Full wwPDB X-ray Structure Validation Report ⓘ

Jun 17, 2024 – 10:51 AM EDT

PDB ID	:	3PAM
Title	:	Crystal structure of a domain of transmembrane protein of ABC-type oligopeptide transport system from Bartonella henselae str. Houston-1
Authors	:	Nocek, B.; Stein, A.; Mack, J.; Buck, K.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on	:	2010-10-19
Resolution	:	2.31 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:

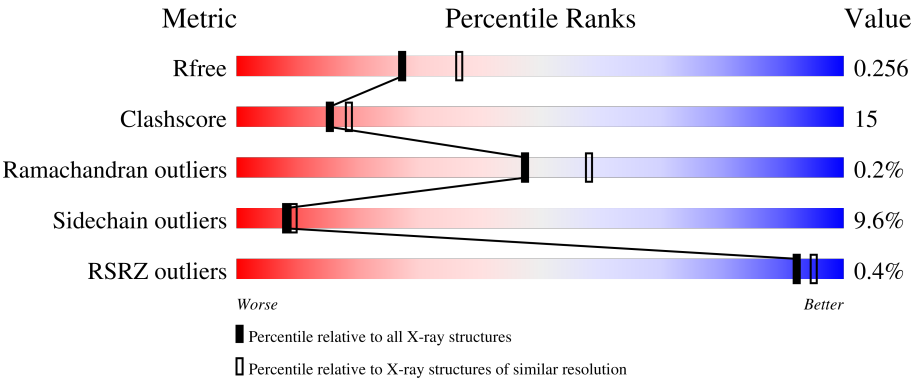
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.31 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	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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 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	259	69% 26%
1	B	259	69% 22% 6%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	EOH	A	1	-	-	X	-
2	EOH	A	5	-	-	X	-
2	EOH	A	6	-	-	X	-
2	EOH	B	9	-	-	X	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3983 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.

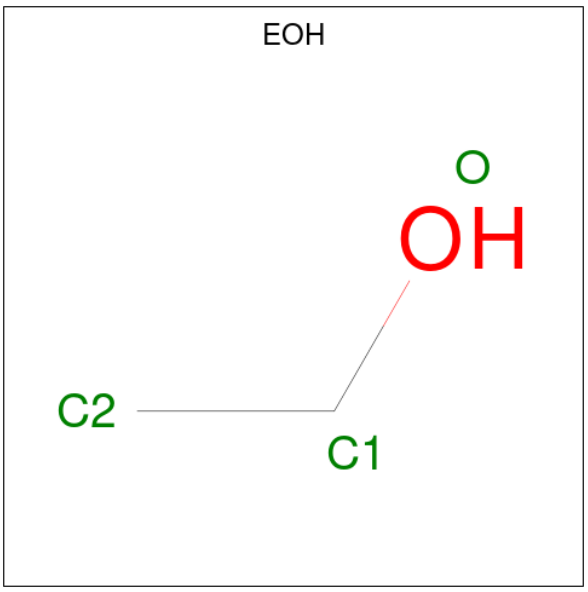
- Molecule 1 is a protein called Transmembrane protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	256	Total	C	N	O	Se	0	1	0
			1956	1246	336	368	6			
1	B	250	Total	C	N	O	Se	0	0	0
			1930	1227	330	367	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	316	SER	-	EXPRESSION TAG	UNP Q6G3A9
A	317	ASN	-	EXPRESSION TAG	UNP Q6G3A9
A	318	ALA	-	EXPRESSION TAG	UNP Q6G3A9
B	316	SER	-	EXPRESSION TAG	UNP Q6G3A9
B	317	ASN	-	EXPRESSION TAG	UNP Q6G3A9
B	318	ALA	-	EXPRESSION TAG	UNP Q6G3A9

- Molecule 2 is ETHANOL (three-letter code: EOH) (formula: C_2H_6O).



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

- Molecule 3 is water.

