



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 03:50 pm GMT

PDB ID : 3CZR  
Title : Crystal Structure of Human 11-beta-Hydroxysteroid Dehydrogenase (HSD1)  
in Complex with Arylsulfonylpiperazine Inhibitor  
Authors : Wang, Z.; Sudom, A.; Walker, N.P.  
Deposited on : 2008-04-29  
Resolution : 2.35 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

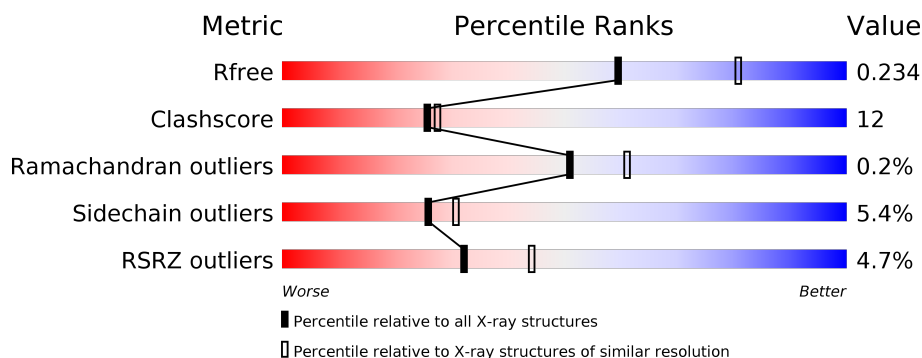
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 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))
$R_{free}$	100719	1522 (2.38-2.34)
Clashscore	112137	1626 (2.38-2.34)
Ramachandran outliers	110173	1605 (2.38-2.34)
Sidechain outliers	110143	1606 (2.38-2.34)
RSRZ outliers	101464	1528 (2.38-2.34)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>8%</div> <div>70%</div> <div>21%</div> <div>7%</div> </div>
1	B	286	<div> <div>8%</div> <div>71%</div> <div>18%</div> <div>8%</div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4390 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 Corticosteroid 11-beta-dehydrogenase isozyme 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	4	0
			2054	1308	348	383	15			
1	B	263	Total	C	N	O	S	0	1	0
			2023	1292	341	375	15			

There are 36 discrepancies between the modelled and reference sequences:

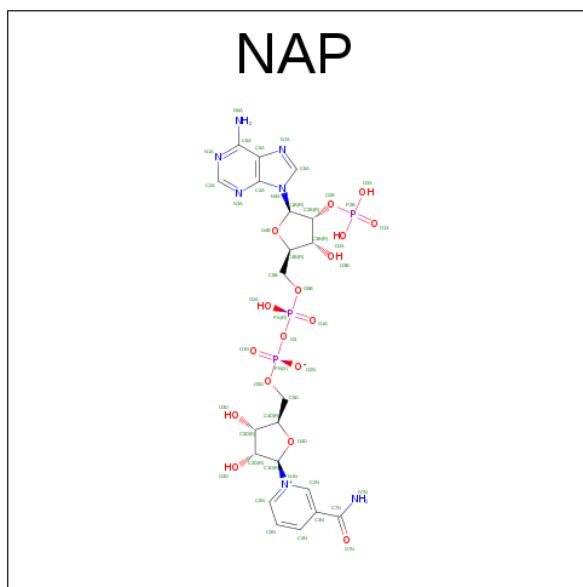
Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MET	-	EXPRESSION TAG	UNP P28845
A	8	LYS	-	EXPRESSION TAG	UNP P28845
A	9	HIS	-	EXPRESSION TAG	UNP P28845
A	10	GLN	-	EXPRESSION TAG	UNP P28845
A	11	HIS	-	EXPRESSION TAG	UNP P28845
A	12	GLN	-	EXPRESSION TAG	UNP P28845
A	13	HIS	-	EXPRESSION TAG	UNP P28845
A	14	GLN	-	EXPRESSION TAG	UNP P28845
A	15	HIS	-	EXPRESSION TAG	UNP P28845
A	16	GLN	-	EXPRESSION TAG	UNP P28845
A	17	HIS	-	EXPRESSION TAG	UNP P28845
A	18	GLN	-	EXPRESSION TAG	UNP P28845
A	19	HIS	-	EXPRESSION TAG	UNP P28845
A	20	GLN	-	EXPRESSION TAG	UNP P28845
A	21	GLN	-	EXPRESSION TAG	UNP P28845
A	22	PRO	-	EXPRESSION TAG	UNP P28845
A	23	LEU	-	EXPRESSION TAG	UNP P28845
A	272	SER	CYS	ENGINEERED	UNP P28845
B	7	MET	-	EXPRESSION TAG	UNP P28845
B	8	LYS	-	EXPRESSION TAG	UNP P28845
B	9	HIS	-	EXPRESSION TAG	UNP P28845
B	10	GLN	-	EXPRESSION TAG	UNP P28845
B	11	HIS	-	EXPRESSION TAG	UNP P28845
B	12	GLN	-	EXPRESSION TAG	UNP P28845
B	13	HIS	-	EXPRESSION TAG	UNP P28845

