



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2014 – 04:04 AM GMT

PDB ID : 3D0H
Title : Crystal structure of spike protein receptor-binding domain from the 2002-2003 SARS coronavirus civet strain complexed with human-civet chimeric receptor ACE2
Authors : Li, F.
Deposited on : 2008-05-01
Resolution : 3.10 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>

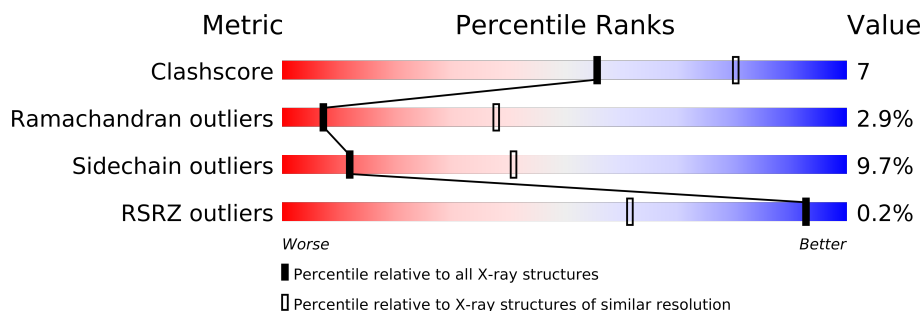
The following versions of software and data (see [references](#)) were used in the production of this report:

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 3.10 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))
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)

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	597	
1	B	597	
2	E	179	
2	F	179	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
5	ZN	A	901	-	X
6	CL	A	902	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12643 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 Angiotensin-convertingenzyme 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	597	Total	C	N	O	S	0	0	0
			4864	3110	803	922	29			
1	B	597	Total	C	N	O	S	0	0	0
			4864	3110	803	922	29			

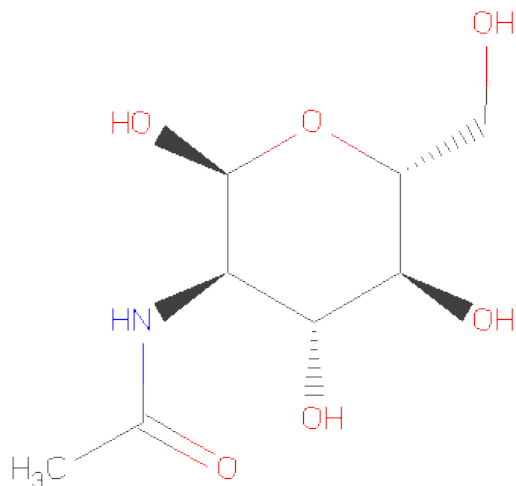
- Molecule 2 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	173	Total	C	N	O	S	0	0	0
			1397	907	227	257	6			
2	F	173	Total	C	N	O	S	0	0	0
			1397	907	227	257	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	479	LYS	ASN	CONFLICT	UNP P59594
E	487	SER	THR	CONFLICT	UNP P59594
F	479	LYS	ASN	CONFLICT	UNP P59594
F	487	SER	THR	CONFLICT	UNP P59594

- Molecule 3 is SUGAR (2-(ACETYLAMINO)-2-DEOXY-A-D-GLUCOPYRANOSE) (three-letter code: NDG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			15	8	1	6		
3	B	1	Total	C	N	O	0	0
			15	8	1	6		
3	B	1	Total	C	N	O	0	0
			15	8	1	6		
3	B	1	Total	C	N	O	0	0
			15	8	1	6		
3	F	1	Total	C	N	O	0	0
			15	8	1	6		

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	E	1	Total	C	N	O	0	0
			15	8	1	6		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Zn	0	0
			1	1		
5	A	1	Total	Zn	0	0
			1	1		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Cl	0	0
			1	1		
6	A	1	Total	Cl	0	0
			1	1		

- Molecule 7 is water.

