



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:42 PM UTC

PDB ID : 1M2Z / pdb_00001m2z
Title : Crystal structure of a dimer complex of the human glucocorticoid receptor ligand-binding domain bound to dexamethasone and a TIF2 coactivator motif
Authors : Bledsoe, R.B.; Montana, V.G.; Stanley, T.B.; Delves, C.J.; Apolito, C.J.; McKee, D.D.; Consler, T.G.; Parks, D.J.; Stewart, E.L.; Willson, T.M.; Lambert, M.H.; Moore, J.T.; Pearce, K.H.; Xu, H.E.
Deposited on : 2002-06-26
Resolution : 2.50 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](#) ①) 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

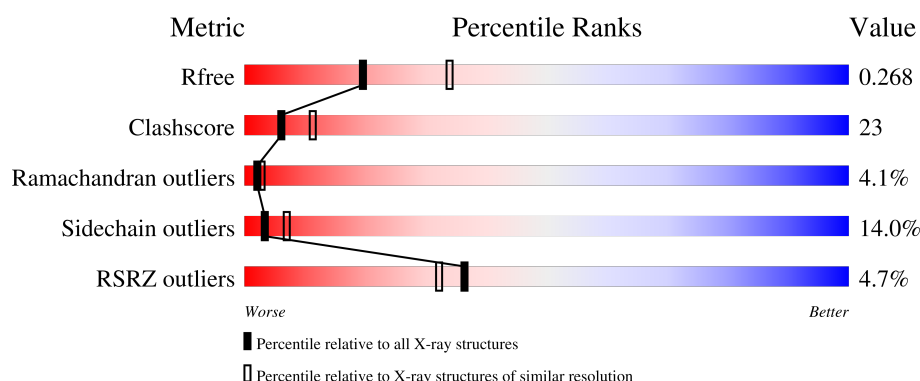
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	257	2% 57% 34% 8%
1	D	257	4% 55% 33% 9%
2	B	21	38% 5% 57% 24% 14%
2	E	21	19% 62% 24% 10% 5%

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
3	BOG	A	501	X	-	-	-
3	BOG	A	778	X	-	-	-
3	BOG	A	779	X	-	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4783 atoms, of which 1 is hydrogen 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 glucocorticoid receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	255	Total	C	N	O	S	0	0	0
			2074	1335	341	380	18			
1	D	253	Total	C	N	O	S	0	0	0
			2058	1324	339	377	18			

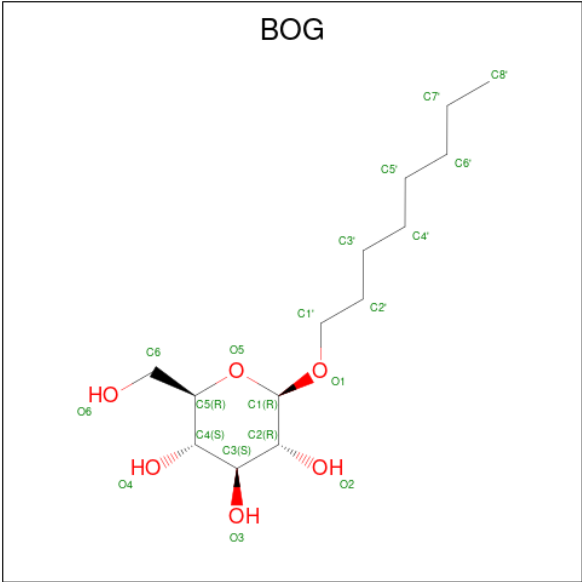
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	602	SER	PHE	engineered mutation	UNP P04150
D	602	SER	PHE	engineered mutation	UNP P04150

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

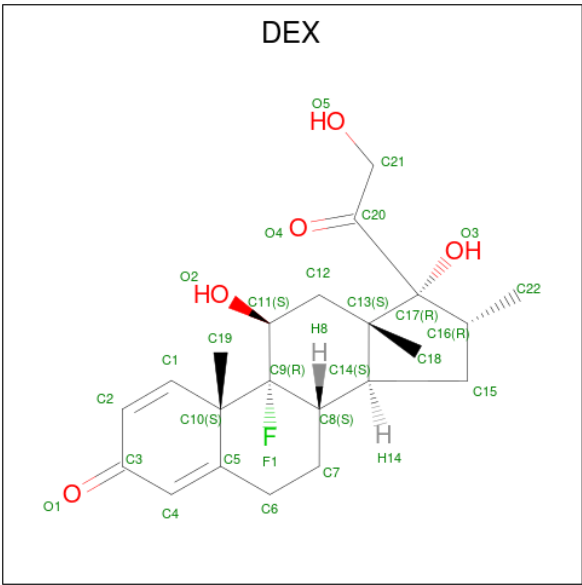
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	21	Total	C	N	O	0	0	0
			172	109	29	34			
2	E	21	Total	C	N	O	0	0	0
			172	109	29	34			

- Molecule 3 is octyl beta-D-glucopyranoside (CCD ID: BOG) (formula: C₁₄H₂₈O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			19	14	5		
3	A	1	Total	C	O	0	0
			12	6	6		
3	A	1	Total	C	O	0	0
			14	8	6		

- Molecule 4 is DEXAMETHASONE (CCD ID: DEX) (formula: C₂₂H₂₉FO₅).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	F	H	O	0	0
			29	22	1	1	5		

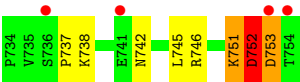
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	D	1	Total	C	F	O	0	0
			28	22	1	5		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	108	Total	O	0	0
			108	108		
5	B	5	Total	O	0	0
			5	5		
5	D	87	Total	O	0	0
			87	87		
5	E	5	Total	O	0	0
			5	5		



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	125.84Å 125.84Å 85.98Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 – 2.50 8.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	81.8 (8.00-2.50) 90.1 (8.00-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.22 (at 2.38Å)	Xtriage
Refinement program	CNX 2000	Depositor
R, R_{free}	0.237 , 0.267 0.253 , 0.268	Depositor DCC
R_{free} test set	2245 reflections (7.97%)	wwPDB-VP
Wilson B-factor (Å ²)	58.2	Xtriage
Anisotropy	0.361	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 58.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.047 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4783	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.99% 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: BOG, DEX

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	0.43	0/2119	0.88	4/2866 (0.1%)
1	D	0.49	1/2103 (0.0%)	0.86	6/2843 (0.2%)
2	B	0.66	0/174	1.23	2/231 (0.9%)
2	E	0.49	0/174	0.81	0/231
All	All	0.47	1/4570 (0.0%)	0.89	12/6171 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	526	PRO	CA-CB	-5.21	1.46	1.53

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	527	GLN	N-CA-C	9.99	132.08	110.80
2	B	750	ASP	N-CA-C	7.15	119.34	109.54
1	A	586	ASN	N-CA-C	-6.82	104.86	113.72
1	D	744	THR	N-CA-C	-6.18	104.65	111.82
1	A	694	ILE	N-CA-C	-6.17	104.48	110.72
1	D	694	ILE	N-CA-C	-6.03	104.63	110.72
1	D	639	MET	N-CA-C	5.95	117.43	111.07
1	D	636	LEU	CA-C-N	5.72	126.99	119.84
1	D	636	LEU	C-N-CA	5.72	126.99	119.84
1	D	760	GLN	N-CA-C	5.55	117.01	111.07
2	B	743	ALA	N-CA-C	-5.31	106.75	113.18
1	A	587	LEU	N-CA-C	-5.16	103.58	110.55

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	2074	0	2097	95	0
1	D	2058	0	2075	93	0
2	B	172	0	182	27	0
2	E	172	0	182	6	0
3	A	45	0	35	5	0
4	A	28	1	29	1	0
4	D	28	0	29	2	0
5	A	108	0	0	1	0
5	B	5	0	0	0	0
5	D	87	0	0	1	0
5	E	5	0	0	1	0
All	All	4782	1	4629	208	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 23.