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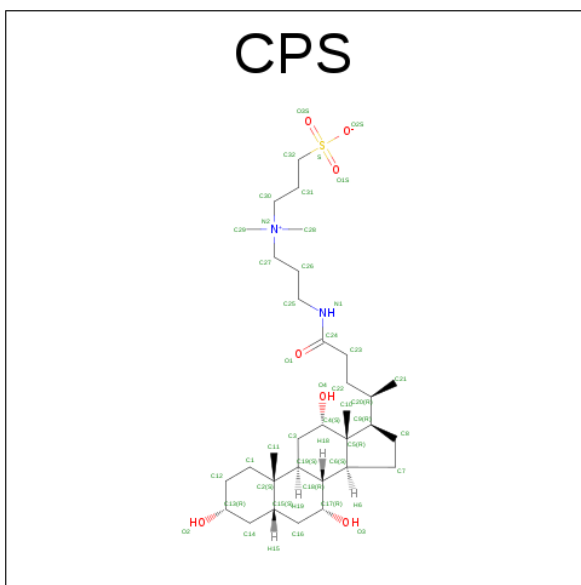
Chain	Residue	Modelled	Actual	Comment	Reference
B	14	GLN	-	EXPRESSION TAG	UNP P28845
B	15	HIS	-	EXPRESSION TAG	UNP P28845
B	16	GLN	-	EXPRESSION TAG	UNP P28845
B	17	HIS	-	EXPRESSION TAG	UNP P28845
B	18	GLN	-	EXPRESSION TAG	UNP P28845
B	19	HIS	-	EXPRESSION TAG	UNP P28845
B	20	GLN	-	EXPRESSION TAG	UNP P28845
B	21	GLN	-	EXPRESSION TAG	UNP P28845
B	22	PRO	-	EXPRESSION TAG	UNP P28845
B	23	LEU	-	EXPRESSION TAG	UNP P28845
B	272	SER	CYS	ENGINEERED	UNP P28845

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula:  $C_{21}H_{28}N_7O_{17}P_3$ ).



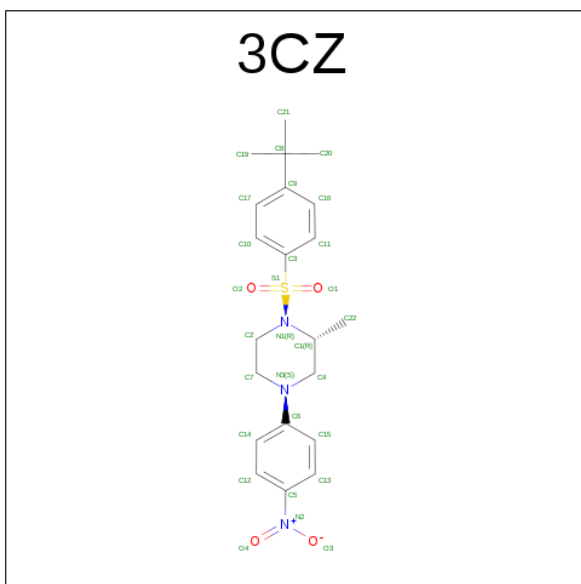
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is 3-[(3-CHOLAMIDOPROPYL)DIMETHYLAMMONIO]-1-PROPANESULFO NATE (three-letter code: CPS) (formula:  $C_{32}H_{58}N_2O_7S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			42	32	2	7	1		