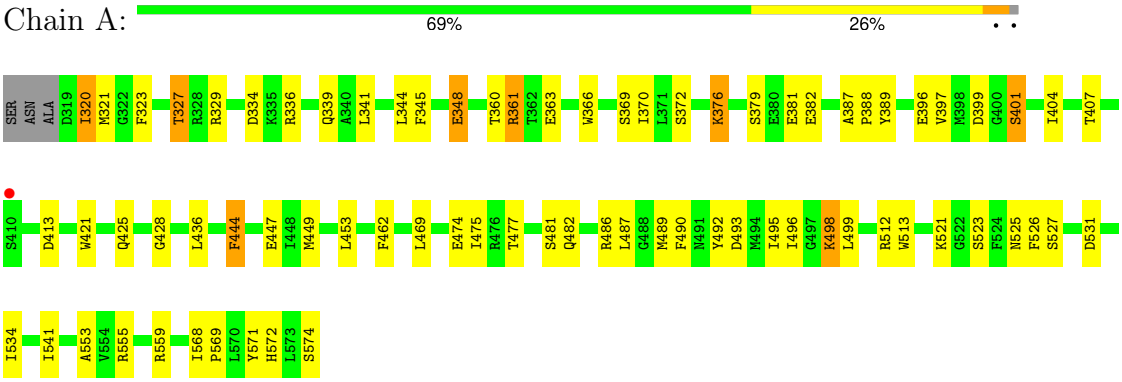
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	45	Total O 45 45	0	0
3	B	22	Total O 22 22	0	0

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.

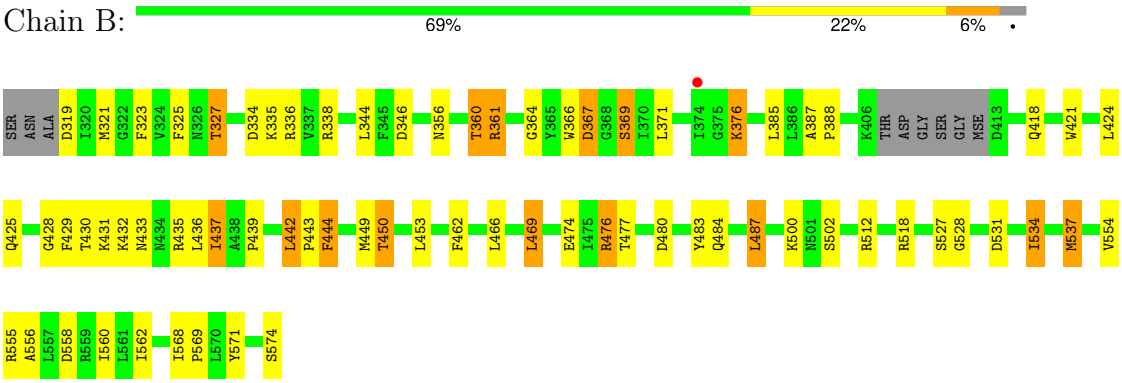
• Molecule 1: Transmembrane protein

Chain A:



• Molecule 1: Transmembrane protein

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	100.85Å 39.72Å 101.35Å 90.00° 92.28° 90.00°	Depositor
Resolution (Å)	36.95 – 2.31 36.95 – 2.40	Depositor EDS
% Data completeness (in resolution range)	88.3 (36.95-2.31) 98.9 (36.95-2.40)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.31 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.223 , 0.257 0.222 , 0.256	Depositor DCC
R_{free} test set	1615 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	44.3	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 21.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	0.075 for l,k,-h 0.049 for h,-k,-l 0.048 for l,-k,h	Xtriage
Reported twinning fraction	0.876 for H, K, L 0.124 for -L, K, H	Depositor
Outliers	0 of 31872 reflections	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	3983	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.31% 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

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

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	0.59	0/1996	0.67	0/2701
1	B	0.53	0/1966	0.66	0/2659
All	All	0.56	0/3962	0.67	0/5360

There are no bond length outliers.

There are no bond angle outliers.

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	1956	0	1841	60	0
1	B	1930	0	1828	56	0
2	A	18	0	36	11	0
2	B	12	0	24	3	0
3	A	45	0	0	1	0
3	B	22	0	0	0	0
All	All	3983	0	3729	114	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 15.

