)	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	233/252 (92%)	201 (86%)	32 (14%)	3	3
1	B	234/252 (93%)	195 (83%)	39 (17%)	2	2
1	C	234/252 (93%)	205 (88%)	29 (12%)	4	4
1	D	231/252 (92%)	201 (87%)	30 (13%)	4	3
All	All	932/1008 (92%)	802 (86%)	130 (14%)	3	3

All (130) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	392	ILE
1	A	407	GLU
1	A	408	LEU
1	A	412	VAL
1	A	449	GLU
1	A	450	LYS
1	A	454	LEU
1	A	459	SER
1	A	460	THR
1	A	468	LEU
1	A	482	ILE
1	A	487	ARG
1	A	488	VAL
1	A	492	SER
1	A	543	GLU
1	A	546	VAL
1	A	548	LEU
1	A	558	LEU
1	A	564	LYS
1	A	571	LEU
1	A	573	SER
1	A	580	VAL
1	A	617	LEU
1	A	619	LEU
1	A	621	GLN
1	A	623	SER
1	A	644	LEU
1	A	648	ASP
1	A	656	GLU
1	A	660	SER
1	A	666	LEU
1	A	668	ARG
1	B	392	ILE

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Mol	Chain	Res	Type
1	B	396	ASN
1	B	403	GLU
1	B	407	GLU
1	B	408	LEU
1	B	412	VAL
1	B	435	LEU
1	B	442	LYS
1	B	447	ASN
1	B	449	GLU
1	B	450	LYS
1	B	454	LEU
1	B	468	LEU
1	B	470	LEU
1	B	476	GLU
1	B	478	SER
1	B	482	ILE
1	B	483	LYS
1	B	487	ARG
1	B	488	VAL
1	B	507	ILE
1	B	510	VAL
1	B	514	GLU
1	B	519	SER
1	B	546	VAL
1	B	548	LEU
1	B	558	LEU
1	B	571	LEU
1	B	573	SER
1	B	580	VAL
1	B	611	ARG
1	B	617	LEU
1	B	619	LEU
1	B	621	GLN
1	B	642	SER
1	B	643	LYS
1	B	645	MET
1	B	648	ASP
1	B	666	LEU
1	C	407	GLU
1	C	408	LEU
1	C	412	VAL
1	C	431	SER

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Mol	Chain	Res	Type
1	C	435	LEU
1	C	438	ASN
1	C	454	LEU
1	C	460	THR
1	C	464	LYS
1	C	468	LEU
1	C	470	LEU
1	C	476	GLU
1	C	487	ARG
1	C	488	VAL
1	C	511	SER
1	C	514	GLU
1	C	546	VAL
1	C	548	LEU
1	C	557	SER
1	C	558	LEU
1	C	571	LEU
1	C	617	LEU
1	C	619	LEU
1	C	621	GLN
1	C	644	LEU
1	C	657	ARG
1	C	664	GLU
1	C	666	LEU
1	C	670	SER
1	D	390	THR
1	D	392	ILE
1	D	396	ASN
1	D	408	LEU
1	D	410	GLU
1	D	412	VAL
1	D	435	LEU
1	D	436	VAL
1	D	442	LYS
1	D	454	LEU
1	D	460	THR
1	D	468	LEU
1	D	476	GLU
1	D	482	ILE
1	D	484	HIS
1	D	485	SER
1	D	488	VAL

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Mol	Chain	Res	Type
1	D	507	ILE
1	D	537	ASP
1	D	546	VAL
1	D	548	LEU
1	D	558	LEU
1	D	571	LEU
1	D	617	LEU
1	D	619	LEU
1	D	642	SER
1	D	644	LEU
1	D	666	LEU
1	D	668	ARG
1	D	670	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	432	HIS
1	A	438	ASN
1	A	484	HIS
1	B	438	ASN
1	B	443	ASN
1	B	447	ASN
1	B	484	HIS
1	B	538	ASN
1	C	438	ASN
1	C	484	HIS
1	C	538	ASN
1	C	585	GLN
1	D	396	ASN
1	D	438	ASN
1	D	443	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	ACY	A	1	-	3,3,3	0.81	0	3,3,3	0.78	0
2	ACY	C	3	-	3,3,3	0.85	0	3,3,3	0.67	0
2	ACY	D	4	-	3,3,3	0.77	0	3,3,3	1.26	0
2	ACY	D	5	-	3,3,3	0.45	0	3,3,3	1.37	0
2	ACY	A	6	-	3,3,3	1.11	0	3,3,3	0.83	0
2	ACY	B	2	-	3,3,3	0.69	0	3,3,3	1.22	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 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	266/286 (93%)	0.06	13 (4%) 35 31	14, 29, 50, 60	0
1	B	267/286 (93%)	0.13	13 (4%) 35 31	15, 30, 48, 56	0
1	C	267/286 (93%)	0.02	8 (2%) 52 49	13, 27, 46, 53	0
1	D	264/286 (92%)	0.10	13 (4%) 35 31	14, 29, 48, 52	0
All	All	1064/1144 (93%)	0.08	47 (4%) 39 36	13, 28, 48, 60	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	390	THR	5.2
1	A	429	SER	4.5
1	B	390	THR	3.7
1	D	487	ARG	3.4
1	C	498	MET	3.4
1	D	434	CYS	3.4
1	D	508	PHE	3.3
1	A	648	ASP	3.2
1	A	430	PHE	3.2
1	A	486	GLY	3.1
1	B	670	SER	3.0
1	D	670	SER	3.0
1	A	487	ARG	2.9
1	A	432	HIS	2.8
1	D	476	GLU	2.8
1	C	670	SER	2.8
1	A	438	ASN	2.7
1	B	498	MET	2.7
1	B	430	PHE	2.6
1	B	496	TRP	2.6
1	D	484	HIS	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	402	GLU	2.6
1	B	487	ARG	2.6
1	B	508	PHE	2.6
1	A	460	THR	2.5
1	B	402	GLU	2.4
1	A	670	SER	2.4
1	D	635	SER	2.4
1	C	476	GLU	2.4
1	B	648	ASP	2.4
1	C	508	PHE	2.3
1	C	438	ASN	2.3
1	A	437	GLY	2.3
1	B	509	GLY	2.3
1	D	390	THR	2.3
1	A	396	ASN	2.2
1	D	485	SER	2.2
1	B	436	VAL	2.2
1	D	641	SER	2.2
1	D	648	ASP	2.1
1	D	430	PHE	2.1
1	B	483	LYS	2.1
1	C	645	MET	2.1
1	D	403	GLU	2.1
1	C	430	PHE	2.0
1	B	429	SER	2.0
1	A	668	ARG	2.0

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](#)

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. 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	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ACY	D	5	4/4	0.78	0.15	27,29,29,29	0
2	ACY	A	6	4/4	0.92	0.10	31,32,32,33	0
2	ACY	B	2	4/4	0.95	0.07	38,39,39,39	0
2	ACY	D	4	4/4	0.95	0.09	31,31,32,32	0
2	ACY	A	1	4/4	0.95	0.08	24,24,26,26	0
2	ACY	C	3	4/4	0.97	0.07	29,29,30,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.