- Molecule 4 is (2R)-1-[(4-TERT-BUTYLPHENYL)SULFONYL]-2-METHYL-4-(4-NITROPHENYL)PIPERAZINE (three-letter code: 3CZ) (formula: C<sub>21</sub>H<sub>27</sub>N<sub>3</sub>O<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			29	21	3	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	81	Total 81	O 81	0	0
5	B	65	Total 65	O 65	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	110.22Å 110.22Å 132.99Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.35 54.56 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-2.35) 99.8 (54.56-2.20)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.96 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.4.0069	Depositor
R, $R_{free}$	0.219 , 0.247 0.215 , 0.234	Depositor DCC
$R_{free}$ test set	1968 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	53.8	Xtriage
Anisotropy	0.066	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 54.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.025 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4390	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.23% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: NAP, CPS, 3CZ

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	0.60	0/2103	0.68	0/2839
1	B	0.56	0/2061	0.66	0/2784
All	All	0.58	0/4164	0.67	0/5623

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	2054	0	2094	46	0
1	B	2023	0	2072	57	0
2	A	48	0	25	0	0
2	B	48	0	25	0	0
3	B	42	0	58	3	0
4	A	29	0	27	1	0
5	A	81	0	0	1	0
5	B	65	0	0	2	0
All	All	4390	0	4301	102	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 12.