All (114) 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:B:537:MSE:HE3	1:B:556:ALA:CB	1.77	1.13
1:B:537:MSE:CE	1:B:556:ALA:HB1	1.87	1.04
1:B:476:ARG:HG3	1:B:476:ARG:HH11	1.23	1.02
1:B:537:MSE:HE3	1:B:556:ALA:HB3	1.47	0.97
1:B:537:MSE:CE	1:B:556:ALA:CB	2.44	0.95
1:B:537:MSE:HE2	1:B:556:ALA:HB1	1.50	0.93
1:B:476:ARG:HH11	1:B:476:ARG:CG	1.87	0.88
1:A:348:GLU:H	1:A:348:GLU:CD	1.80	0.85
1:A:379:SER:OG	1:A:382:GLU:HG3	1.77	0.83
1:A:449:MSE:HE1	1:A:486:ARG:HD3	1.59	0.83
1:A:327:THR:HB	1:A:527:SER:O	1.80	0.82
1:B:450:THR:HG22	1:B:477:THR:HG23	1.62	0.79
1:B:476:ARG:HG3	1:B:476:ARG:NH1	2.02	0.72
1:A:449:MSE:HE1	1:A:486:ARG:CD	2.21	0.70
1:B:361:ARG:NH1	1:B:569:PRO:O	2.25	0.70
1:A:336:ARG:NH2	2:A:6:EOH:H12	2.07	0.69
1:A:336:ARG:HH22	2:A:6:EOH:H12	1.57	0.69
1:A:421:TRP:CE2	1:A:425:GLN:NE2	2.60	0.69
1:A:376:LYS:O	1:A:559:ARG:NH2	2.27	0.68
1:A:361:ARG:NH1	1:A:569:PRO:O	2.26	0.68
1:B:323:PHE:HB2	1:B:568:ILE:HB	1.76	0.68
1:A:397:VAL:HG12	1:A:559:ARG:HG2	1.76	0.68
1:A:348:GLU:HG2	1:A:407:THR:OG1	1.94	0.67
1:A:399:ASP:OD2	1:A:401:SER:HB3	1.94	0.67
1:A:513:TRP:CH2	2:A:1:EOH:H22	2.31	0.65
1:A:366:TRP:O	1:A:372:SER:HB2	1.97	0.65
1:B:474:GLU:OE2	1:B:476:ARG:NH1	2.29	0.64
1:B:484:GLN:HE21	1:B:484:GLN:HA	1.64	0.62
1:A:421:TRP:NE1	1:A:425:GLN:NE2	2.48	0.62
1:B:476:ARG:CG	1:B:476:ARG:NH1	2.57	0.61
1:B:360:THR:HG21	1:B:574:SER:HB2	1.82	0.61
1:B:558:ASP:O	1:B:562:ILE:HG13	2.02	0.60
2:B:7:EOH:H23	2:B:9:EOH:C1	2.31	0.60
1:B:518:ARG:HD2	1:B:528:GLY:O	2.01	0.60
1:B:487:LEU:HD11	2:B:3:EOH:H21	1.82	0.60
1:A:334:ASP:OD1	1:A:336:ARG:HD3	2.02	0.60
1:A:449:MSE:HE1	1:A:486:ARG:NE	2.17	0.59
1:A:320:ILE:O	1:A:498:LYS:HA	2.02	0.59
1:A:323:PHE:HB2	1:A:568:ILE:HB	1.85	0.59
1:A:376:LYS:HE3	1:A:555:ARG:NH1	2.17	0.59
1:B:531:ASP:O	1:B:534:ILE:HD13	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:430:THR:O	1:B:437:ILE:HG12	2.03	0.58
1:B:531:ASP:HB3	1:B:534:ILE:HG23	1.85	0.58
1:A:475:ILE:H	1:B:433:ASN:ND2	2.00	0.58
1:A:363:GLU:HG2	1:A:404:ILE:CG2	2.33	0.58
1:B:334:ASP:HA	2:B:9:EOH:H22	1.86	0.57
1:A:360:THR:HG23	1:A:572:HIS:CE1	2.40	0.57
1:B:344:LEU:HD21	1:B:469:LEU:HD13	1.86	0.56
1:A:381:GLU:H	2:A:5:EOH:H23	1.71	0.56
1:A:321:MSE:CE	1:A:571:TYR:O	2.54	0.56
1:A:320:ILE:HG22	1:A:499:LEU:HB2	1.88	0.56
1:B:385:LEU:HB3	1:B:537:MSE:HE1	1.89	0.55
1:A:329:ARG:HH12	2:A:2:EOH:H22	1.71	0.55
1:A:348:GLU:CD	1:A:348:GLU:N	2.55	0.55
1:B:385:LEU:CB	1:B:537:MSE:HE1	2.38	0.54
1:B:450:THR:HB	1:B:476:ARG:O	2.07	0.54
1:A:477:THR:HB	1:B:431:LYS:HB2	1.90	0.54
1:B:484:GLN:HA	1:B:484:GLN:NE2	2.23	0.53
1:A:513:TRP:CZ2	2:A:1:EOH:H22	2.43	0.53