All (208) 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)
3:A:501:BOG:C1	3:A:501:BOG:C1'	2.28	1.11
1:A:570:GLN:HB3	1:A:604:MET:HE2	1.51	0.92
1:D:544:LEU:HD21	1:D:570:GLN:HG2	1.60	0.84
2:B:742:ASN:OD1	2:B:745:LEU:HB2	1.79	0.82
1:D:565:MET:HE3	1:D:750:PRO:HB3	1.61	0.80
1:A:680:LEU:H	1:A:683:GLN:HG2	1.47	0.79
2:B:751:LYS:O	2:B:751:LYS:HD3	1.84	0.78
1:A:760:GLN:HB3	1:A:764:TYR:HD1	1.48	0.77
1:A:633:ARG:HA	1:A:636:LEU:CD1	2.16	0.76
1:D:639:MET:HE3	1:D:639:MET:HA	1.66	0.76
1:A:560:MET:HE3	1:A:747:ILE:HD13	1.72	0.70
1:D:760:GLN:HB3	1:D:764:TYR:HD1	1.56	0.70
1:A:761:ILE:CG2	1:A:762:PRO:HD3	2.21	0.70
1:D:701:ILE:HG23	1:D:714:ARG:HG2	1.72	0.69
1:A:588:HIS:HD2	1:A:590:ASP:HB2	1.56	0.69
1:A:591:ASP:CG	1:A:680:LEU:HB3	2.17	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:548:TYR:HD1	1:D:562:THR:HG21	1.57	0.68
1:D:757:ILE:O	1:D:761:ILE:HG12	1.95	0.67
1:A:524:THR:O	1:A:525:LEU:HD12	1.94	0.67
1:A:753:LEU:O	1:A:757:ILE:HD12	1.95	0.66
1:D:558:ARG:O	1:D:562:THR:HG23	1.96	0.66
1:A:761:ILE:HG22	1:A:762:PRO:HD3	1.76	0.66
1:A:630:ASN:OD1	1:D:545:TYR:HE1	1.79	0.65
1:A:588:HIS:CD2	1:A:681:LYS:HD2	2.32	0.65
1:A:759:ASN:HA	2:B:741:GLU:HG2	1.80	0.64
1:A:568:GLY:HA2	1:A:753:LEU:HD13	1.80	0.63
1:D:544:LEU:H	1:D:544:LEU:HD23	1.63	0.63
1:A:761:ILE:HD13	1:A:761:ILE:O	1.99	0.62
1:A:543:VAL:HG11	1:A:625:PRO:HD3	1.82	0.62
2:B:740:LYS:HE2	2:B:740:LYS:HA	1.80	0.62
1:A:759:ASN:HA	2:B:741:GLU:CG	2.30	0.61
1:D:593:MET:HE1	2:E:746:ARG:CZ	2.30	0.61
2:E:751:LYS:O	2:E:752:ASP:HB2	1.99	0.61
1:A:598:TYR:CE2	1:A:769:ILE:HG12	2.36	0.61
1:A:646:MET:O	1:A:649:VAL:HG12	2.00	0.61
1:D:548:TYR:CD1	1:D:562:THR:HG21	2.36	0.61
1:A:742:ASP:OD1	1:A:745:MET:HE3	2.00	0.61
1:A:701:ILE:HD11	1:A:718:LEU:HD12	1.82	0.60
1:A:575:VAL:O	1:A:579:LYS:HG3	2.01	0.60
1:A:752:MET:HE1	2:B:748:LEU:CD1	2.31	0.60
1:D:560:MET:HE3	1:D:642:GLN:HE22	1.67	0.60
1:D:707:ASN:HB3	1:D:710:GLN:OE1	2.01	0.60
1:D:701:ILE:HD11	1:D:718:LEU:HD12	1.83	0.60
1:D:680:LEU:N	1:D:680:LEU:HD23	2.17	0.59
1:A:591:ASP:OD1	1:A:680:LEU:HB3	2.03	0.59
1:A:602:SER:OG	1:A:670:LEU:HG	2.02	0.59
1:A:579:LYS:HD3	2:B:749:LEU:HA	1.84	0.59
1:D:699:LYS:O	1:D:702:VAL:HG22	2.02	0.59
1:D:568:GLY:HA2	1:D:753:LEU:HD13	1.84	0.59
1:A:633:ARG:HA	1:A:636:LEU:HD13	1.84	0.59
2:B:734:PRO:O	2:B:735:VAL:HG13	2.03	0.58
1:D:661:GLU:OE1	1:D:703:LYS:HE2	2.04	0.58
1:D:675:VAL:HB	1:D:680:LEU:CD2	2.33	0.58
2:B:738:LYS:HE3	2:B:741:GLU:HB3	1.86	0.57
1:D:725:MET:HA	1:D:728:VAL:HG13	1.87	0.57
1:D:762:PRO:O	1:D:766:ASN:OD1	2.22	0.57
1:A:631:GLU:O	1:A:635:THR:HG22	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:737:PRO:HA	2:B:739:LYS:HE2	1.87	0.57
1:A:670:LEU:HD13	1:A:722:LEU:HD22	1.88	0.56
1:A:759:ASN:CG	2:B:741:GLU:HG3	2.31	0.56
1:D:675:VAL:HB	1:D:680:LEU:HD21	1.87	0.56
1:D:726:HIS:HE1	1:D:772:LEU:O	1.89	0.56
1:A:545:TYR:HE1	1:A:625:PRO:HB2	1.70	0.55
1:A:559:ILE:O	1:A:563:LEU:HG	2.06	0.55
1:A:759:ASN:CB	2:B:741:GLU:HG3	2.36	0.55
2:E:737:PRO:O	2:E:738:LYS:HB2	2.07	0.55
1:A:761:ILE:HD13	1:A:761:ILE:C	2.31	0.55
2:B:735:VAL:O	2:B:737:PRO:HD3	2.05	0.55
1:D:666:MET:HB3	1:D:722:LEU:HD21	1.88	0.55
1:D:675:VAL:HB	1:D:676:PRO:HD2	1.90	0.54
3:A:501:BOG:C1'	3:A:501:BOG:O5	2.56	0.54
1:D:591:ASP:OD1	1:D:680:LEU:HB3	2.08	0.52
1:D:677:LYS:O	1:D:678:ASP:CG	2.52	0.52
1:D:568:GLY:O	1:D:572:ILE:HG13	2.09	0.52
1:A:698:GLY:CA	3:A:779:BOG:H62	2.40	0.52
1:A:525:LEU:HA	1:A:526:PRO:C	2.35	0.52
1:D:755:GLU:HG2	5:E:104:HOH:O	2.10	0.51
1:D:705:GLU:HG3	1:D:710:GLN:HG2	1.91	0.51
1:A:690:ARG:HD3	3:A:501:BOG:O3	2.11	0.51
1:D:735:TYR:O	1:D:739:THR:HG23	2.10	0.51
1:A:655:ARG:HH21	1:A:656:LEU:HD21	1.75	0.50
1:D:755:GLU:HG3	2:E:742:ASN:HD22	1.75	0.50
2:E:751:LYS:O	2:E:752:ASP:CB	2.59	0.50
1:A:725:MET:O	1:A:729:VAL:HG23	2.11	0.50
1:D:676:PRO:HD2	1:D:680:LEU:HD22	1.92	0.50
1:A:720:LYS:HD2	1:A:775:HIS:HD2	1.76	0.50
1:A:589:LEU:O	1:A:589:LEU:HD23	2.10	0.49
1:D:560:MET:HE3	1:D:642:GLN:NE2	2.28	0.49
1:D:737:PHE:CG	1:D:761:ILE:HD13	2.48	0.49
1:D:685:LEU:HD22	1:D:689:ILE:HG13	1.93	0.49
1:A:720:LYS:HD2	1:A:775:HIS:CD2	2.48	0.49
2:B:739:LYS:O	2:B:740:LYS:CB	2.59	0.49
2:E:752:ASP:O	2:E:753:ASP:HB2	2.13	0.49
1:A:579:LYS:HD3	2:B:749:LEU:HD23	1.94	0.48
2:B:751:LYS:N	2:B:751:LYS:HD2	2.28	0.48
1:D:557:TRP:CZ3	1:D:746:SER:O	2.66	0.48
1:D:615:GLN:NE2	1:D:628:ILE:HD11	2.28	0.48
1:A:615:GLN:HG3	1:D:615:GLN:HG2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:742:ASN:CG	2:B:745:LEU:HB2	2.36	0.48
2:B:750:ASP:O	2:B:751:LYS:HB3	2.13	0.48
1:D:560:MET:HE3	1:D:642:GLN:OE1	2.12	0.48
1:A:589:LEU:HD23	1:A:589:LEU:C	2.38	0.48
1:D:600:TRP:O	1:D:604:MET:HG2	2.13	0.48
2:B:750:ASP:O	2:B:751:LYS:CB	2.59	0.48
1:A:733:LEU:HG	1:A:737:PHE:CZ	2.49	0.48
1:D:684:GLU:HG2	1:D:685:LEU:H	1.79	0.48