All (102) 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:230:ILE:HG13	1:B:232:HIS:NE2	1.63	1.13
1:A:231:VAL:CG1	1:A:232:HIS:N	2.15	1.08
1:A:231:VAL:HG13	1:A:232:HIS:H	1.21	1.03
1:A:231:VAL:CG1	1:A:232:HIS:H	1.72	1.02
1:B:230:ILE:CD1	1:B:232:HIS:CE1	2.45	0.99
1:A:96:MET:HE1	1:A:146:SER:HA	1.45	0.97
1:A:231:VAL:HG12	1:A:232:HIS:N	1.76	0.96
1:B:224:MET:CE	1:B:224:MET:HA	2.00	0.91
1:B:155:LEU:HB3	1:B:156:PRO:HD3	1.54	0.88
1:B:224:MET:HE3	1:B:224:MET:HA	1.53	0.88
1:B:230:ILE:HD12	1:B:232:HIS:CE1	2.10	0.87
1:B:263:TRP:O	1:B:267:LEU:HD12	1.75	0.86
1:B:75:VAL:HG21	1:B:88:TYR:HB3	1.60	0.82
1:B:230:ILE:CD1	1:B:232:HIS:HE1	1.91	0.81
1:A:284:TYR:HE2	1:B:232:HIS:HD1	1.30	0.80
1:B:178:PRO:O	1:B:179:MET:HB2	1.81	0.80
1:A:96:MET:HE2	1:A:96:MET:HA	1.63	0.80
1:A:122:THR:O	1:A:124:THR:HG22	1.82	0.79
1:B:103:VAL:HG11	1:B:154:ALA:HB2	1.65	0.77
1:A:96:MET:HA	1:A:96:MET:CE	2.15	0.76
1:A:279:LEU:O	1:A:283:SER:HB2	1.86	0.76
1:B:230:ILE:CG1	1:B:232:HIS:NE2	2.46	0.75
1:A:284:TYR:HE2	1:B:232:HIS:ND1	1.87	0.72
1:B:230:ILE:HD11	1:B:232:HIS:CE1	2.25	0.71
1:A:191:ASP:O	1:A:195:SER:HB2	1.94	0.67
1:B:230:ILE:HD11	1:B:232:HIS:HE1	1.58	0.67
1:B:101:GLN:HE21	1:B:101:GLN:HA	1.60	0.67
1:B:200:GLU:OE1	5:B:411:HOH:O	2.14	0.66
1:B:155:LEU:HB3	1:B:156:PRO:CD	2.26	0.64
1:A:231:VAL:HG13	1:A:232:HIS:N	1.95	0.64
1:A:216:GLY:O	1:A:218:ILE:HG12	1.98	0.63
1:B:97:THR:O	1:B:101:GLN:HG2	2.03	0.59
1:A:175:VAL:HG23	1:A:177:TYR:CE1	2.38	0.58
1:B:230:ILE:CG1	1:B:232:HIS:CE1	2.87	0.57
1:B:224:MET:HE3	1:B:227:VAL:CG2	2.35	0.57
1:A:134[B]:HIS:NE2	1:A:138:LYS:NZ	2.53	0.56
1:B:224:MET:CE	1:B:224:MET:CA	2.78	0.56
1:B:224:MET:CE	1:B:227:VAL:CG2	2.85	0.55
1:B:230:ILE:HG13	1:B:232:HIS:CE1	2.38	0.55
1:A:215:LEU:HD11	1:A:245:ILE:HD11	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:60:HIS:CD2	1:B:84:ALA:HB3	2.41	0.55
1:A:139:SER:O	1:A:143:ASN:HB2	2.07	0.54
1:B:178:PRO:O	1:B:179:MET:CB	2.49	0.54
1:B:224:MET:HE2	1:B:224:MET:HA	1.84	0.54
1:B:36:LYS:O	1:B:113:LEU:HD12	2.07	0.54
1:A:155:LEU:HB3	1:A:156:PRO:HD3	1.89	0.54
1:B:42:ALA:HB3	1:B:63:VAL:HB	1.89	0.54
1:B:139:SER:O	1:B:143:ASN:HB2	2.08	0.53
1:B:105:GLN:O	1:B:109:LEU:HD13	2.08	0.53
1:B:127:ASN:ND2	5:B:386:HOH:O	2.42	0.52
1:A:221:GLU:O	1:A:225:LYS:HD3	2.09	0.52
1:A:212:LEU:O	1:A:255:GLU:HA	2.10	0.52
1:B:75:VAL:CG2	1:B:88:TYR:HB3	2.36	0.51
1:A:119:ASN:HD22	1:A:168:VAL:HG21	1.75	0.51
1:B:36:LYS:HG2	1:B:110:MET:HB3	1.92	0.51
1:B:146:SER:O	1:B:150:LEU:HD12	2.10	0.51
1:A:223:ALA:O	1:A:227:VAL:HG22	2.11	0.51
1:A:54:LEU:HA	1:A:57:MET:HE3	1.93	0.50
1:A:178:PRO:O	1:A:179:MET:HB2	2.12	0.50
1:A:27:PHE:CD2	1:A:247:LYS:HD3	2.47	0.49
1:A:133:ILE:HD13	1:B:149:VAL:HG22	1.94	0.49
1:B:75:VAL:HG13	1:B:86:ALA:HB1	1.94	0.49
1:A:191:ASP:O	1:A:195:SER:CB	2.60	0.48
1:A:227:VAL:O	1:A:228:SER:C	2.52	0.48
3:B:1:CPS:H262	3:B:1:CPS:H30A	1.41	0.48
1:B:37:VAL:HG13	1:B:115:MET:HB3	1.95	0.47
1:B:63:VAL:HG23	1:B:71:LEU:HD22	1.97	0.47
1:A:71:LEU:O	1:A:75:VAL:HG23	2.15	0.47
1:A:161:SER:O	1:A:162:ASN:HB2	2.14	0.46
1:B:103:VAL:HG11	1:B:154:ALA:CB	2.41	0.46
1:B:243:LEU:HG	1:B:247:LYS:HE3	1.97	0.46
1:A:140:MET:HE3	1:A:144:PHE:HB3	1.98	0.46
1:B:220:THR:O	1:B:224:MET:HG2	2.17	0.45
1:A:266:LEU:O	1:A:269:ARG:HG2	2.16	0.45
1:A:45:GLY:O	1:A:49:GLU:HG2	2.17	0.44
1:B:103:VAL:CG1	1:B:154:ALA:HB2	2.42	0.44
1:B:64:THR:O	1:B:65:ALA:HB2	2.17	0.44
1:B:236:ALA:HB2	1:B:260:SER:HB3	2.00	0.44
1:B:205:ARG:HG3	1:B:205:ARG:NH1	2.33	0.44
1:A:284:TYR:O	1:A:285:ASN:HB3	2.17	0.44
1:A:126:LEU:HD11	1:A:227:VAL:HG12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:71:LEU:O	1:B:75:VAL:HG23	2.18	0.43
1:A:158:LEU:HD22	1:A:164:SER:H	1.82	0.43
1:A:128:LEU:HD23	1:B:200:GLU:HB3	2.00	0.43
1:B:270:ASN:HD21	1:B:272:SER:HB2	1.82	0.43
1:A:54:LEU:HA	1:A:57:MET:CE	2.49	0.42
1:B:212:LEU:O	1:B:255:GLU:HA	2.19	0.42
1:B:180:VAL:O	1:B:184:SER:HB2	2.19	0.42
4:A:293:3CZ:H7A	4:A:293:3CZ:H15	1.87	0.42
1:A:53:HIS:O	1:A:57:MET:HG3	2.19	0.42
1:A:49:GLU:HB3	5:A:347:HOH:O	2.19	0.42
1:A:185:ALA:HB2	1:B:193:PHE:HB2	2.02	0.42
1:B:205:ARG:HG3	1:B:205:ARG:HH11	1.84	0.42
1:A:224:MET:HA	1:A:224:MET:CE	2.50	0.41
1:A:133:ILE:H	1:A:133:ILE:HG13	1.64	0.41
1:B:224:MET:HE3	1:B:224:MET:CA	2.36	0.41
1:A:132:ASP:O	1:A:136:VAL:HG23	2.20	0.41
1:A:61:VAL:O	1:A:86:ALA:HA	2.21	0.41
3:B:1:CPS:O2S	3:B:1:CPS:C30	2.69	0.40
3:B:1:CPS:O2S	3:B:1:CPS:H30	2.18	0.40
1:B:101:GLN:NE2	1:B:101:GLN:HA	2.33	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	265/286 (93%)	247 (93%)	18 (7%)	0	100	100
1	B	262/286 (92%)	244 (93%)	17 (6%)	1 (0%)	38	44
All	All	527/572 (92%)	491 (93%)	35 (7%)	1 (0%)	51	61