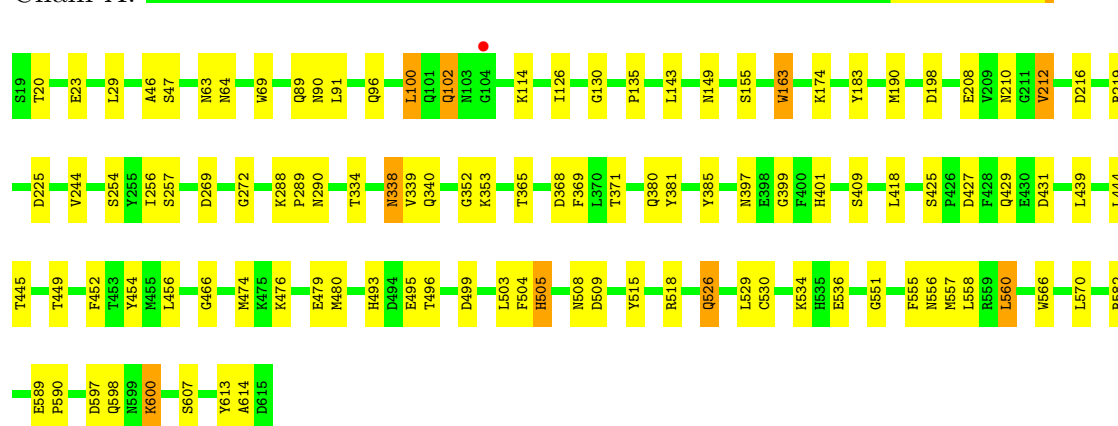
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	21	Total	O	0	0
			21	21		
7	F	6	Total	O	0	0
			6	6		

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.

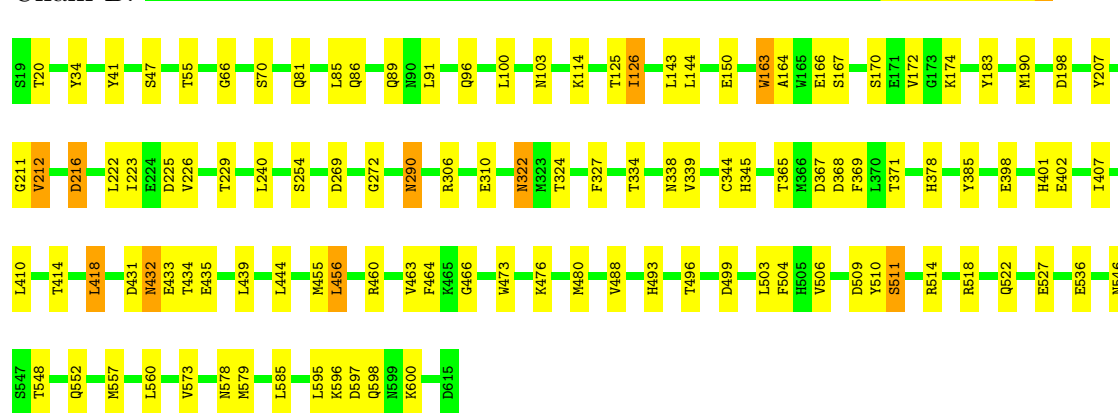
• Molecule 1: Angiotensin-convertingenzyme 2

Chain A:



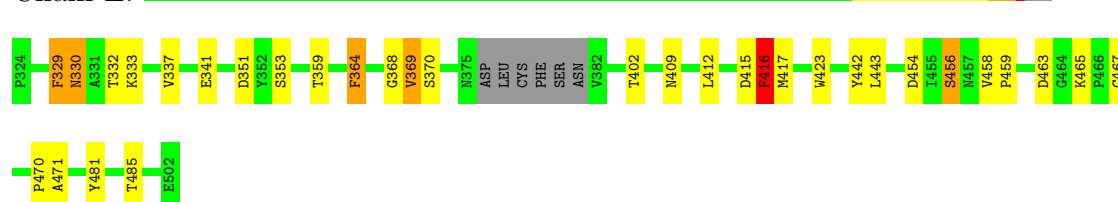
• Molecule 1: Angiotensin-convertingenzyme 2

Chain B:

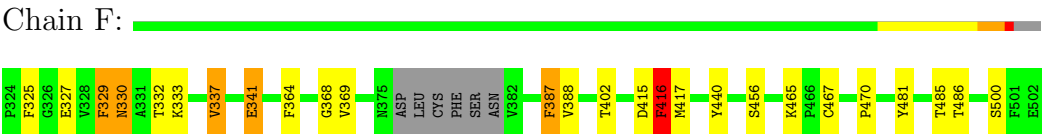


• Molecule 2: Spike protein S1

Chain E:



● Molecule 2: Spike protein S1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	80.35Å 119.84Å 109.42Å 90.00° 95.89° 90.00°	Depositor
Resolution (Å)	37.50 – 3.10 37.50 – 3.05	Depositor EDS
% Data completeness (in resolution range)	90.3 (37.50-3.10) 87.7 (37.50-3.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 3.06Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.221 , 0.302 0.238 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	69.7	Xtriage
Anisotropy	0.155	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 28.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 38306 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	12643	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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: ZN, NAG, NDG, CL

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	0.51	0/5000	0.62	0/6796
1	B	0.55	0/5000	0.65	0/6796
2	E	0.54	0/1442	0.64	0/1961
2	F	0.55	0/1442	0.65	0/1961
All	All	0.53	0/12884	0.64	0/17514

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	4864	0	0	30	0
1	B	4864	0	0	38	0
2	E	1397	0	0	8	0
2	F	1397	0	0	9	0
3	A	15	0	0	1	0
3	B	45	0	0	2	0
3	F	15	0	0	0	0
4	E	15	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	B	21	0	0	0	0
7	F	6	0	0	0	0
All	All	12643	0	0	83	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 7.

All (83) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:F:416:PHE:CD1	2:F:416:PHE:N	2.61	0.69
2:E:416:PHE:CD1	2:E:416:PHE:N	2.61	0.68
1:B:183:TYR:OH	1:B:509:ASP:OD1	2.17	0.63
1:A:90:ASN:OD1	3:A:616:NDG:O1L	2.20	0.60
2:F:329:PHE:CD2	2:F:329:PHE:N	2.70	0.60
1:A:338:ASN:O	1:A:340:GLN:N	2.36	0.59
1:B:324:THR:O	1:B:327:PHE:N	2.37	0.57
2:F:329:PHE:O	2:F:330:ASN:CB	2.53	0.56
2:E:329:PHE:O	2:E:330:ASN:CB	2.56	0.54
1:B:322:ASN:ND2	3:B:617:NDG:O7	2.42	0.53
1:B:511:SER:O	1:B:514:ARG:NH1	2.41	0.53
2:E:329:PHE:N	2:E:329:PHE:CD2	2.77	0.52
1:B:546:ASN:ND2	3:B:618:NDG:C1	2.73	0.52
1:A:174:LYS:NZ	1:A:496:THR:CG2	2.73	0.51
1:B:407:ILE:CD1	1:B:522:GLN:O	2.59	0.51
1:B:504:PHE:CD2	1:B:504:PHE:C	2.85	0.50
1:A:352:GLY:O	1:A:353:LYS:C	2.49	0.50
1:A:566:TRP:O	1:A:570:LEU:N	2.45	0.50
1:B:460:ARG:NH1	1:B:510:TYR:O	2.45	0.49
1:B:269:ASP:OD2	1:B:272:GLY:N	2.46	0.49
1:B:41:TYR:OH	2:F:486:THR:OG1	2.30	0.49
1:A:63:ASN:O	1:A:64:ASN:C	2.50	0.49
2:F:341:GLU:CA	2:F:341:GLU:OE1	2.60	0.48
1:A:183:TYR:OH	1:A:509:ASP:OD1	2.31	0.48
1:B:34:TYR:CD2	2:F:440:TYR:OH	2.66	0.48
1:B:464:PHE:C	1:B:466:GLY:N	2.66	0.48
1:B:166:GLU:OE1	1:B:493:HIS:CE1	2.65	0.48
1:A:269:ASP:OD2	1:A:272:GLY:N	2.47	0.48
1:A:598:GLN:OE1	1:A:598:GLN:CA	2.61	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:460:ARG:NH2	1:B:506:VAL:CA	2.78	0.47