1:A:541:ILE:HG13	1:A:553:ALA:HB1	1.90	0.52
1:A:487:LEU:HD21	1:A:495:ILE:HD13	1.91	0.52
1:B:449:MSE:HE3	1:B:483:TYR:CD1	2.45	0.52
1:A:379:SER:HB2	2:A:5:EOH:H12	1.91	0.52
1:B:435:ARG:O	1:B:437:ILE:HD11	2.09	0.51
1:A:321:MSE:HE3	1:A:571:TYR:H	1.76	0.50
1:B:344:LEU:HD21	1:B:469:LEU:CD1	2.41	0.50
1:B:321:MSE:HE1	1:B:571:TYR:CE1	2.46	0.50
1:A:320:ILE:CG2	1:A:499:LEU:HB2	2.41	0.49
1:B:442:LEU:HD22	1:B:443:PRO:HD2	1.95	0.49
1:A:490:PHE:HA	1:A:492:TYR:CE2	2.49	0.48
1:A:489:MSE:HA	1:A:521:LYS:HG2	1.95	0.48
1:B:435:ARG:O	1:B:437:ILE:CD1	2.62	0.48
1:A:387:ALA:HB3	1:A:388:PRO:HD3	1.94	0.47
1:B:421:TRP:O	1:B:425:GLN:HB2	2.13	0.47
1:A:447:GLU:O	1:A:493:ASP:HB2	2.14	0.47
1:A:344:LEU:HD21	1:A:469:LEU:HD22	1.97	0.47
1:A:321:MSE:HE1	1:A:571:TYR:CE2	2.50	0.47
1:B:325:PHE:CG	1:B:338:ARG:HG2	2.50	0.47
1:A:474:GLU:HA	1:B:433:ASN:HD21	1.80	0.47
1:A:449:MSE:HE1	1:A:486:ARG:CZ	2.44	0.46
1:B:500:LYS:O	1:B:512:ARG:NH2	2.35	0.46
1:B:371:LEU:HB3	1:B:554:VAL:HG11	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:449:MSE:CE	1:A:486:ARG:CZ	2.94	0.46
1:B:325:PHE:CD1	1:B:338:ARG:HG2	2.51	0.46
1:B:556:ALA:O	1:B:560:ILE:HG13	2.16	0.45
1:A:436:LEU:HD23	1:A:444:PHE:CD2	2.51	0.45
1:A:321:MSE:HE1	1:A:571:TYR:CD2	2.52	0.45
1:B:327:THR:HB	1:B:527:SER:O	2.17	0.45
1:B:432:LYS:HB3	1:B:437:ILE:HD11	1.98	0.45
1:B:462:PHE:CE2	1:B:466:LEU:HD11	2.52	0.45
1:B:346:ASP:OD1	1:B:346:ASP:C	2.55	0.45
1:B:364:GLY:N	1:B:367:ASP:OD1	2.41	0.44
1:A:339:GLN:HG3	3:A:49:HOH:O	2.17	0.44
1:B:424:LEU:O	1:B:429:PHE:HB2	2.18	0.43
1:A:388:PRO:HB2	1:A:389:TYR:CE2	2.53	0.43
1:A:526:PHE:H	2:A:1:EOH:H12	1.83	0.43
1:A:348:GLU:HG2	1:A:407:THR:HG1	1.83	0.43
1:A:428:GLY:HA2	2:A:4:EOH:H12	2.00	0.43
1:A:531:ASP:HB3	1:A:534:ILE:HG13	2.01	0.43
1:B:334:ASP:OD1	1:B:336:ARG:HB2	2.19	0.43
1:A:421:TRP:CD1	1:A:425:GLN:NE2	2.87	0.42
1:A:436:LEU:HD23	1:A:444:PHE:HD2	1.85	0.42
1:A:379:SER:HB2	2:A:5:EOH:C1	2.49	0.42
1:B:366:TRP:O	1:B:369:SER:HB3	2.20	0.41
1:B:436:LEU:HD23	1:B:444:PHE:CD2	2.56	0.41
1:A:482:GLN:HE21	1:A:486:ARG:HH11	1.69	0.41
1:A:526:PHE:N	2:A:1:EOH:H12	2.35	0.41
1:B:387:ALA:N	1:B:388:PRO:CD	2.84	0.41
1:B:480:ASP:O	1:B:484:GLN:HG2	2.20	0.41
1:A:512:ARG:O	1:A:525:ASN:HA	2.21	0.40
1:B:321:MSE:HE2	1:B:571:TYR:O	2.21	0.40
1:A:345:PHE:HB2	1:A:462:PHE:CE1	2.56	0.40
1:B:376:LYS:HD2	1:B:555:ARG:CZ	2.52	0.40
1:B:428:GLY:O	1:B:439:PRO:HG3	2.22	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	255/259 (98%)	248 (97%)	7 (3%)	0	100 100
1	B	246/259 (95%)	240 (98%)	5 (2%)	1 (0%)	34 41
All	All	501/518 (97%)	488 (97%)	12 (2%)	1 (0%)	47 58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	502	SER