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	65	ALA

### 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	226/243 (93%)	215 (95%)	11 (5%)	29	36
1	B	221/243 (91%)	208 (94%)	13 (6%)	23	26
All	All	447/486 (92%)	423 (95%)	24 (5%)	26	31

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	LYS
1	A	85	SER
1	A	96	MET
1	A	109	LEU
1	A	124	THR
1	A	179	MET
1	A	233	MET
1	A	266	LEU
1	A	269	ARG
1	A	281	SER
1	A	285	ASN
1	B	26	GLU
1	B	70	THR
1	B	101	GLN
1	B	124	THR
1	B	126	LEU
1	B	127	ASN
1	B	170	SER
1	B	184	SER
1	B	224	MET
1	B	266	LEU
1	B	267	LEU
1	B	268	ILE

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Mol	Chain	Res	Type
1	B	270	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	GLN
1	A	119	ASN
1	A	127	ASN
1	A	162	ASN
1	A	285	ASN
1	B	87	HIS
1	B	101	GLN
1	B	270	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

4 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	NAP	A	1	-	44,52,52	1.59	4 (9%)	51,80,80	1.99	8 (15%)
4	3CZ	A	293	-	30,31,31	1.22	3 (10%)	45,47,47	1.13	4 (8%)
3	CPS	B	1	-	45,45,45	1.38	2 (4%)	68,70,70	1.32	5 (7%)
2	NAP	B	2	-	44,52,52	1.54	3 (6%)	51,80,80	2.06	5 (9%)

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
2	NAP	A	1	-	-	0/27/67/67	0/5/5/5
4	3CZ	A	293	-	-	0/24/39/39	0/3/3/3
3	CPS	B	1	-	-	0/25/90/90	0/4/4/4
2	NAP	B	2	-	-	0/27/67/67	0/5/5/5