1:A:208:GLU:OE1	1:A:210:ASN:ND2	2.48	0.47
1:B:211:GLY:N	1:B:216:ASP:OD2	2.47	0.46
1:A:425:SER:O	1:A:427:ASP:N	2.48	0.46
1:B:432:ASN:OD1	1:B:432:ASN:N	2.48	0.45
1:A:505:HIS:CE1	1:A:515:TYR:CE2	3.04	0.45
1:B:578:ASN:CG	1:B:579:MET:N	2.70	0.45
1:B:514:ARG:O	1:B:518:ARG:CB	2.64	0.45
1:A:208:GLU:OE2	1:A:219:ARG:NH1	2.50	0.45
2:E:415:ASP:O	2:E:416:PHE:C	2.54	0.45
2:F:337:VAL:CG1	2:F:387:PHE:CD1	3.00	0.45
1:A:551:GLY:O	1:A:555:PHE:N	2.49	0.45
1:A:556:ASN:O	1:A:560:LEU:CD1	2.64	0.45
1:A:474:MET:N	1:A:495:GLU:OE1	2.50	0.45
1:B:597:ASP:O	1:B:600:LYS:N	2.50	0.44
1:A:288:LYS:NZ	1:A:431:ASP:OD1	2.50	0.44
1:A:454:TYR:C	1:A:454:TYR:CD2	2.90	0.44
2:F:415:ASP:O	2:F:416:PHE:C	2.54	0.44
1:B:431:ASP:OD2	1:B:433:GLU:N	2.51	0.44
1:A:135:PRO:CD	1:A:163:TRP:NE1	2.80	0.44
1:A:46:ALA:O	1:A:47:SER:C	2.56	0.44
1:A:452:PHE:CD1	1:A:452:PHE:C	2.90	0.44
1:B:163:TRP:O	1:B:164:ALA:C	2.56	0.44
1:A:589:GLU:N	1:A:590:PRO:CD	2.80	0.44
1:A:397:ASN:OD1	1:A:399:GLY:N	2.51	0.44
1:B:344:CYS:O	1:B:345:HIS:C	2.56	0.44
1:A:126:ILE:O	1:A:130:GLY:N	2.51	0.44
1:B:434:THR:OG1	1:B:435:GLU:N	2.50	0.43
1:B:207:TYR:CE1	1:B:398:GLU:OE2	2.71	0.43
1:B:493:HIS:CD2	1:B:499:ASP:OD1	2.71	0.43
1:B:414:THR:O	1:B:418:LEU:CD2	2.66	0.43
1:B:174:LYS:NZ	1:B:496:THR:OG1	2.52	0.43
1:A:505:HIS:CE1	1:A:515:TYR:OH	2.72	0.43
1:B:226:VAL:O	1:B:229:THR:CG2	2.66	0.43
1:B:222:LEU:O	1:B:223:ILE:C	2.58	0.42
1:B:456:LEU:C	1:B:456:LEU:CD1	2.87	0.42
1:A:493:HIS:CD2	1:A:499:ASP:OD1	2.73	0.42
2:E:351:ASP:C	2:E:353:SER:N	2.73	0.42
1:B:66:GLY:O	1:B:70:SER:OG	2.38	0.42
1:A:505:HIS:N	1:A:505:HIS:CD2	2.88	0.41
1:A:256:ILE:CG2	1:A:257:SER:N	2.83	0.41
1:B:548:THR:O	1:B:552:GLN:N	2.53	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:E:458:VAL:O	2:E:459:PRO:C	2.59	0.41
1:B:125:THR:O	1:B:126:ILE:C	2.58	0.41
1:A:526:GLN:O	1:A:530:CYS:SG	2.79	0.41
1:B:597:ASP:O	1:B:598:GLN:C	2.59	0.41
1:B:595:LEU:O	1:B:596:LYS:C	2.60	0.41
1:A:100:LEU:O	1:A:102:GLN:N	2.54	0.41
2:F:325:PHE:C	2:F:327:GLU:N	2.73	0.41
2:E:454:ASP:OD2	2:E:456:SER:N	2.53	0.40
1:B:306:ARG:O	1:B:310:GLU:CB	2.70	0.40
2:E:442:TYR:CE1	2:E:443:LEU:CG	3.04	0.40
1:B:143:LEU:O	1:B:144:LEU:C	2.59	0.40
1:B:378:HIS:NE2	1:B:402:GLU:OE1	2.55	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	595/597 (100%)	511 (86%)	68 (11%)	16 (3%)	8	39
1	B	595/597 (100%)	509 (86%)	75 (13%)	11 (2%)	13	52
2	E	169/179 (94%)	135 (80%)	24 (14%)	10 (6%)	2	17
2	F	169/179 (94%)	135 (80%)	27 (16%)	7 (4%)	4	27
All	All	1528/1552 (98%)	1290 (84%)	194 (13%)	44 (3%)	7	38

All (44) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	289	PRO
1	A	504	PHE
1	B	212	VAL
1	B	290	ASN
1	B	536	GLU
2	E	330	ASN