1:D:707:ASN:CB	1:D:710:GLN:OE1	2.62	0.48
1:A:736:CYS:HA	4:A:301:DEX:O4	2.15	0.47
2:B:738:LYS:O	2:B:738:LYS:HD3	2.14	0.47
2:B:739:LYS:O	2:B:740:LYS:HG2	2.15	0.47
1:D:609:GLY:HA3	1:D:649:VAL:HG22	1.96	0.47
1:A:757:ILE:O	1:A:761:ILE:HB	2.15	0.47
1:A:755:GLU:O	1:A:759:ASN:HB2	2.14	0.47
1:A:527:GLN:C	1:A:529:THR:H	2.23	0.47
1:A:632:GLN:O	1:A:635:THR:HG23	2.16	0.46
1:A:761:ILE:HG23	1:A:762:PRO:HD3	1.96	0.46
1:D:706:GLY:O	1:D:707:ASN:HB2	2.14	0.46
1:A:531:THR:O	1:A:534:SER:HB3	2.15	0.46
1:A:613:TYR:CE1	1:A:654:HIS:HA	2.51	0.46
1:D:545:TYR:HB3	1:D:626:ASP:OD2	2.15	0.46
1:A:662:GLU:O	1:A:666:MET:HG3	2.16	0.46
1:D:626:ASP:OD1	1:D:626:ASP:C	2.59	0.46
1:D:705:GLU:CG	1:D:710:GLN:HG2	2.45	0.45
1:D:572:ILE:CG1	1:D:752:MET:HG3	2.46	0.45
1:D:675:VAL:CB	1:D:680:LEU:HD21	2.46	0.45
1:A:606:PHE:HB2	1:A:725:MET:HE2	1.99	0.45
1:D:760:GLN:O	1:D:761:ILE:C	2.60	0.45
1:A:572:ILE:HG12	1:A:752:MET:CE	2.47	0.45
1:D:571:VAL:O	1:D:575:VAL:HG23	2.16	0.45
1:D:602:SER:HB2	1:D:729:VAL:HG21	1.99	0.45
2:B:747:TYR:O	2:B:751:LYS:HE2	2.16	0.45
1:A:531:THR:CG2	1:A:533:VAL:HG12	2.46	0.45
1:A:690:ARG:O	1:A:694:ILE:HG13	2.17	0.45
1:A:698:GLY:HA2	3:A:779:BOG:H62	1.99	0.45
1:A:568:GLY:O	1:A:572:ILE:HG13	2.17	0.44
1:D:613:TYR:CE1	1:D:654:HIS:HA	2.52	0.44
1:D:670:LEU:HA	1:D:673:SER:HB3	1.98	0.44
1:D:661:GLU:CD	1:D:703:LYS:HE2	2.42	0.44
2:B:752:ASP:OD1	2:B:752:ASP:O	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:729:VAL:O	1:A:733:LEU:HB2	2.17	0.44
1:D:658:VAL:HG11	1:D:666:MET:HE1	2.00	0.44
1:A:543:VAL:HG11	1:A:625:PRO:CD	2.46	0.44
2:B:739:LYS:O	2:B:740:LYS:HB2	2.17	0.44
1:D:608:LEU:HD13	1:D:623:PHE:HA	2.00	0.44
1:D:762:PRO:HG2	1:D:763:LYS:H	1.83	0.43
1:D:529:THR:O	1:D:529:THR:HG23	2.18	0.43
1:D:726:HIS:CE1	1:D:771:LYS:HB3	2.52	0.43
1:D:568:GLY:CA	1:D:753:LEU:HD13	2.49	0.43
1:D:556:THR:HG22	1:D:560:MET:SD	2.58	0.43
1:D:706:GLY:O	1:D:707:ASN:CB	2.66	0.43
1:D:710:GLN:H	1:D:710:GLN:CD	2.27	0.43
1:A:759:ASN:ND2	2:B:741:GLU:HG3	2.34	0.43
1:A:588:HIS:CD2	1:A:590:ASP:H	2.36	0.43
1:A:630:ASN:OD1	1:D:545:TYR:CE1	2.67	0.43
1:D:560:MET:HE2	4:D:401:DEX:H122	2.00	0.43
1:A:711:ASN:HD22	1:A:711:ASN:HA	1.59	0.43
1:A:752:MET:HE1	2:B:748:LEU:HD13	2.01	0.43
1:D:639:MET:HA	1:D:639:MET:CE	2.44	0.43
1:D:544:LEU:H	1:D:544:LEU:CD2	2.32	0.42
1:D:675:VAL:CG1	1:D:680:LEU:HD21	2.49	0.42
1:D:751:GLU:HA	1:D:751:GLU:OE1	2.18	0.42
1:A:759:ASN:O	1:A:762:PRO:HD2	2.18	0.42
1:D:703:LYS:O	1:D:703:LYS:HG3	2.19	0.42
1:A:634:MET:HE3	1:A:647:LEU:HD11	2.02	0.42
1:D:642:GLN:HB2	4:D:401:DEX:C22	2.50	0.42
1:D:707:ASN:O	1:D:708:SER:CB	2.68	0.42
1:A:527:GLN:C	1:A:529:THR:N	2.78	0.42
1:A:577:TRP:CZ2	1:A:581:ILE:HD11	2.55	0.42
1:A:556:THR:O	1:A:560:MET:HG3	2.20	0.42
1:A:758:THR:O	1:A:761:ILE:HG22	2.19	0.42
1:D:761:ILE:HB	1:D:762:PRO:CD	2.49	0.42
1:A:536:LEU:HA	1:A:539:ILE:HG12	2.02	0.42
1:A:625:PRO:O	1:D:625:PRO:O	2.38	0.42
1:A:627:LEU:C	1:A:627:LEU:HD13	2.44	0.42
1:D:535:LEU:HD22	1:D:582:PRO:CG	2.50	0.42
1:A:577:TRP:CE2	1:A:581:ILE:HD11	2.55	0.41
1:A:776:GLN:H	1:A:776:GLN:HG3	1.72	0.41
1:D:575:VAL:O	1:D:579:LYS:HG3	2.20	0.41
1:D:632:GLN:O	1:D:635:THR:HG23	2.19	0.41
1:D:752:MET:HE3	1:D:756:ILE:HD11	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:527:GLN:HG3	1:A:534:SER:OG	2.20	0.41
1:A:570:GLN:HE21	1:A:604:MET:HG3	1.86	0.41
1:A:621:LEU:HG	1:A:647:LEU:CD2	2.51	0.41
1:A:761:ILE:HG23	1:A:762:PRO:CD	2.51	0.41
1:D:754:ALA:O	1:D:758:THR:OG1	2.38	0.41
1:A:660:TYR:O	1:A:663:TYR:HB3	2.21	0.41
1:A:740:PHE:CE2	1:A:758:THR:HG23	2.55	0.41
1:D:627:LEU:HD13	1:D:627:LEU:C	2.46	0.41
1:A:632:GLN:O	1:A:635:THR:CG2	2.69	0.41
1:A:634:MET:SD	1:A:640:TYR:HD1	2.44	0.41
1:D:645:HIS:O	1:D:648:TYR:HB3	2.21	0.41
1:D:663:TYR:HA	1:D:666:MET:HE3	2.03	0.41
1:D:563:LEU:HD13	1:D:623:PHE:CE1	2.56	0.41
1:A:525:LEU:HA	1:A:526:PRO:O	2.20	0.41
1:A:567:GLY:O	1:A:571:VAL:HG23	2.21	0.41
1:D:631:GLU:O	1:D:635:THR:HG22	2.21	0.41
1:A:531:THR:HG22	1:A:533:VAL:HG12	2.02	0.40
1:D:705:GLU:HB3	1:D:706:GLY:H	1.69	0.40
1:D:725:MET:HA	1:D:728:VAL:CG1	2.50	0.40
1:D:681:LYS:HA	5:D:157:HOH:O	2.19	0.40
1:A:542:GLU:HB2	5:A:80:HOH:O	2.22	0.40
1:D:701:ILE:CD1	1:D:718:LEU:HD12	2.49	0.40
1:A:524:THR:HB	1:A:528:LEU:HD12	2.04	0.40
1:A:743:LYS:HA	1:A:743:LYS:HD3	1.81	0.40
1:D:752:MET:O	1:D:756:ILE:HG13	2.21	0.40
1:D:776:GLN:HE21	1:D:776:GLN:HB2	1.64	0.40
1:A:586:ASN:HD22	1:A:586:ASN:HA	1.70	0.40
2:B:751:LYS:O	2:B:751:LYS:CD	2.63	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	253/257 (98%)	232 (92%)	17 (7%)	4 (2%)	7	14
1	D	251/257 (98%)	227 (90%)	15 (6%)	9 (4%)	2	3
2	B	19/21 (90%)	11 (58%)	2 (10%)	6 (32%)	0	0
2	E	19/21 (90%)	12 (63%)	4 (21%)	3 (16%)	0	0
All	All	542/556 (98%)	482 (89%)	38 (7%)	22 (4%)	2	3