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	196/214 (92%)	178 (91%)	18 (9%)	9 10
1	B	199/214 (93%)	179 (90%)	20 (10%)	7 8
All	All	395/428 (92%)	357 (90%)	38 (10%)	8 9

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	320	ILE
1	A	327	THR
1	A	341	LEU
1	A	348	GLU
1	A	361	ARG
1	A	369	SER
1	A	370	ILE
1	A	376	LYS
1	A	396	GLU
1	A	401	SER
1	A	413	ASP

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Mol	Chain	Res	Type
1	A	444	PHE
1	A	453	LEU
1	A	481	SER
1	A	496	ILE
1	A	498	LYS
1	A	523	SER
1	A	574	SER
1	B	319	ASP
1	B	327	THR
1	B	335	LYS
1	B	356	ASN
1	B	360	THR
1	B	361	ARG
1	B	367	ASP
1	B	369	SER
1	B	376	LYS
1	B	418	GLN
1	B	437	ILE
1	B	442	LEU
1	B	444	PHE
1	B	450	THR
1	B	453	LEU
1	B	469	LEU
1	B	476	ARG
1	B	487	LEU
1	B	534	ILE
1	B	537	MSE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	353	HIS
1	A	433	ASN
1	A	445	GLN
1	A	463	GLN
1	A	465	ASN
1	B	353	HIS
1	B	418	GLN
1	B	433	ASN
1	B	465	ASN
1	B	484	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

10 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	EOH	A	5	-	2,2,2	0.65	0	1,1,1	0.45	0
2	EOH	B	7	-	2,2,2	0.49	0	1,1,1	0.44	0
2	EOH	B	10	-	2,2,2	0.66	0	1,1,1	0.56	0
2	EOH	A	1	-	2,2,2	0.57	0	1,1,1	0.06	0
2	EOH	B	9	-	2,2,2	0.46	0	1,1,1	0.35	0
2	EOH	A	2	-	2,2,2	0.60	0	1,1,1	0.01	0
2	EOH	B	3	-	2,2,2	0.64	0	1,1,1	0.49	0
2	EOH	A	4	-	2,2,2	0.59	0	1,1,1	0.40	0
2	EOH	A	6	-	2,2,2	0.60	0	1,1,1	0.67	0
2	EOH	A	8	-	2,2,2	0.54	0	1,1,1	0.33	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.

8 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	5	EOH	3	0
2	B	7	EOH	1	0
2	A	1	EOH	4	0
2	B	9	EOH	2	0
2	A	2	EOH	1	0
2	B	3	EOH	1	0
2	A	4	EOH	1	0
2	A	6	EOH	2	0

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	249/259 (96%)	-0.05	1 (0%)	92	95	29, 45, 77, 96	0
1	B	244/259 (94%)	-0.05	1 (0%)	92	95	32, 50, 74, 96	0
All	All	493/518 (95%)	-0.05	2 (0%)	92	95	29, 47, 77, 96	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	410	SER	2.3
1	B	374	ILE	2.3

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

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, 95^{th} 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(Å^2)	Q<0.9
2	EOH	B	10	3/3	0.80	0.19	28,28,31,32	0
2	EOH	B	7	3/3	0.89	0.20	26,26,26,27	0
2	EOH	A	8	3/3	0.90	0.16	27,27,28,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	EOH	A	1	3/3	0.91	0.32	18,18,19,22	0
2	EOH	A	5	3/3	0.92	0.24	26,26,27,28	0
2	EOH	A	6	3/3	0.93	0.15	24,24,25,25	0
2	EOH	A	2	3/3	0.93	0.11	21,21,25,26	0
2	EOH	B	9	3/3	0.94	0.24	27,27,27,27	0
2	EOH	A	4	3/3	0.95	0.12	22,22,23,24	0
2	EOH	B	3	3/3	0.96	0.07	25,25,27,27	0

6.5 Other polymers (i)

There are no such residues in this entry.