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Mol	Chain	Res	Type
2	E	369	VAL
2	E	402	THR
2	F	330	ASN
2	F	402	THR
1	A	91	LEU
1	A	212	VAL
1	B	91	LEU
1	B	126	ILE
1	B	163	TRP
1	B	463	VAL
1	B	473	TRP
2	E	370	SER
2	E	471	ALA
1	A	20	THR
1	A	338	ASN
1	B	322	ASN
2	E	364	PHE
2	E	368	GLY
2	E	416	PHE
1	A	163	TRP
1	A	339	VAL
1	A	466	GLY
1	A	508	ASN
1	B	339	VAL
2	F	416	PHE
2	F	465	LYS
2	F	470	PRO
1	A	254	SER
1	A	505	HIS
1	A	600	LYS
1	A	614	ALA
1	B	338	ASN
1	A	409	SER
1	A	534	LYS
2	F	368	GLY
2	F	387	PHE
2	E	465	LYS
2	E	470	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	527/527 (100%)	477 (90%)	50 (10%)	12	42
1	B	527/527 (100%)	479 (91%)	48 (9%)	14	45
2	E	151/157 (96%)	133 (88%)	18 (12%)	8	27
2	F	151/157 (96%)	136 (90%)	15 (10%)	11	39
All	All	1356/1368 (99%)	1225 (90%)	131 (10%)	12	41

All (131) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	GLU
1	A	29	LEU
1	A	69	TRP
1	A	89	GLN
1	A	96	GLN
1	A	100	LEU
1	A	102	GLN
1	A	114	LYS
1	A	143	LEU
1	A	149	ASN
1	A	155	SER
1	A	190	MET
1	A	198	ASP
1	A	212	VAL
1	A	216	ASP
1	A	225	ASP
1	A	244	VAL
1	A	290	ASN
1	A	334	THR
1	A	365	THR
1	A	368	ASP
1	A	369	PHE
1	A	371	THR
1	A	380	GLN
1	A	381	TYR
1	A	385	TYR

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Mol	Chain	Res	Type
1	A	401	HIS
1	A	418	LEU
1	A	429	GLN
1	A	439	LEU
1	A	444	LEU
1	A	445	THR
1	A	449	THR
1	A	456	LEU
1	A	476	LYS
1	A	479	GLU
1	A	480	MET
1	A	503	LEU
1	A	518	ARG
1	A	526	GLN
1	A	529	LEU
1	A	536	GLU
1	A	557	MET
1	A	558	LEU
1	A	560	LEU
1	A	582	ARG
1	A	597	ASP
1	A	600	LYS
1	A	607	SER
1	A	613	TYR
1	B	20	THR
1	B	47	SER
1	B	55	THR
1	B	81	GLN
1	B	85	LEU
1	B	86	GLN
1	B	89	GLN
1	B	96	GLN
1	B	100	LEU
1	B	103	ASN
1	B	114	LYS
1	B	150	GLU
1	B	167	SER
1	B	170	SER
1	B	172	VAL
1	B	190	MET
1	B	198	ASP
1	B	212	VAL

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Mol	Chain	Res	Type
1	B	216	ASP
1	B	225	ASP
1	B	240	LEU
1	B	254	SER
1	B	290	ASN
1	B	334	THR
1	B	365	THR
1	B	367	ASP
1	B	368	ASP
1	B	369	PHE
1	B	371	THR
1	B	385	TYR
1	B	401	HIS
1	B	410	LEU
1	B	418	LEU
1	B	432	ASN
1	B	439	LEU
1	B	444	LEU
1	B	455	MET
1	B	456	LEU
1	B	476	LYS
1	B	480	MET
1	B	488	VAL
1	B	503	LEU
1	B	511	SER
1	B	527	GLU
1	B	557	MET
1	B	560	LEU
1	B	573	VAL
1	B	585	LEU
2	E	329	PHE
2	E	332	THR
2	E	333	LYS
2	E	337	VAL
2	E	341	GLU
2	E	359	THR
2	E	364	PHE
2	E	369	VAL
2	E	409	ASN
2	E	412	LEU
2	E	416	PHE
2	E	417	MET

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Mol	Chain	Res	Type
2	E	423	TRP
2	E	456	SER
2	E	463	ASP
2	E	467	CYS
2	E	481	TYR
2	E	485	THR
2	F	329	PHE
2	F	332	THR
2	F	333	LYS
2	F	337	VAL
2	F	341	GLU
2	F	364	PHE
2	F	369	VAL
2	F	388	VAL
2	F	416	PHE
2	F	417	MET
2	F	456	SER
2	F	467	CYS
2	F	481	TYR
2	F	485	THR
2	F	500	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 for Mogul analysis.