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	527	GLN
1	A	637	PRO
2	B	740	LYS
2	B	751	LYS
2	B	753	ASP
1	D	526	PRO
1	D	707	ASN
1	D	708	SER
2	E	751	LYS
2	E	753	ASP
2	B	739	LYS
2	B	741	GLU
1	D	678	ASP
1	D	705	GLU
1	A	530	PRO
1	D	762	PRO
2	E	752	ASP
1	A	742	ASP
2	B	742	ASN
1	D	637	PRO
1	D	761	ILE
1	D	625	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	234/236 (99%)	206 (88%)	28 (12%)	5	10
1	D	232/236 (98%)	199 (86%)	33 (14%)	3	7
2	B	20/20 (100%)	12 (60%)	8 (40%)	0	0
2	E	20/20 (100%)	18 (90%)	2 (10%)	7	15
All	All	506/512 (99%)	435 (86%)	71 (14%)	3	7

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	525	LEU
1	A	526	PRO
1	A	529	THR
1	A	532	LEU
1	A	535	LEU
1	A	557	TRP
1	A	560	MET
1	A	595	LEU
1	A	604	MET
1	A	627	LEU
1	A	630	ASN
1	A	635	THR
1	A	670	LEU
1	A	683	GLN
1	A	685	LEU
1	A	688	GLU
1	A	711	ASN
1	A	721	LEU
1	A	727	GLU
1	A	728	VAL
1	A	743	LYS
1	A	744	THR
1	A	757	ILE
1	A	758	THR
1	A	761	ILE
1	A	763	LYS
1	A	764	TYR
1	A	776	GLN
2	B	736	SER
2	B	738	LYS
2	B	739	LYS
2	B	741	GLU
2	B	744	LEU

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Mol	Chain	Res	Type
2	B	745	LEU
2	B	751	LYS
2	B	754	THR
1	D	526	PRO
1	D	527	GLN
1	D	544	LEU
1	D	557	TRP
1	D	565	MET
1	D	589	LEU
1	D	613	TYR
1	D	625	PRO
1	D	626	ASP
1	D	632	GLN
1	D	635	THR
1	D	637	PRO
1	D	639	MET
1	D	641	ASP
1	D	649	VAL
1	D	656	LEU
1	D	667	LYS
1	D	669	LEU
1	D	680	LEU
1	D	685	LEU
1	D	704	ARG
1	D	705	GLU
1	D	707	ASN
1	D	711	ASN
1	D	721	LEU
1	D	728	VAL
1	D	743	LYS
1	D	744	THR
1	D	748	GLU
1	D	758	THR
1	D	764	TYR
1	D	766	ASN
1	D	776	GLN
2	E	745	LEU
2	E	752	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	570	GLN
1	A	586	ASN
1	A	588	HIS
1	A	619	ASN
1	A	642	GLN
1	A	683	GLN
1	A	707	ASN
1	A	710	GLN
1	A	713	GLN
1	A	717	GLN
1	A	738	GLN
1	D	570	GLN
1	D	597	GLN
1	D	615	GLN
1	D	707	ASN
1	D	711	ASN
1	D	713	GLN
1	D	717	GLN
1	D	726	HIS
1	D	760	GLN
1	D	776	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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
4	DEX	D	401	-	31,31,31	1.35	5 (16%)	53,53,53	1.87	12 (22%)
3	BOG	A	778	-	12,12,20	0.69	0	17,17,25	4.24	15 (88%)
3	BOG	A	779	-	14,14,20	0.61	0	19,19,25	4.28	16 (84%)
3	BOG	A	501	-	18,18,20	0.68	0	21,21,25	3.59	13 (61%)
4	DEX	A	301	-	31,31,31	1.35	5 (16%)	53,53,53	1.95	14 (26%)

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
4	DEX	D	401	-	-	0/8/84/84	0/4/4/4
3	BOG	A	778	-	5/5/5/5	2/2/22/31	0/1/1/1
3	BOG	A	779	-	5/5/5/5	4/5/25/31	0/1/1/1
3	BOG	A	501	-	4/4/4/5	1/7/24/31	0/1/1/1
4	DEX	A	301	-	-	2/8/84/84	0/4/4/4

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	301	DEX	C10-C9	-4.08	1.53	1.57
4	D	401	DEX	C10-C9	-4.00	1.53	1.57
4	D	401	DEX	C17-C13	-3.25	1.53	1.56
4	A	301	DEX	C17-C13	-3.21	1.53	1.56
4	A	301	DEX	C17-C16	-2.57	1.53	1.56
4	D	401	DEX	C17-C16	-2.57	1.53	1.56
4	A	301	DEX	F1-C9	-2.02	1.36	1.43
4	D	401	DEX	C9-C11	-2.01	1.53	1.54
4	D	401	DEX	F1-C9	-2.01	1.36	1.43
4	A	301	DEX	C4-C3	2.01	1.50	1.45