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1	CPS	C32-S	-7.39	1.66	1.77
3	B	1	CPS	C30-N2	-2.06	1.47	1.52
2	A	1	NAP	P2B-O2B	2.19	1.63	1.59
4	A	293	3CZ	O1-S1	2.37	1.46	1.43
2	B	2	NAP	C2A-N1A	2.63	1.38	1.33
2	B	2	NAP	C2A-N3A	2.70	1.36	1.32
2	A	1	NAP	C2A-N1A	2.71	1.39	1.33
4	A	293	3CZ	C3-S1	3.04	1.80	1.76
4	A	293	3CZ	O2-S1	3.20	1.47	1.43
2	A	1	NAP	C2A-N3A	3.65	1.38	1.32
2	B	2	NAP	O7N-C7N	7.78	1.40	1.24
2	A	1	NAP	O7N-C7N	7.83	1.40	1.24

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	NAP	N3A-C2A-N1A	-11.75	118.62	128.86
2	A	1	NAP	N3A-C2A-N1A	-10.72	119.52	128.86
3	B	1	CPS	C19-C18-C17	-3.83	107.42	111.92
2	A	1	NAP	O7N-C7N-C3N	-3.45	115.59	119.62
2	B	2	NAP	O2B-P2B-O1X	-3.34	96.16	109.26
2	A	1	NAP	C3N-C2N-N1N	-2.89	117.52	120.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	293	3CZ	O1-S1-N1	-2.51	102.15	106.97
4	A	293	3CZ	C13-C5-N2	-2.43	117.56	119.41
2	A	1	NAP	C1B-N9A-C4A	-2.19	122.84	126.64
2	A	1	NAP	C4D-O4D-C1D	-2.13	107.50	109.77
2	A	1	NAP	O2N-PN-O1N	2.12	123.23	112.28
2	B	2	NAP	C2A-N1A-C6A	2.18	122.59	118.77
2	A	1	NAP	C4B-O4B-C1B	2.23	112.14	109.77
4	A	293	3CZ	C7-C2-N1	2.32	111.04	109.00
2	B	2	NAP	C3N-C7N-N7N	2.39	120.50	117.77
3	B	1	CPS	O3S-S-C32	2.48	108.92	106.79
3	B	1	CPS	C9-C5-C4	2.50	119.97	117.67
3	B	1	CPS	C19-C18-C6	2.50	113.04	109.64
4	A	293	3CZ	O2-S1-O1	2.94	124.41	119.46
2	B	2	NAP	C2N-C3N-C4N	2.94	121.62	118.26
2	A	1	NAP	C3N-C7N-N7N	4.07	122.42	117.77
3	B	1	CPS	O1S-S-C32	4.69	110.82	106.79

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	293	3CZ	1	0
3	B	1	CPS	3	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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	265/286 (92%)	0.20	3 (1%) 80 88	35, 56, 79, 95	0
1	B	263/286 (91%)	0.44	22 (8%) 12 17	35, 64, 95, 107	0
All	All	528/572 (92%)	0.32	25 (4%) 32 44	35, 60, 92, 107	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	112	GLY	5.8
1	B	233	MET	5.3
1	B	23	LEU	5.2
1	B	81	LEU	4.1
1	B	32	LEU	3.9
1	B	33	GLN	3.5
1	B	280[A]	TYR	3.3
1	B	21	GLN	3.2
1	B	59	ALA	3.1
1	B	208	VAL	2.8
1	A	112	GLY	2.8
1	B	24	ASN	2.6
1	B	37	VAL	2.6
1	B	60	HIS	2.6
1	B	232	HIS	2.4
1	B	30	GLU	2.4
1	A	60	HIS	2.4
1	B	62	VAL	2.4
1	B	36	LYS	2.4
1	B	158	LEU	2.4
1	B	111	GLY	2.2
1	B	110	MET	2.2
1	B	87	HIS	2.1
1	B	160	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	130	HIS	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 carbohydrates 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. 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, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	3CZ	A	293	29/29	0.97	0.15	-0.17	45,49,67,70	0
3	CPS	B	1	42/42	0.88	0.14	-0.24	48,53,97,98	0
2	NAP	A	1	48/48	0.96	0.12	-0.31	38,46,60,63	0
2	NAP	B	2	48/48	0.98	0.11	-0.65	38,45,54,56	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.