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	NDG	A	616	-	15,15,15	0.61	0	21,21,21	1.01	1 (4%)
3	NDG	B	616	-	15,15,15	0.41	0	21,21,21	1.15	3 (14%)
3	NDG	B	617	-	15,15,15	0.89	1 (6%)	21,21,21	1.82	3 (14%)
3	NDG	B	618	-	15,15,15	0.57	0	21,21,21	1.78	5 (23%)
4	NAG	E	91	-	15,15,15	0.64	0	21,21,21	1.16	2 (9%)
3	NDG	F	91	-	15,15,15	0.55	0	21,21,21	1.12	3 (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
3	NDG	A	616	-	-	0/6/26/26	0/1/1/1
3	NDG	B	616	-	-	0/6/26/26	0/1/1/1
3	NDG	B	617	-	-	2/6/26/26	0/1/1/1
3	NDG	B	618	-	-	0/6/26/26	0/1/1/1
4	NAG	E	91	-	-	0/6/26/26	0/1/1/1
3	NDG	F	91	-	-	0/6/26/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	617	NDG	C1-C2	2.16	1.55	1.53

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	617	NDG	O-C1-C2	6.21	115.90	109.61
3	B	618	NDG	O-C1-C2	3.89	113.55	109.61
3	B	618	NDG	C1-O-C5	3.71	120.04	113.40
3	B	617	NDG	C1-O-C5	3.09	118.94	113.40
4	E	91	NAG	O5-C1-C2	2.99	112.64	109.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	91	NAG	C1-O5-C5	2.98	118.73	113.40
3	B	618	NDG	O-C5-C4	2.97	115.26	109.76
3	A	616	NDG	C1-C2-N2	2.94	114.25	110.85
3	B	618	NDG	C4-C3-C2	2.79	114.41	110.44
3	B	618	NDG	C1-C2-C3	2.71	114.47	110.59
3	B	616	NDG	O-C5-C4	2.63	114.62	109.76
3	B	616	NDG	C1-O-C5	2.60	118.06	113.40
3	F	91	NDG	C1-O-C5	2.45	117.79	113.40
3	B	616	NDG	C3-C4-C5	2.30	114.32	110.20
3	B	617	NDG	O4-C4-C5	2.28	115.29	109.28
3	F	91	NDG	C4-C3-C2	2.23	113.61	110.44
3	F	91	NDG	O-C1-C2	2.16	111.80	109.61

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	617	NDG	C8-C7-N2-C2
3	B	617	NDG	O7-C7-N2-C2

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	597/597 (100%)	-0.11	1 (0%) 93 61	37, 71, 118, 142	0
1	B	597/597 (100%)	-0.17	0 100 100	31, 67, 116, 143	0
2	E	173/179 (96%)	-0.08	0 100 100	53, 78, 116, 120	0
2	F	173/179 (96%)	-0.09	0 100 100	54, 79, 115, 119	0
All	All	1540/1552 (99%)	-0.13	1 (0%) 93 70	31, 72, 116, 143	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	104	GLY	2.5

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(\AA^2)	Q<0.9
5	ZN	A	901	1/1	0.38	3.50	102,102,102,102	0
6	CL	A	902	1/1	0.26	2.69	78,78,78,78	0
5	ZN	B	901	1/1	0.35	1.23	110,110,110,110	0
3	NDG	B	616	15/15	0.28	1.11	105,107,108,108	0
3	NDG	B	618	15/15	0.19	0.70	56,63,70,70	0
3	NDG	B	617	15/15	0.27	0.43	98,102,103,104	0
3	NDG	A	616	15/15	0.22	-0.26	114,120,121,121	0
6	CL	B	902	1/1	0.17	-1.03	52,52,52,52	0
4	NAG	E	91	15/15	0.38	-	147,148,148,148	0
3	NDG	F	91	15/15	0.32	-	117,118,118,118	0

6.5 Other polymers ⓘ

There are no such residues in this entry.