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	779	BOG	O1-C1-C2	6.53	118.19	108.27
3	A	779	BOG	O5-C5-C4	6.35	121.14	109.70
3	A	501	BOG	O2-C2-C3	5.98	122.53	110.15
3	A	779	BOG	O5-C1-C2	5.92	122.53	110.37
4	A	301	DEX	C21-C20-C17	5.92	122.62	117.63
3	A	501	BOG	O2-C2-C1	5.87	122.66	109.22
3	A	778	BOG	O5-C5-C6	5.73	120.63	106.44
3	A	778	BOG	O5-C1-C2	5.69	120.30	110.30
3	A	779	BOG	O5-C5-C6	5.54	120.18	106.44
4	D	401	DEX	C21-C20-C17	5.53	122.29	117.63
3	A	778	BOG	O2-C2-C1	5.46	121.84	109.25
3	A	501	BOG	O3-C3-C2	5.43	121.13	110.05
3	A	778	BOG	O4-C4-C5	5.39	122.60	109.32
3	A	501	BOG	O4-C4-C5	5.25	122.25	109.32
3	A	501	BOG	O5-C5-C6	5.21	117.81	107.66
3	A	778	BOG	O4-C4-C3	5.16	122.53	110.38
3	A	778	BOG	O2-C2-C3	5.01	122.18	110.38
3	A	779	BOG	O4-C4-C5	4.89	121.37	109.32
3	A	778	BOG	O3-C3-C2	4.81	121.72	110.38
3	A	779	BOG	O4-C4-C3	4.79	121.67	110.38
4	D	401	DEX	C6-C5-C10	4.74	118.83	115.70
3	A	779	BOG	O2-C2-C1	4.73	121.35	110.08
3	A	778	BOG	O3-C3-C4	4.73	121.53	110.38
3	A	501	BOG	O3-C3-C4	4.72	121.50	110.38
3	A	779	BOG	O3-C3-C4	4.69	121.42	110.38
3	A	501	BOG	O4-C4-C3	4.68	121.40	110.38
3	A	779	BOG	O2-C2-C3	4.66	121.35	110.38
4	A	301	DEX	C6-C5-C10	4.64	118.76	115.70
3	A	779	BOG	O3-C3-C2	4.63	121.30	110.38
3	A	778	BOG	O5-C5-C4	4.55	117.91	109.70
3	A	778	BOG	O1-C1-C2	4.22	121.22	108.98
4	D	401	DEX	C1-C2-C3	-4.10	118.03	121.49
4	A	301	DEX	C1-C2-C3	-4.10	118.03	121.49
3	A	779	BOG	O5-C1-O1	3.86	119.17	110.04
3	A	501	BOG	O5-C5-C4	3.84	120.18	110.83
4	A	301	DEX	C13-C17-C16	3.80	106.15	102.85
4	A	301	DEX	C12-C11-C9	3.73	115.83	112.96
3	A	501	BOG	C2-C3-C4	3.70	117.38	110.86
3	A	779	BOG	C3-C4-C5	3.70	116.95	110.23
3	A	779	BOG	C4-C3-C2	3.67	117.28	110.83
3	A	501	BOG	C6-C5-C4	3.66	122.01	113.02
4	D	401	DEX	C13-C17-C16	3.56	105.94	102.85
3	A	501	BOG	C1-C2-C3	3.48	114.72	109.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	779	BOG	C1-C2-C3	3.46	117.28	110.01
3	A	778	BOG	C6-C5-C4	3.36	121.28	113.02
3	A	778	BOG	C4-C3-C2	3.35	116.71	110.83
3	A	501	BOG	C3-C4-C5	3.34	116.30	110.23
4	D	401	DEX	C12-C11-C9	3.25	115.46	112.96
4	A	301	DEX	C10-C5-C4	3.05	124.34	122.15
4	A	301	DEX	C7-C8-C9	3.00	114.38	110.98
4	A	301	DEX	C10-C1-C2	3.00	126.64	124.37
4	D	401	DEX	C7-C8-C9	2.96	114.32	110.98
4	A	301	DEX	C5-C4-C3	-2.89	120.09	122.72
4	D	401	DEX	C10-C5-C4	2.89	124.22	122.15
4	D	401	DEX	C5-C4-C3	-2.88	120.11	122.72
4	D	401	DEX	C10-C1-C2	2.79	126.49	124.37
3	A	778	BOG	O1-C1-O5	2.72	118.48	110.41
3	A	778	BOG	C1-C2-C3	2.70	115.87	110.36
4	A	301	DEX	C9-C8-C14	2.69	111.70	109.34
4	D	401	DEX	C9-C8-C14	2.64	111.66	109.34
3	A	778	BOG	C3-C4-C5	2.55	114.85	110.23
4	A	301	DEX	C6-C5-C4	-2.48	116.90	120.86
4	D	401	DEX	C6-C5-C4	-2.45	116.95	120.86
3	A	501	BOG	O5-C1-C2	2.42	116.55	110.79
3	A	779	BOG	C1'-O1-C1	-2.32	108.83	113.91
3	A	779	BOG	C6-C5-C4	2.30	118.67	113.02
4	A	301	DEX	C15-C14-C8	2.27	121.21	119.08
4	D	401	DEX	C15-C14-C8	2.12	121.07	119.08
4	A	301	DEX	F1-C9-C8	-2.11	104.00	105.96
4	A	301	DEX	O4-C20-C17	-2.00	120.41	122.78

All (14) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	501	BOG	C3
3	A	501	BOG	C5
3	A	501	BOG	C2
3	A	501	BOG	C4
3	A	778	BOG	C5
3	A	778	BOG	C4
3	A	778	BOG	C1
3	A	778	BOG	C3
3	A	778	BOG	C2
3	A	779	BOG	C5
3	A	779	BOG	C4

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Mol	Chain	Res	Type	Atom
3	A	779	BOG	C1
3	A	779	BOG	C3
3	A	779	BOG	C2

All (9) torsion outliers are listed below:

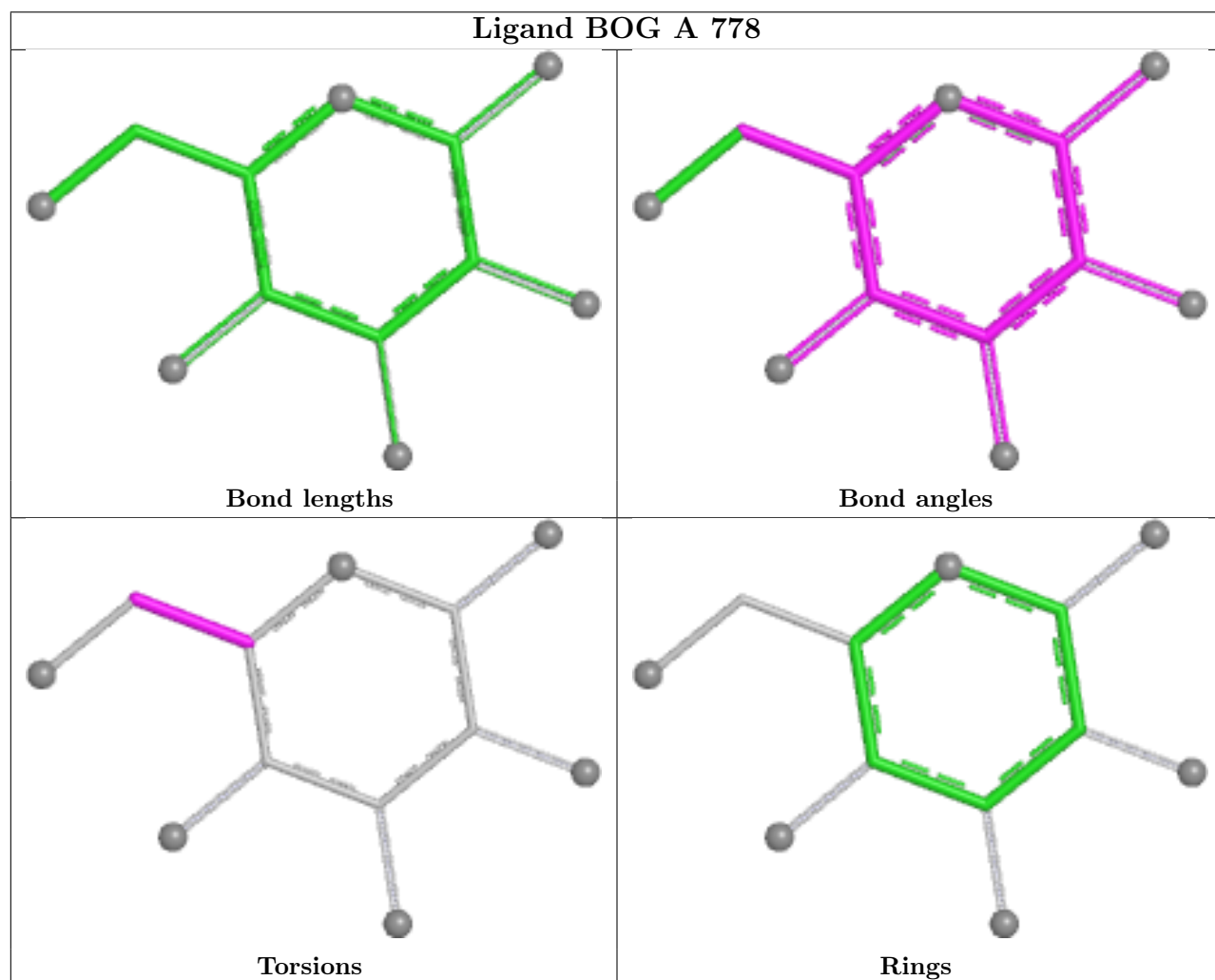
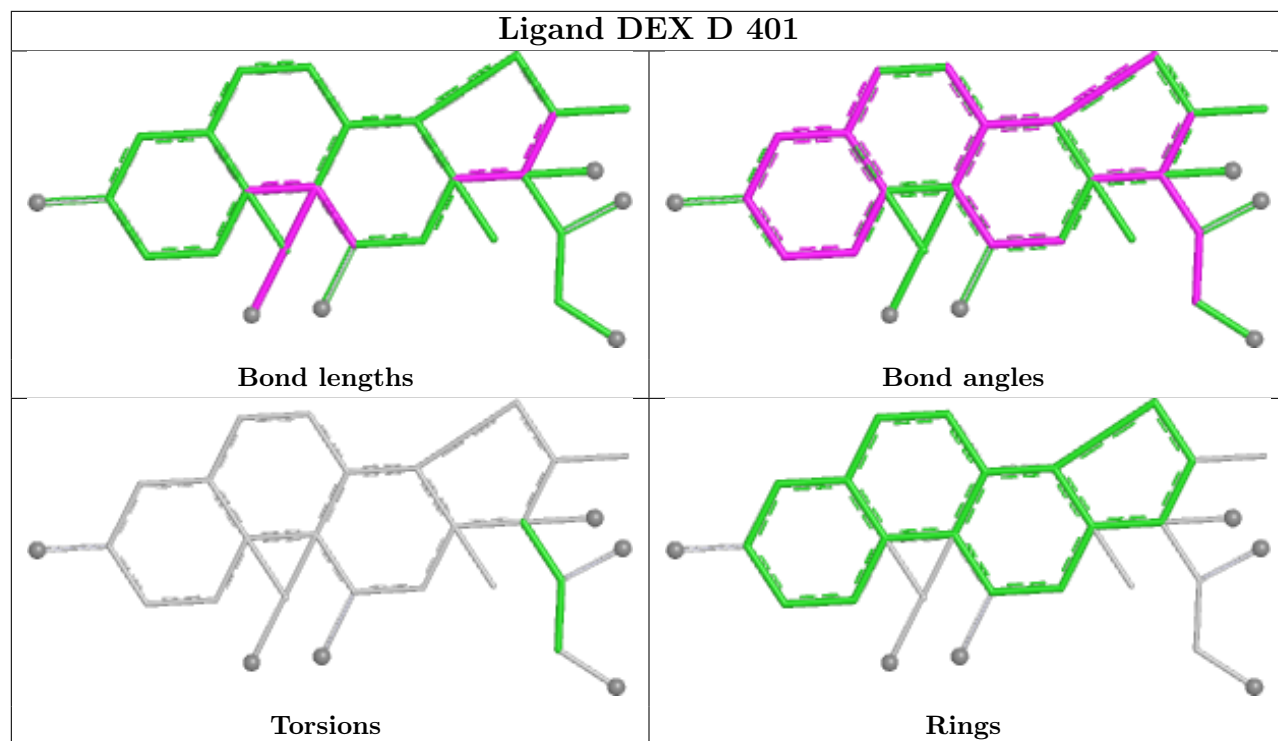
Mol	Chain	Res	Type	Atoms
4	A	301	DEX	C17-C20-C21-O5
4	A	301	DEX	O4-C20-C21-O5
3	A	778	BOG	C4-C5-C6-O6
3	A	779	BOG	C4-C5-C6-O6
3	A	501	BOG	O5-C5-C6-O6
3	A	779	BOG	O5-C5-C6-O6
3	A	779	BOG	O5-C1-O1-C1'
3	A	778	BOG	O5-C5-C6-O6
3	A	779	BOG	C2'-C1'-O1-C1

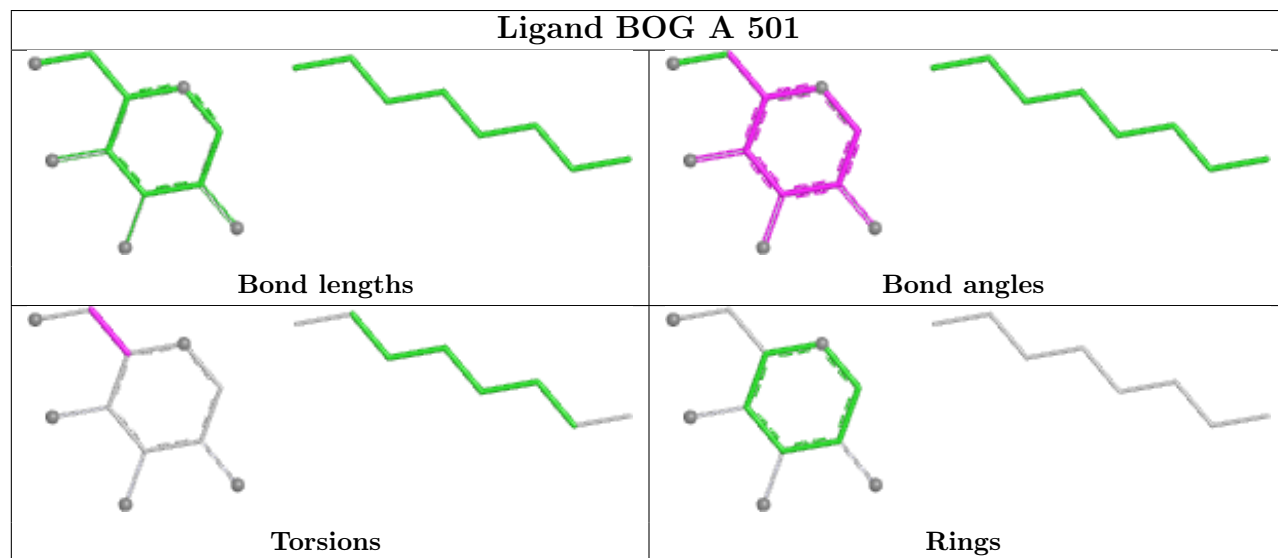
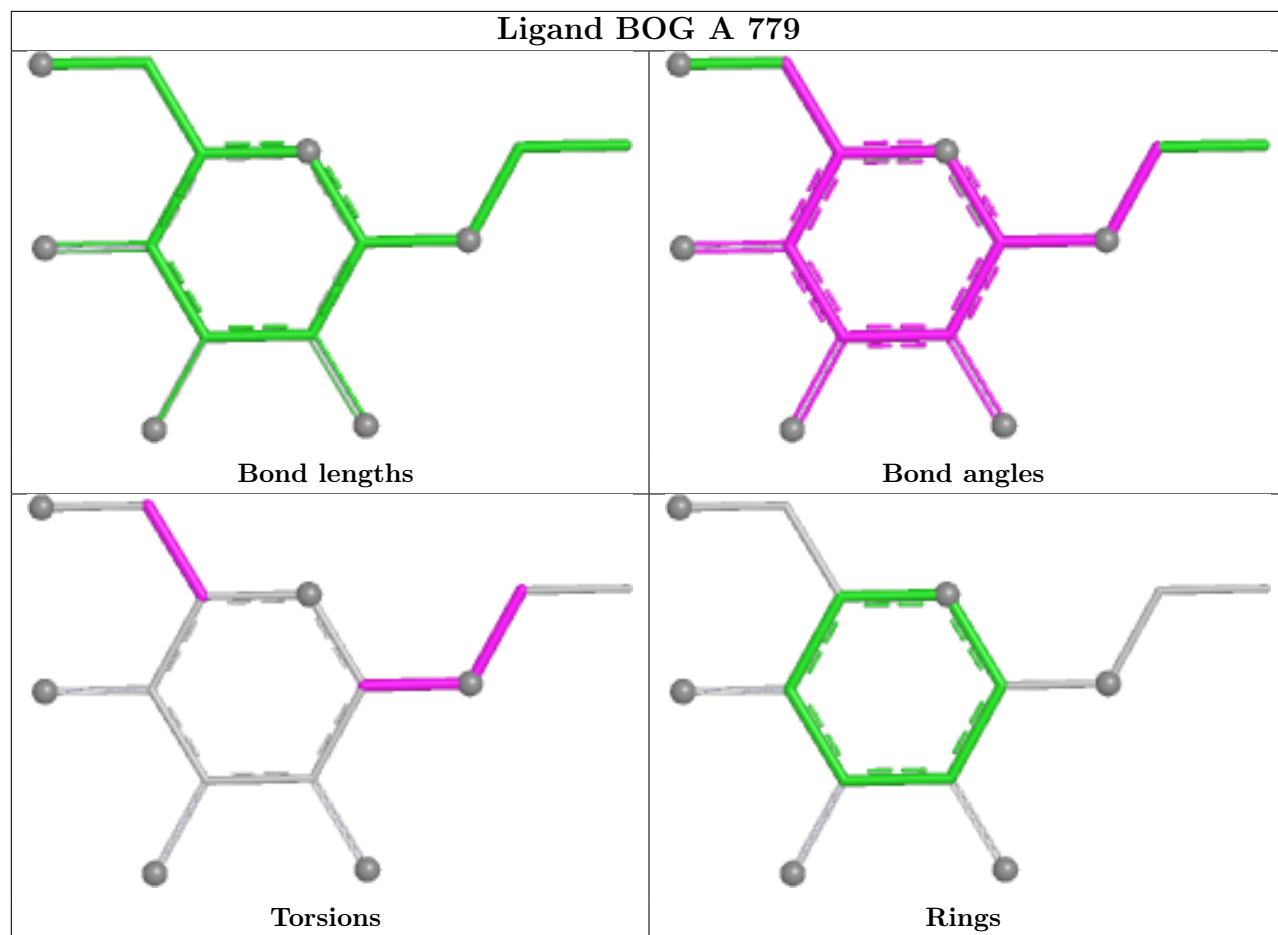
There are no ring outliers.

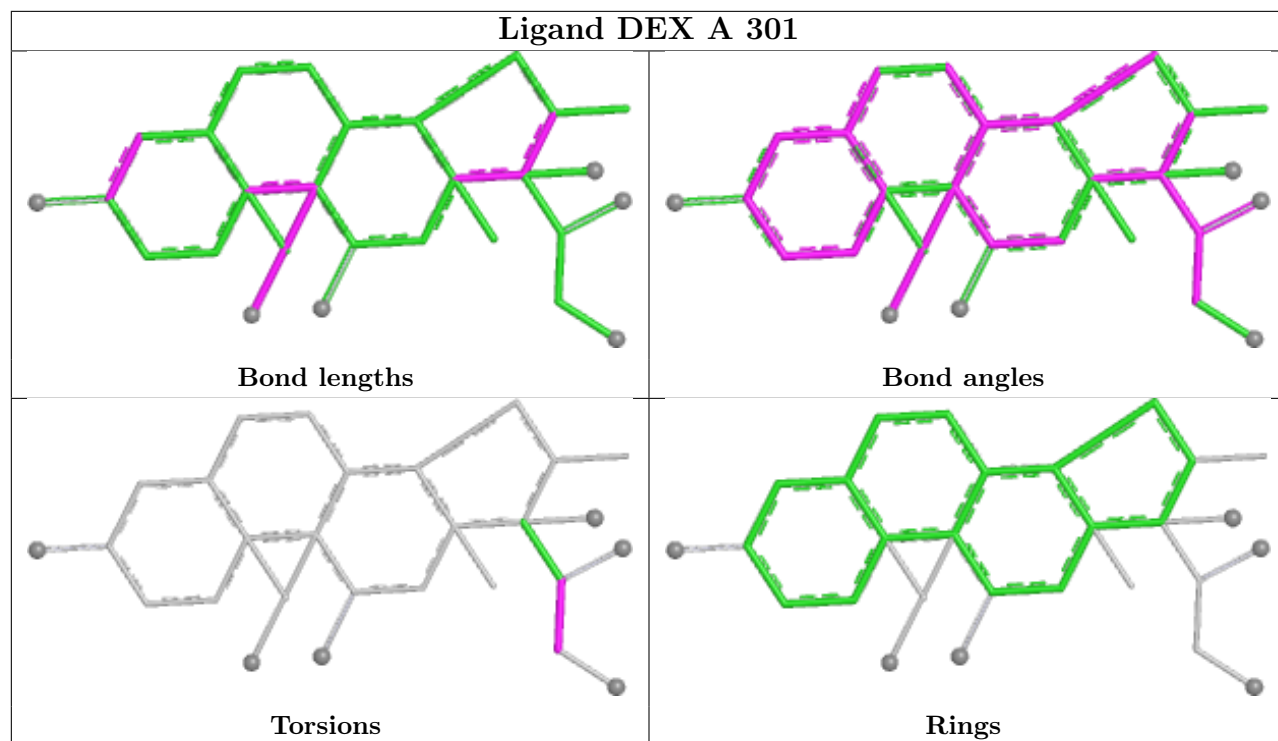
4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	401	DEX	2	0
3	A	779	BOG	2	0
3	A	501	BOG	3	0
4	A	301	DEX	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







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	255/257 (99%)	-0.13	4 (1%) 70 67	34, 61, 103, 127	0
1	D	253/257 (98%)	-0.03	10 (3%) 42 38	34, 59, 109, 139	0
2	B	21/21 (100%)	1.39	8 (38%) 1 0	55, 109, 157, 160	0
2	E	21/21 (100%)	0.87	4 (19%) 3 2	59, 110, 168, 171	0
All	All	550/556 (98%)	0.01	26 (4%) 36 32	34, 62, 121, 171	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	708	SER	4.7
1	D	709	SER	3.5
2	E	754	THR	3.3
2	B	736	SER	3.2
1	A	706	GLY	3.2
1	A	527	GLN	3.1
2	B	739	LYS	3.0
1	D	706	GLY	3.0
2	B	754	THR	3.0
1	D	765	SER	2.8
2	E	736	SER	2.7
2	B	750	ASP	2.7
2	B	743	ALA	2.6
1	A	707	ASN	2.5
1	D	766	ASN	2.5
1	D	705	GLU	2.5
1	D	625	PRO	2.4
1	A	525	LEU	2.4
1	D	638	CYS	2.3
2	B	735	VAL	2.3
2	E	753	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	737	PRO	2.2
2	E	741	GLU	2.1
1	D	557	TRP	2.1
1	D	707	ASN	2.1
2	B	752	ASP	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](#)

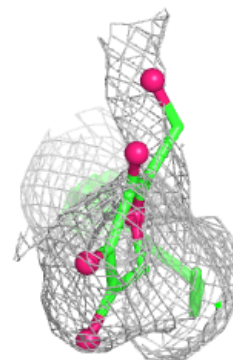
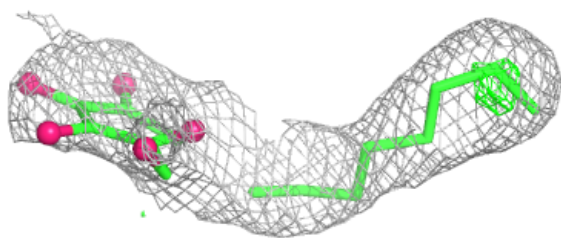
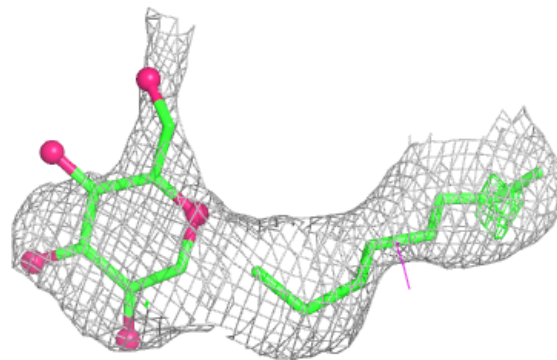
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	BOG	A	501	19/20	0.74	0.12	79,95,100,101	0
3	BOG	A	779	14/20	0.78	0.13	76,87,90,90	0
3	BOG	A	778	12/20	0.85	0.11	112,113,114,115	0
4	DEX	A	301	28/28	0.93	0.07	48,52,59,62	0
4	DEX	D	401	28/28	0.93	0.07	51,55,59,60	0

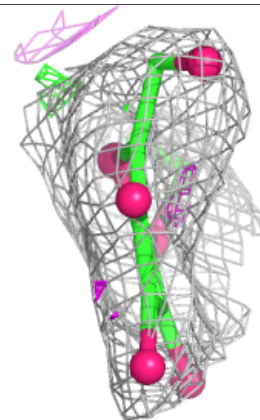
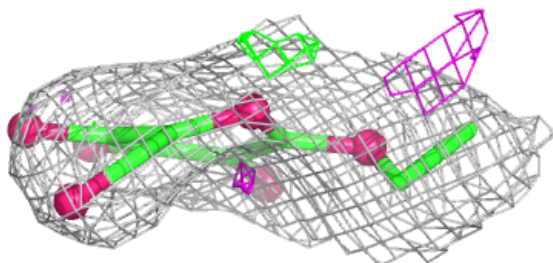
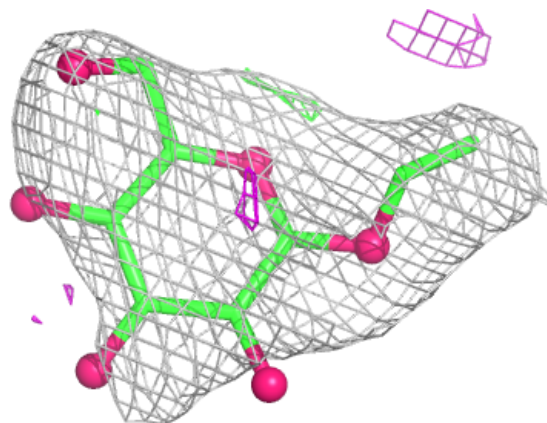
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around BOG A 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

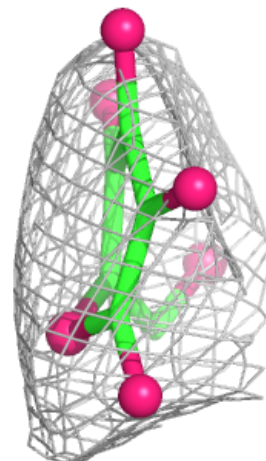
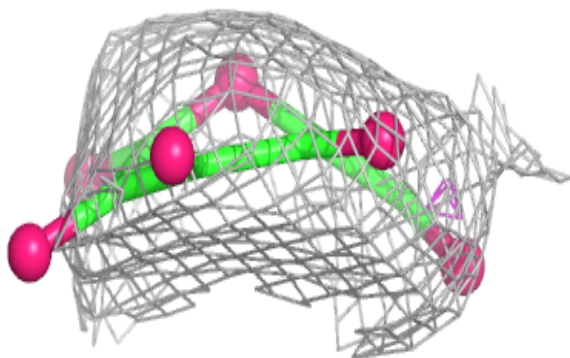
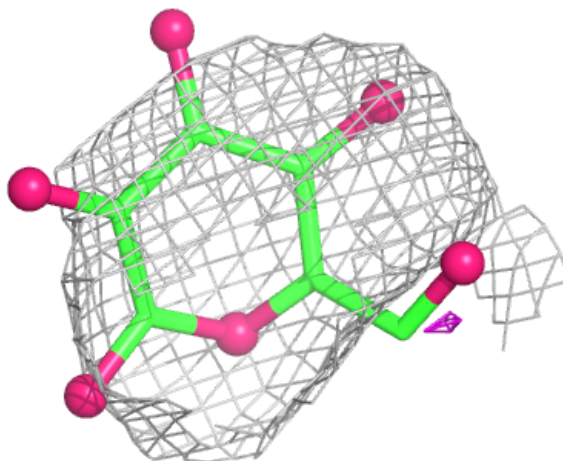
**Electron density around BOG A 779:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



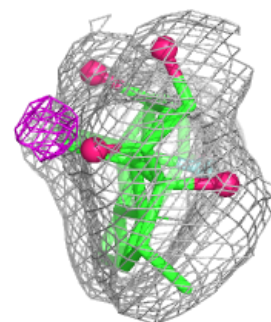
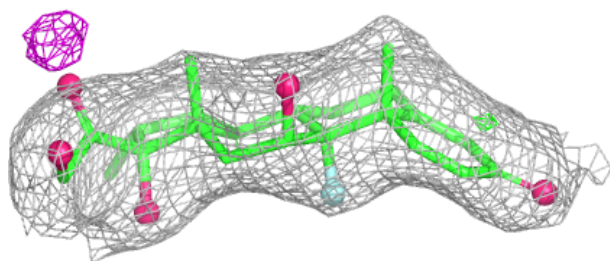
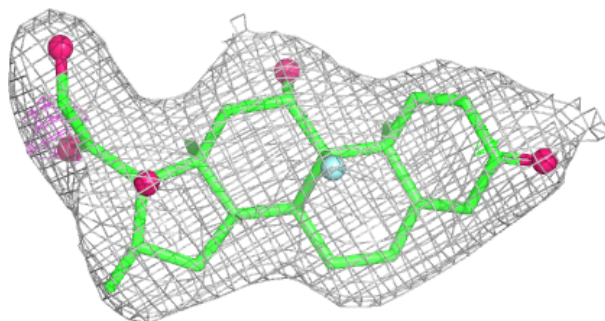
Electron density around BOG A 778:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

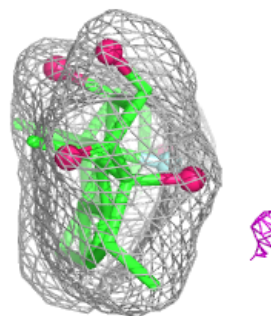
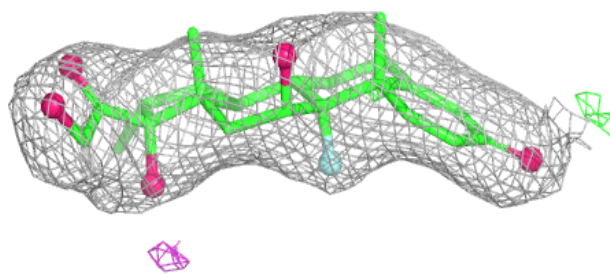
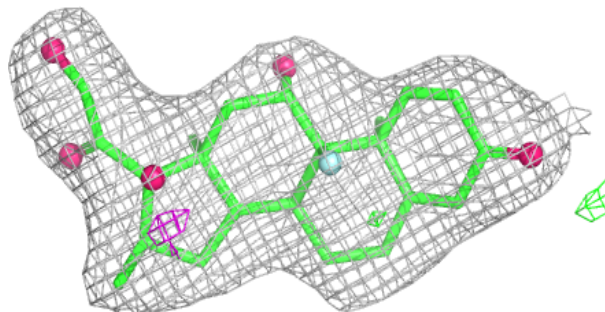


Electron density around DEX A 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around DEX D 401:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.